

(12) INTERNATIONAL APPLICATION PUBLISHED

UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 April 2001 (19.04.2001)

PCT

(10) International Publication Number
WO 01/27158 A2

(51) International Patent Classification⁷: **C07K 14/705**

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(21) International Application Number: **PCT/US00/27582**

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(22) International Filing Date: 6 October 2000 (06.10.2000)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data: 8 October 1999 (08.10.1999) US
60/158,615 24 February 2000 (24.02.2000) US
60/184,800

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(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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Published:

— Without international search report and to be republished
upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

WO 01/27158 A2

(54) Title: OLFACTORY RECEPTOR SEQUENCES

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensa-
tion. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these
polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides
for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides.
Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of
polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent pro-
file) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present
invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.

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OLFACTORY RECEPTOR SEQUENCES

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims priority benefit of United States Provisional Patent Application Serial No. 60/158,615, filed on October 9, 1999, and United States Provisional Patent Application Serial No. 60/184,809, filed on February 4, 2000. The contents of those applications are hereby incorporated by reference herein in their entirety.

STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER **FEDERALLY SPONSORED RESEARCH**

Not applicable.

TECHNICAL FIELD

15 The present invention is in the field of human olfactory receptors and their use in screening for olfactory agonists and antagonists. The present invention pertains to isolated nucleotide sequences which encode human olfactory receptors and also to the proteins
20 encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of secondary scents and the identification of
25 combinations of odor receptors which are encoded to detect such secondary scents.

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BACKGROUND ART

Our sense of smell plays an important role not only in our appreciation of our surroundings such as the smell of flowers or new mown grass, but also evolved as a survival skill. Numerous odorant molecules can be detected at extremely low concentrations, providing early warning of danger, such as the smell of smoke or contaminated food. Indeed, a potent example of this is that most pregnant women experience a heightened sense of smell, presumably to protect the fetus from the deleterious effects of food poisoning.

It is estimated that humans can detect millions of different molecular species; however, our nose can discriminate only a fraction of these different chemicals (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320), usually estimated at about 10,000 odorants (Axel, *Scientific American* 1995, October, 154-159). Odorants for terrestrial species such as humans, are volatile (air born) ligands which are detected by the olfactory system. Odorants have vastly different chemical structures and subtle differences can lead to pronounced changes in the perceived odor (Mombaerts, *supra*). For instance, when the hydroxyl group of octanol is replaced by a carboxyl group to give octanoic acid, its perceived odor changes from orange and rose-like to rancid and sweaty (Malnic *et al.*, *Cell* 1999 96, 713-723). The basis for these feats of sensory perception are just beginning to be understood at a cellular and molecular level.

The olfactory system contains millions of olfactory sensory neurons (OSNs) located in the olfactory epithelium of the nasal cavity. In humans, the olfactory epithelium occupies an area of approximately 5 cm². The OSNs are bipolar with one end extending through the supporting cell into the mucosal layer, terminating in hairlike cilia. These cilia are the site of the olfactory receptors (OR) where the odorant ligands are thought to bind (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320, Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). The OSNs also have a single unbranched axon which leads to the olfactory bulb, a part of the brain containing approximately 2000 glomeruli where the axons terminate and initial processing of the sensory code takes place. OSNs expressing the same OR are randomly interspersed throughout the olfactory epithelium, but in both the nose and the bulb, information derived from different ORs is strictly segregated; each OSN in the nose and each glomerulus in the olfactory bulb appear to be dedicated to input from one or few OR type(s) (Malnic *et al.*, *Cell* 1999 96, 713-723). It also appears that the location of the glomeruli are conserved across individuals of a species, providing the first spatial processing of particular odorant patterns (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). The domains in the olfactory bulb for

different odors may overlap, but the overall patterns are distinct (Hildebrand *et al.*, *supra*), therefore, it should be possible to identify and reproduce the characteristic pattern of a given odorant. Output neurons project from the olfactory bulb to the primary olfactory cortex and from there to the higher cortical areas of the brain and to the limbic system (Malnic *et al.*, *supra*; Hildebrand *et al.*, *supra*, 20, 595-631).

Until the identification of a large family of genes encoding putative odorant receptors (Buck & Axel *Cell* 1991 65, 175-187), progress towards understanding the process of odor recognition was negligible. In recent years there has been an explosion in this field as more and more putative odor receptors are isolated and cloned. The odorant receptor gene products have thus far been characterized through homology as seven transmembrane domain G protein-coupled receptors (GPCR). It is estimated that there are probably 500-750 OR-like sequences in humans, while there are 500-1000 OR genes in rat and mouse (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). In mice, OR-like sequences make up approximately 1% of their genome, the largest known family in the mammalian genome, surpassing the complexity of even the immunoglobulin and T-cell antigen receptor gene families (Mombaerts, *supra*). The OR are concentrated on the surface of the OSN's mucus coated cilia and it is thought that odorant molecules bind to the OR in the olfactory epithelium and thereby initiate signal transduction. Current interpretation of recent experimental evidence favors the idea that each neuron expresses only one, or very few, ORs. Since mammals can detect at least 10,000 odors and there are approximately 1,000 or fewer ORs, each of the ORs must respond to several odorant molecules, and each odorant molecule must bind to several receptors. It is believed that various receptors respond to discrete parts of an odorant molecule's structure and that an odorant consists of several chemical groups each of which bind a characteristic receptor (Axel *Scientific American* 1995, October, 154-159; Malnic *et al.*, *Cell* 1999 96, 713-723).

The main signal transduction pathway mediated by OR homologues in vertebrate species involves G protein-mediated stimulation of adenylyl cyclase activity, resulting in cAMP elevation that opens cyclic-nucleotide gated channels with a non-specific cation selectivity (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). However, there are still numerous unanswered questions and recently it has come to light that 38-76% of the human gene OR sequences that are being reported may be pseudogenes and therefore incapable of expressing the proteins that encode the olfactory receptors. Some of the incidences may be due to the method of extracting the genomic DNA libraries (Mombaerts, *supra*). Few pseudogenes have been found in other vertebrates and their incidence in libraries from testicular DNA is also

rare (Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). cDNA should not contain pseudogenes. There are a number of examples of ORs which have been successfully expressed and reactions to certain odorant ligands have been determined (Malnic *et al.*, *Cell* 1999 96, 713-723; Mombaerts, *supra*; Zhao *et al.*, *Science* 1998 279, 237-242).

5 Some attempts to express the ORs in heterologous cell lines resulted in the formation of inclusion bodies rather than the insertion of the proteins into the membrane (Kiefer *et al.*, *infra*). However, purification of the receptors after expression in *E. coli* and their insertion into lipid vesicles facilitates the use of these receptors in odorant ligand screening using a combination of photoaffinity labeling and Trp fluorescence (Kiefer *et al.*, *Biochemistry* 1996 10 35, 16077-16084). In addition, a functional human OR receptor protein has been expressed in HEK-293 cells and oocytes and found to interact with odorant ligands (Wetzel *et al.*, *J. Neurosci.* 1999 19, 7426-7433). There have also been, a number of successful efforts of expressing cDNA in insect Sf9 cells using *baculovirus* vectors (Mombaerts *Annu. Rev. Neuorsci.* 1999) as well as assays with neuronal tissue (Malnic *et al.*, *Cell* 1999 96, 713-723; 15 Zhao *et al.*, 1998; Firestein *et al.*, WO 98/50081). In addition, recent work accomplished the expression of chimeric mouse olfactory receptor sequences in HEK-293 cells and showed their reactivity towards a panel of odorant ligands, some at micromolar concentrations (Krautwurst *et al.*, *Cell* 1998 95 917-926). The drawback to expression in heterologous cell systems is the lack of working signal transduction pathways which can be used to detect responses to odorant 20 ligands; these drawbacks can be overcome with methods known in the art (e. g. U.S. Pat. No. 5,798, 275). There are also methods of expressing and assaying functional neuronal receptors in neuronal cells, including methods for detecting particular odorant ligand specificity (Malnic *et al.*, *supra*; Zhao, *supra*; Firestein *et al.*, *supra*).

25 Other publications of interest are: *Chemical Senses* 6: 343-349 (1981); *Proc. Natl. Acad. Sci. USA* 79: 670-674 (1982); *Proc. Natl. Acad. Sci. USA* 81(6): 1859-1863 (1984); *Nature* 316: 255-258 (1985); *Brain Research* 368: 329-338 (1986); *J. Biol. Chem.* 261: 1299-1305 (1986); *Proc. Natl. Acad. Sci. USA* 83(13): 4947-4951 (1986); *J. Neurosci.* 6: 2146-2154 (1986); *J. Neurochem.* 47: 1527-1533 (1986); *Chemical Senses* 13: 191-204 30 (1988); *Biochem. J.* 260:121-126 (1989); *J. Biol. Chem.* 264: 6780-6785 (1989); *Biochim. Biophys. Acta* 1013: 68-72 (1989); *J. Biol. Chem.* 264: 18803-18807 (1989); *Biochemistry* 29: 7433-7440 (1990); *FEBS lett.* 270: 24-29 (1990); *Chemical Senses* 15: 529-536 (1990); *Eur. J. Biochem.* 196: 51-58 (1991); *Nature* 349: 790-793 (1991); *Neurosci. Lett.* 141: 115-

118 (1992); Developmental Brain Res. 73: 7-16 (1993); Proc. Natl. Acad. Sci., USA 90: 3715-3719 (1993); Human Mol. Genetics 3: 229-235 (1994); Eur. J. Biochem. 225: 1157-1168 (1994); European Journal of Biochemistry 238: 28-37 (1996); Receptors and Channels 4: 141-147 (1996); Genomics 37(2): 147-160 (1996); Protein Science 8: 969-977 (1999); Genomics 53: 56-68 (1998); Genomics 61:24-36 (1999); Genomics 63: 227-245 (2000); Trends in Neurosci. 7:35-36 (1984); Ann. Rev. Neurosci. 9:329-355 (1986); Trends Biochem. Sci. 12:63-66 (1987); Nature 351: 275-276 (1991); Nature 353: 799-800 (1991); Current Biol. 3(10): 668-674 (1993); Nature 372:321-322 (1994); Essays in Biochemistry. 33: 93-104 (1998); and Nature, 398 (6725): 285-287 (1999).

10 However, despite the forgoing, there has been relatively little work with human olfactory receptors, in particular in determining the sequences of large numbers of receptors, and less progress in determining the correspondence between particular human olfactory receptors and the scent(s) to which they respond.

15 All publications cited herein are hereby incorporated by reference in their entirety.

DISCLOSURE OF THE INVENTION

20 An object of the invention is to determine the correspondence between ORs and the scent(s) to which they respond. Once this is accomplished, scents can be both analyzed and re-created for enhancing human experiences or eliciting particular responses. The present invention pertains to isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation. The present invention also pertains to the proteins encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the
25 nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of receptor complex scent components and the identification of combinations of odor receptors which are encoded to detect such receptor complex scent
30 components scents.

The invention provides isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation that are isolated from human olfactory epithelial tissue. The invention further provides expression vectors containing such nucleotide sequences. Also provided by the invention are purified polypeptides encoded by the nucleotide sequences. The invention further provides transformed cells which comprise a suitable host cell transfected with a suitable expression vector containing the nucleotide sequence encoding the receptor. The present invention also encompasses nucleotide sequences isolated from human olfactory epithelial tissue which encode receptors capable of binding odorant molecules. The invention further provides expression vectors containing such nucleotide sequences and homologues of both the polynucleotides and polypeptides. Further, the invention provides a means of using the nucleotide sequences of the invention in a method of screening odorant ligands to determine the specific binding of odorant molecules to a particular receptors, and further, determining the component odorant molecules of subjectively experienced smells, determining the combination odorant molecules and receptor stimulation or inhibition to re-create a particular scent. The binding of odorant molecules by the receptors encompassed in the present invention includes binding resulting in both the agonism (excitation/activation) and antagonism (inhibition/blocking) of receptor function(s) upon binding of the molecule.

Accordingly, the invention includes an isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence at least 95% homologous to said sequences. The invention also encompasses the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention. The invention further encompasses fragments of said polynucleotides which can be used as probes or primers to identify additional polynucleotide sequences through techniques known in the art, including those fragments depicted in SEQ ID NOs: 74-105.

The invention also includes additional isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides

encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:153 through SEQ ID NO: 1084, or a nucleotide sequence at least 95% homologous to said sequences. The invention also comprises the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing
5 such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

10 The invention also encompasses an isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function. Host cells expressing such polypeptides and phages displaying such
15 polypeptides are also encompassed by the invention. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

Scents can be captured, analyzed and recorded by a sensory device using various
20 methods. Scent capture can be initiated by the user or by an automatic sensing system. A scent can be analyzed in terms of its interaction with olfactory neurons of a mammalian, preferably human, olfactory system, or by the expression of individual receptors under appropriate conditions and appropriate assay conditions in multiwell plates or in terms of its perception by a panel of mammalian, preferably human, subjects. The interaction with olfactory neurons can
25 be determined experimentally, in vitro, by determining the interaction of an odorant with olfactory receptors of a given type. Alternatively, the interaction with olfactory receptor can be determined using a computer simulation which provides information regarding the interaction of an odorant with the olfactory receptors. A panel of subjects can be used to represent odors in terms of their perception. The data so generated can be used to represent a scent in a manner
30 which can be recorded in digital or other format, stored in media such as computer memory, disks, or printed format, and transmitted over a data network. The representation of the scent can be used to re-create the scent at a local or remote site using an emitter module. The

representation of the scent allows for scent editing, where desirable aspects of an odor are enhanced or added and undesirable aspects are attenuated or eliminated.

Accordingly, the invention also embraces libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084, where the polynucleotides encode functional olfactory receptors; or functional fragments of the expression products. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

Also encompassed by the invention are libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, where the polypeptides are functional olfactory receptors; or functional fragments of the polypeptides. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

The invention also embraces methods for determining the binding pattern of a composition with olfactory receptors, involving exposing the composition to an olfactory receptor library, and determining whether the composition binds to each olfactory receptor, thereby determining the overall binding pattern of the composition. In additional embodiments, the method also involves determining the approximate binding constant with which the composition, or the various chemicals within the composition, bind to the receptors; determining whether a receptor or functional fragment thereof is activated; and determining the absolute amount of activation, or amount of activation relative to another receptor or a control substance. The composition can consist essentially of one compound or chemical, or can comprise at least two compounds or chemicals.

The invention also embraces DNA arrays or DNA chips comprising the DNA segments derived from any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084. The invention also embraces a method of determining differences among one or more individuals with respect to their olfactory faculties, comprising the steps of comparing the olfactory DNA of each individual against the array or chip.

The invention also embraces a method to determine single nucleotide polymorphisms in olfactory receptors, comprising the steps of uniquely amplifying olfactory receptor sequences from DNA obtained from one or more individuals, based on

primers designed according to the first 25 bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084, and determining the similarities and differences between said amplified DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

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Brief Description of the Drawings

Figure 1 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 1 - 73.

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Figure 2 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 111 - 152.

Detailed Description of the Invention

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The present invention provides isolated polynucleotides comprising sequences that encode polypeptides which are involved in olfactory sensation and which can be used to screen odorant ligands, *e.g.*, odorant receptor agonists and antagonists.

Definitions

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The term "olfactory receptor" (OR) refers to a polypeptide involved in olfactory sensation. An "olfactory receptor polynucleotide" or "OR polynucleotide" is a polynucleotide encoding a polypeptide involved in olfactory sensation.

The term "odorant ligand" as employed herein refers to a molecule that has the potential to bind to an olfactory receptor. Equivalent terms employed herein include "odorant", "odorant molecule" and "odorant compound". The term "binding" or "interaction" as used herein with respect to odorant ligands refers to the interaction of ligands with the receptor polypeptide where the ligands may serve as either agonists and/or antagonists of a given receptor or receptor function. An odorant ligand may thus directly cause a perception of odor (an agonist), or may block the perception of odor (an antagonist). An odorant ligand may include, but is not limited to, molecules which interact with polypeptides involved in olfactory

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sensation. Odorant ligands and molecules which interact with olfactory receptors are generally small, approximately 1000 Daltons, more preferably approximately 750 Daltons, more preferably approximately 500 Daltons, or even more preferably approximately 300 Daltons, hydrophobic molecules with a variety of functional groups. Small changes in structure can induce profound changes in odorant ligand binding and hence in the odor perceived by an individual.

A more detailed description of these sequences, as well as how these sequences were obtained, is provided below.

As used herein, a "polynucleotide" is a polymeric form of nucleotides of any length, which contain deoxyribonucleotides, ribonucleotides, and/or their analogs. The terms "polynucleotide", "nucleotide" and "nucleic acid" as used herein are used interchangeably. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The term "polynucleotide" includes double-, single-stranded, and triple-helical molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double stranded form. Not all linkages in a polynucleotide need be identical.

The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, primers, and adaptors. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The use of uracil as a substitute for thymine in a deoxyribonucleic acid is also considered an analogous form of pyrimidine.

In the context of polynucleotides, a "linear sequence" or a "sequence" is an order of nucleotides in a polynucleotide in a 5' to 3' direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polynucleotide. A "partial sequence" is a linear sequence of part of a polynucleotide which is known to comprise additional residues in one or both directions.

If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by

conjugation with a labeling component. Other types of modifications included in this definition are, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, cabamates, etc.) and with
5 charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., α -anomeric nucleic acids, peptide nucleic acids,
10 etc.), as well as unmodified forms of the polynucleotide(s).

Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH groups can be phosphorylated or substituted with amines or organic
15 capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups.

Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, but not limited to, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carboxycyclic sugar analogs, α -anomeric sugars, epimeric sugars such
20 as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside.

Although conventional sugars and bases will be used in applying the method of the invention, substitution of analogous forms of sugars, purines and pyrimidines can be advantageous in designing a final product, as can alternative backbone structures like a
25 polyamide backbone such as those used in peptide nucleic acids (PNAs).

A polynucleotide or polynucleotide region has a certain percentage (for example, 75%, 80%, 85%, 90%, 95% or 99%) of "sequence identity" to another sequence means that, when aligned, that percentage of bases are the same in comparing the two sequences.

Homology, as described herein, means that the polypeptide sequences that are encoded
30 by the nucleic acids demonstrate a certain relatedness (i.e., there exists regions of conserved amino acids), but not the same amino acid identity. There is complete or 100% homology at a particular amino acid residue when the amino acids of sequences being compared are the same (there is identity) or represent a conservative amino acid substitution (there is homology). A

“conservative amino acid substitution” occurs when a particular amino acid is substituted by an alternate amino acid of similar charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Ile). A “nonconservative amino acid substitution” occurs when a particular amino acid is substituted by an alternative amino acid of differing properties, that is, charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Tyr). The nucleic acid sequences within the scope of the present invention include those nucleic acids which differ in exact sequence from those listed in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152 but which encode identical or homologous polypeptide amino acid sequences.

A “primer” is a short polynucleotide, generally with a free 3' -OH group, that binds to a target potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target.

An “adaptor” is a short, partially-duplexed polynucleotide that has a blunt, double-stranded end and a protruding, single-stranded end. It can be ligated, through its double-stranded end, to the double-stranded end of another polynucleotide. This provides known sequences at the ends of thus modified polynucleotides. Often adaptors contain specific sequences for primer binding and/or restriction endonuclease digestion.

A “probe” when used in the context of polynucleotide manipulation refers to a polynucleotide which is provided as a reagent to detect a target potentially present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and enzymes.

“Transformation” or “transfection” refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, lipofection, transduction, infection or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

A polynucleotide is said to “encode” a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the polypeptide, a homologous polypeptide or a fragment thereof. For purposes of this invention, and to avoid cumbersome referrals to complementary strands, the anti-sense (or complementary) strand of such a polynucleotide is also said to encode the

sequence; that is, a polynucleotide sequence that "encodes" a polypeptide includes both the conventional coding strand and the complementary sequence (or strand).

The terms "polypeptide", "oligopeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, it may be interrupted by non-amino acids, and it may be assembled into a complex of more than one polypeptide chain. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), as well as other modifications known in the art.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an N-terminal to C-terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide which is known to comprise additional residues in one or both directions.

"Recombinant," as applied to a polynucleotide or gene, means that the polynucleotide is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature.

A "vector" is a self-replicating nucleic acid molecule that can be used to transfer an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of a nucleic acid molecule into a cell, vectors that function primarily for the amplification of nucleic acid, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the above functions.

"Expression vectors" are defined as polynucleotides which, when introduced into an appropriate host cell, can be transcribed into a mRNA capable of being translated into a polypeptide(s). An expression vector also comprises control elements operatively linked to the coding region to enable and/or facilitate expression of the polypeptide in the target cell. These can include transcriptional, translational, posttranscriptional, and posttranslational control elements, as are known in the art. An "expression system" usually connotes a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

A "host cell" includes an individual cell or cell culture which can be or has been a recipient for vector(s) or for incorporation of nucleic acid molecules and/or proteins. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in-vivo with a polynucleotide(s) of this invention.

A "cell line" or "cell culture" denotes eukaryotic cells, derived from higher, multicellular organisms, grown or maintained in vitro. It is understood that the descendants of a cell may not be completely identical (either morphologically, genotypically, or phenotypically) to the parent cell. Cells described as "uncultured" are obtained directly from a living organism, and are generally maintained for a limited amount of time away from the organism (i.e., not long enough or under conditions for the cells to undergo substantial replication).

As used herein, "expression" includes transcription and/or translation.

"Heterologous" means derived from (i.e., obtained from) a genotypically distinct entity from the rest of the entity to which it is being compared. For example, a polynucleotide may be placed by genetic engineering techniques into a plasmid or vector derived from a different source, thus becoming a heterologous polynucleotide. A promoter which is linked to a coding sequence with which it is not naturally linked is a heterologous promoter.

An "isolated" or "purified" polynucleotide, polypeptide or cell is one that is substantially free of the materials with which it is associated in nature. By substantially free is meant at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90%, even more preferably at least 99%, and even more preferably at least 99.9% free of the materials with which it is associated in nature. As used herein, an "isolated" polynucleotide or polypeptide also refers to recombinant polynucleotides or polypeptides, which, by virtue of origin or manipulation: (1) are not associated with all or a portion of a polynucleotide or polypeptide with which they are associated in nature, (2) are linked to a polynucleotide or polypeptide other than that to which they are linked in nature, or (3) do not occur in nature, or (4) in the case of polypeptides, arise from expression of recombinant polynucleotides. Thus, for example, an isolated substance may be prepared by using a purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, by specific activity or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this invention are increasingly more preferred.

Thus, for example, a 2-fold enrichment is preferred, 10-fold enrichment is more preferred, 100-fold enrichment is more preferred, 1000-fold enrichment is even more preferred. A substance can also be provided in an isolated state by processes such as chemical synthesis or recombinant expression.

5 A "reagent" polynucleotide, polypeptide, or antibody, is a substance provided for a reaction, the substance having some known and desirable function in the reaction. A reaction mixture may also contain a "target", such as a polynucleotide, antibody, polypeptide, or assembly of polypeptides that the reagent is capable of reacting with. For example, in some types of diagnostic tests, the presence and/or amount of the target in a sample is determined by
10 adding a reagent, allowing the reagent and target to react, and measuring the amount of reaction product (if any).

 "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any
15 other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of an amplification reaction such as PCR, or the enzymatic cleavage of a polynucleotide by a ribozyme.

20 When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, those polynucleotides are described as "complementary". A double-stranded polynucleotide can be "complementary" to another polynucleotide if hybridization can occur between one of the strands of the first polynucleotide and the second. The degree to which one polynucleotide is complementary with another is quantifiable in terms of the proportion of bases in
25 opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules of A-T, A-U and G-C.

 A "stable duplex" of polynucleotides, or a "stable complex" formed between any two or more components in a biochemical reaction, refers to a duplex or complex that is sufficiently long-lasting to persist between formation of the duplex or complex and subsequent detection,
30 including any optional washing steps or other manipulation that may take place in the interim.

 A substance is said to be "selective" or "specific" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance than it does with alternative cells or substances. An odorant ligand "specifically

binds" to a target if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances.

As used herein, "naturally occurring," "native," or "wild type" refers to endogenous polynucleotides and the protein(s) expressed thereby. These terms include full-length and
5 processed polynucleotides and polypeptides. Processing can occur in one or more steps, and these terms encompass all stages of processing. For instance, polypeptides having or lacking a signal sequence are encompassed by the invention. "Non-naturally occurring", "non-native", or "non-wild type" refer to all other polynucleotides and polypeptides.

A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made
10 of a target polynucleotide using one or more primers, and a catalyst of polymerization, such as a reverse transcriptase or a DNA polymerase, and particularly a thermally stable polymerase enzyme. Methods for PCR are taught in U.S. Patent Nos. 4,683,195 (Mullis) and 4,683,202 (Mullis et al.). All processes of producing replicate copies of the same polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "amplification."

According to this invention, a "genomic DNA library" is a clone library which contains representative nucleotide sequences from the DNA of a given genome. It is constructed using various techniques that are well known in the art, for instance, by enzymatically or mechanically fragmenting the DNA from an organism, organ, or tissue of interest, linking the fragments to a suitable vector, and introducing the vector into appropriate cells so as to
20 establish the genomic library. A genomic library contains both transcribed DNA fragments as well as nontranscribed DNA fragments.

In comparison, a "cDNA library" is a clone library that differs from a genomic library in that it contains only transcribed DNA sequences and no nontranscribed DNA sequences. It is established using techniques that are well known in the art, i.e., selection of mRNA (e.g. by
25 polyA) making single stranded DNA from a population of cytoplasmic mRNA molecules using the enzyme RNA-dependent DNA polymerase (i.e., reverse transcriptase), converting the single-stranded DNA into double-stranded DNA, cloning the resultant molecules into a vector, and introducing the vector into appropriate cells so as to establish the cDNA library. Alternately, a cDNA library need not be cloned into a vector and/or established in cells, but can
30 be screened using PCR with gene-specific primers, as is well known in the art.

An "individual" is a vertebrate, preferably a mammal, more preferably a human.

General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as: "Molecular Cloning: A Laboratory Manual", second edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987 and annual updates); "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994); "Current Protocols in Immunology" (J.E. Coligan et al., eds., 1991).

Basis for identification and description of the polynucleotides and polypeptides

The polynucleotide sequences were identified using oligonucleotide primers which were complementary to OR membrane-spanning regions. A number of different primers were used to elicit a variety of nucleotide sequences which encode polypeptides involved in olfactory sensation. The identification and isolation of nucleotide sequences which encode polypeptides involved in olfactory sensation and the polypeptides that they encode is vital for determining the response of receptors to odorant molecules, the elucidation of scent representations, profiles, or fingerprints, the reproduction of scent representations, profiles, or fingerprints and the editing of scent representations, profiles, or fingerprints.

Polynucleotides encoding polypeptides involved in olfactory sensation

The present invention provides isolated polynucleotides encoding polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. These polynucleotides are isolated and/or produced by chemical and/or recombinant methods, or a combination of these methods. The present invention includes polynucleotides isolated from the human olfactory epithelium which encode polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. Unless specifically stated otherwise,

“polynucleotides” shall include all embodiments of the polynucleotides of this invention. These polynucleotides are useful as probes, primers, in expression systems, and, in a preferred embodiment, in screening methods as described herein. In one embodiment the polynucleotides of the present invention can be isolated by creating a cDNA library using template RNA from human olfactory epithelium tissue. A detailed example is related in Example 1, below.

The advantage of constructing a cDNA library for isolation of the desired nucleotide sequences is that the likelihood of obtaining pseudogenes is greatly reduced compared to using a genomic DNA library for the same purpose. cDNA libraries contain only mRNA expressed in the tissue used for the construction of the library, in this case, the human olfactory epithelium. The preferred olfactory epithelium tissue should express only those nucleotide sequences which are relevant for olfactory function, thereby excluding nonfunctioning pseudogenes and also GPCRs which may be similar in primary structure (amino acid sequence) but are not encoded in OSNs. As the number of GPCRs utilized in human signal transduction pathways is extremely wide and varied, cDNA libraries constructed using olfactory tissue are preferable for isolating nucleotide sequences that encode polypeptides which are involved in olfactory sensation, inasmuch as genomic libraries can contain abundant nucleotide sequences which encode for a variety of GPCRs performing numerous functions, and are likely to contain pseudogenes.

The isolation of polynucleotide sequences which encode polypeptides involved in olfactory sensation is described in Example 1. Accordingly, this invention provides isolated polynucleotides that contain sequences encoding polypeptides or portions thereof which are involved in olfactory sensation, wherein the polypeptide is at least 10 amino acids in length, and wherein the polynucleotide sequences are depicted in SEQ ID NOs:1-73 and SEQ ID NOs:111-152.

The invention includes modifications to said polynucleotides described above such as deletions, substitutions, additions, or changes in the nature of any nucleic acid moieties. A “modification” is any difference in nucleotide sequence as compared to a polynucleotide shown herein to encode a polypeptide involved in olfactory sensation, and/or any difference in the nucleic acid moieties of the polynucleotide(s), wherein such a modified polynucleotide encodes a polypeptide involved in olfactory sensation or a variant of said polypeptide that is useful in the practice of the invention. Such changes can be useful to facilitate cloning and modify expression of polynucleotides encoding polypeptides which are involved in olfactory

sensation. Such changes also can be useful for conferring desirable properties to the polynucleotide(s), such as stability. The definition of polynucleotide provided herein gives examples of these modifications. Hence, the invention also includes variants of the nucleic acid sequences disclosed herein, which include nucleic acid substitutions, additions, and/or deletions.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, including polynucleotides that are full-length, processed, coding, non-coding (including flanking region) or portions thereof, provided that these polynucleotides contain a region encoding at least a portion of a polypeptide involved in olfactory sensation. (That is, the region encodes a functional fragment of an olfactory receptor or other polypeptide involved in olfactory sensation.) Also embodied are the mRNA, cDNA and genomic DNA sequences and fragments thereof that include a polynucleotide sequence comprising a coding sequence for a portion of a polypeptide involved in olfactory sensation.

Genes encoding human olfactory receptors, and optionally including related genomic sequences such as regulatory sequences, can be obtained using olfactory receptor cDNAs as hybridization probes. Under high stringency hybridization conditions, an OR cDNA will hybridize to its cognate OR gene. Use of lower stringency hybridization conditions allows the isolation of OR genes that are related to, but not identical with, the gene corresponding to a particular OR cDNA.

Conditions for hybridization are well-known to those of skill in the art and can be varied within relatively wide limits. Hybridization stringency refers to the degree to which hybridization conditions disfavor the formation of hybrids containing mismatched nucleotides, thereby promoting the formation of perfectly matched hybrids or hybrids containing fewer mismatches; with higher stringency correlated with a lower tolerance for mismatched hybrids. Factors that affect the stringency of hybridization include, but are not limited to, temperature, pH, ionic strength, and concentration of organic solvents such as formamide and dimethylsulfoxide. As is well known to those of skill in the art, hybridization stringency is increased by higher temperatures and/or lower ionic strengths. See, for example, Ausubel et al., supra; Sambrook et al., supra; M.A. Innis et al. (eds.) PCR Protocols, Academic Press, San Diego, 1990; B.D. Hames et al. (eds.) Nucleic Acid Hybridisation: A Practical Approach, IRL Press, Oxford, 1985; and van Ness et al., (1991) Nucleic Acids Res. 19:5143-5151. The degree of stringency can be adjusted not only during a hybridization reaction, but also in post-hybridization washes, as is known to those of skill in the art.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, functionally equivalent variants and derivatives of full-length polypeptides involved in olfactory sensation and functionally equivalent fragments. For instance, changes in a DNA sequence that do not change the encoded amino acid sequence, as well as those that result in conservative substitutions of amino acid residues, non-deleterious non-conservative substitutions, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs, will not significantly affect properties of the encoded polypeptide. Polypeptides homologous to the polypeptides encoded by the polynucleotides described herein can also be identified using algorithms and methods well-known to those of skill in the art, such as those described in Ausubel, "Current Protocols in Molecular Biology," Chapter 19; see also Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656. A preferred method of determining homology is the BLAST set of similarity search programs (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410. Polypeptides which are 40% homologous, 50% homologous, 60% homologous, 70% homologous, 80% homologous, 90% homologous, 95% homologous, or 99% homologous to the polypeptides encoded by the polynucleotides described herein are encompassed by the invention.

Nucleotide substitutions that do not alter the amino acid residues encoded can be useful for optimizing gene expression in different systems. Suitable substitutions are known to those of skill in the art and are made, for instance, to reflect preferred codon usage in the particular expression systems. In another example, alternatively spliced polynucleotides can give rise to different functionally equivalent fragments or variants of an polypeptide involved in olfactory sensation. Alternatively processed polynucleotide sequence variants are defined as polynucleotide sequences corresponding to mRNAs that differ in sequence from one another but are derived from the same genomic region, for example, mRNAs that result from: 1) the

use of alternative promoters; 2) the use of alternative polyadenylation sites; and/or 3) the use of alternative splice sites.

Preparation of polynucleotides involved in olfactory sensation

5 The polynucleotides of this invention can be obtained using chemical synthesis, recombinant methods, or PCR.

Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

10 For preparing polynucleotides which encode polypeptides involved in olfactory sensation using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct
15 uptake, endocytosis, transfection, F-mating, particle bombardment, liposome mediation, or electroporation. Once introduced, an exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide encoding a polypeptide involved in olfactory sensation can be isolated from the host cell by methods well known within the art. See, e.g., Sambrook et al. (1989).

20 Alternatively, PCR allows amplification of DNA sequences. PCR technology is well known in the art and is described in U.S. Pat. Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as *PCR: The Polymerase Chain Reaction*, Mullis et al. eds., Birkhausw Press, Boston (1994).

25 RNA can be obtained in a number of ways in an appropriate vector and the vector is transformed into a suitable host cell. When the inserted DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook et al., (1989), for example. RNA can also be obtained through in vitro reactions. For example, the polynucleotide, which encodes a polypeptide involved in olfactory sensation, can be inserted into a vector that contains appropriate transcription promoter sequences.

30 Commercially available RNA polymerases will specifically initiate transcription at their promoter sites and continue the transcription process through the adjoining DNA polynucleotides. Placing the polynucleotide sequences which encode polypeptides involved in

olfactory sensation between two such promoters allows the generation of sense or antisense strands of desired RNA.

5 ***Cloning and expression vectors comprising polynucleotide sequences encoding polypeptides involved in olfactory sensation***

The present invention further includes a variety of vectors containing polynucleotides encoding polypeptides involved in olfactory sensation. These vectors can be used for expression of recombinant polypeptides as well as a source of polynucleotides which encode polypeptides involved in olfactory sensation. Cloning vectors can be used to obtain replicate
10 copies of the polynucleotides, which encode polypeptides involved in olfactory sensation, they contain, or as a means of storing the polynucleotides in a depository for future recovery. Expression vectors (and host cells containing these expression vectors) can be used to obtain polypeptides produced from the polynucleotides they contain. Suitable cloning and expression vectors include any known in the art, e.g., those for use in in vitro, bacterial, mammalian, yeast
15 and insect expression systems. Specific vectors and suitable host cells are known in the art and need not be described in detail herein. For example, see Gacesa and Ramji, *Vectors*, John Wiley & Sons (1994).

Cloning and expression vectors typically contain a selectable marker (for example, a gene encoding a protein necessary for the survival or growth of a host cell transformed with the
20 vector), although such a marker gene can be carried on another polynucleotide sequence co-introduced into the host cell. Only those host cells into which a selectable marker has been introduced will survive and/or grow under selective conditions. Typical selectable markers encode protein(s) that (a) confer resistance to antibiotics or other toxins substances, e.g., ampicillin, neomycin, methotrexate, etc.; (b) complement auxotrophic deficiencies; or (c)
25 supply critical nutrients not available from complex media. The choice of the proper marker gene will depend on the host cell, and appropriate genes for different hosts are known in the art. Cloning and expression vectors also typically contain a replication system recognized by the host.

Suitable cloning vectors may be constructed according to standard techniques, or may
30 be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate in an appropriate host, may possess a single target for one or more particular restriction endonucleases, and/or may carry genes for a marker

that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, m13mp18, m13mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Stratagene, and

5 Invitrogen.

Expression vectors generally are replicatable polynucleotide constructs that contain a polynucleotide encoding an polypeptide involved in olfactory sensation of interest. The polynucleotide, which encodes a polypeptide involved in olfactory sensation, encoding the polypeptide is operatively linked to suitable transcriptional controlling elements, such as
10 promoters, enhancers and terminators. For expression (i.e., translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons. These controlling elements (transcriptional and translational) may be derived from the gene encoding polypeptides involved in olfactory sensation, or they may be heterologous (i.e., derived from other genes and/or other organisms).
15 A polynucleotide sequence encoding a signal peptide can also be included to allow a polypeptide involved in olfactory sensation to cross and/or lodge in cell membranes or be secreted from the cell. A number of expression vectors suitable for expression in eukaryotic cells including yeast, insect, avian, plant and mammalian cells are known in the art. Common vectors, such as YEpl3 and the Sikorski series pRS303-306, 313-316, 423-426 can also be
20 used. Vectors pDBV52 and pDBV53 are suitable for expression. Another example of an expression vector/host cell system is the baculovirus (e.g., nuclear polyhedrosis virus)/insect cell (e.g., sf9 cells) system.

Human olfactory receptor polypeptides are expressed from olfactory receptor cDNA by methods well-known to those of skill in the art. A cDNA or portion thereof is inserted in an
25 expression vector using standard molecular cloning techniques. Coupled in vitro transcription and translation of such a vector results in expression of the OR protein encoded by the cDNA. In vivo expression of a OR polypeptide is accomplished by inserting an OR cDNA into a eucaryotic or procaryotic expression vector, of which many are known in the art, to generate an OR expression construct. The OR expression construct is introduced into an appropriate
30 host cell in which the OR sequences are expressed (by transcription and translation) and optionally secreted, and the expressed OR polypeptide is obtained from the cell growth medium and/or from cell lysates.

A number of expression vectors are known in the art. Prokaryotic expression vectors include, but are not limited to, T7 RNA polymerase/T7 promoter-based vectors, bacteriophage λ -based vectors and various types of fusion vectors. Fusion vectors include, but are not limited to, lacZ and trpE fusion vectors, maltose binding protein fusion vectors, glutathione-S-transferase fusion vectors, and thioredoxin fusion vectors. Baculovirus-based vectors are used for expression in insect cell systems. Expression in mammalian cells (such as HEK, COS and CHO cells) utilizes vectors containing a mammalian origin of replication (such as, for example, a SV40 origin), an efficient promoter (optionally including one or more enhancer sequences), mRNA processing signals (e.g., splice sites and polyadenylation sites), one or more selectable markers, and optionally a prokaryotic replicon to allow propagation and manipulation of the construct in prokaryotic cells. Alternatively, expression in mammalian cells is achieved through the use of any of a number of mammalian viral vectors including, but not limited to, retroviruses, lentiviruses, Semliki Forest viruses, vaccinia viruses, adenoviruses and adeno-associated viruses.

Vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, direct injection, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent, such as a virus). The choice of means of introducing vectors or polynucleotides encoding polypeptides involved in olfactory sensation will often depend on the host cell, as will be well known to those of skill in the art.

Host cells transformed with polynucleotides encoding polypeptides involved in olfactory sensation

Another embodiment of this invention are host cells transformed with (i.e., comprising) polynucleotides encoding polypeptides involved in olfactory sensation, and/or vectors having polynucleotide(s) sequences encoding polypeptides involved in olfactory sensation, as described above. Both prokaryotic and eukaryotic host cells may be used. Prokaryotic hosts include bacterial cells, for example *E. coli*, *B. subtilis*, and mycobacteria. Among eukaryotic hosts are yeast, insect, avian, plant and mammalian cells. Host systems are known in the art and need not be described in detail herein.

The host cells of this invention can be used, *inter alia*, as repositories of polynucleotides encoding polypeptides involved in olfactory sensation, and/or vehicles for

production of polynucleotides encoding polypeptides involved in olfactory sensation, and/or polypeptides involved in olfactory sensation . They may also be used as vehicles for *in vivo* delivery of polypeptides involved in olfactory sensation .

5 ***Uses for and methods using polynucleotides encoding polypeptides involved in olfactory sensation***

To determine whether a vector containing polynucleotides is capable of expressing in eukaryotic cells, cells such as, for example, COS-7 (primate origin), CHO (rodent origin), HEK-293 (human origin), or HeLa (human origin) cells can be transfected with the vector.

- 10 Expression of a polypeptide(s) encoded by the vector is then determined by, for example, RIA, ELISA, immunofluorescence of fixed cells, or western blotting of cell lysate using an antibody as a probe. Antibodies can be obtained using, as immunogen, peptide sequences synthesized from the protein sequences encoded by the known polynucleotide sequence. Polypeptides can be purified by, for example, phase partitioning, affinity methods, gel filtration and ion
- 15 exchange, as well as additional methods known by those skilled in the art. Further characterization of the expressed polypeptide can be achieved by purification of the polypeptide using techniques known in the art.

Polypeptides involved in olfactory sensation

- 20 The present invention encompasses polypeptides involved in olfactory sensation. Expression of said polypeptides is localized in the olfactory neurons located in the olfactory epithelium, as described earlier. The polypeptides may comprise any novel sequence encoded by a nucleotide sequence as depicted in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152.
- 25 The invention includes modifications to polypeptides involved in olfactory sensation including functionally equivalent fragments of the polypeptides involved in olfactory sensation which do not significantly affect their properties and variants which may have enhanced or decreased activity. Collectively, these modifications may be termed "analogs" of or a fragment of polypeptides involved in olfactory sensation. Modification of polypeptides is routine practice in
- 30 the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues which can be conservatively substituted for

one another include but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. Such conservative substitutions are known in the art, and preferably, the amino acid substitutions would be such that the substituted amino acid would possess

5 similar chemical properties as that of the original amino acid. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different sugars, acetylation, and phosphorylation. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region. Other methods of
10 modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modified polypeptides involved in olfactory sensation are made using established procedures in the art.

The invention also encompasses fusion proteins comprising one or more polypeptides involved in olfactory sensation. For purposes of this invention, an fusion protein contains one
15 or more polypeptides involved in olfactory sensation and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region. Useful heterologous sequences include, but are not limited to, sequences that provide for secretion from a host cell, intracellular trafficking, and stability/degradation. Other useful heterologous sequences are ones which facilitate
20 purification. Examples of such sequences are known in the art and include those encoding epitopes such as Myc, HA (derived from influenza virus hemagglutinin), His-6, or FLAG. Other heterologous sequences that facilitate purification are derived from proteins such as glutathione S-transferase (GST), maltose-binding protein (MBP), or the Fc portion of
immunoglobulin.

Preparation of polypeptides involved in olfactory sensation

The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by recombinant methods (i.e., single or fusion polypeptides) or by chemical synthesis. Polypeptides, especially shorter polypeptides up to about 50 amino
30 acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available. For example, a polypeptide can be produced by an automated polypeptide synthesizer employing the solid phase method. Polypeptides can also be made by chemical synthesis using techniques known in the art.

Polypeptides can also be made by expression systems, using recombinant methods. The availability of polynucleotides encoding polypeptides permits the construction of expression vectors encoding intact (i.e., native) polypeptide, functional equivalents and functional fragments thereof, modified forms or recombinant forms. A polynucleotide encoding the desired polypeptide, or a fusion protein, can be ligated into an expression vector suitable for any convenient host. Both eukaryotic and prokaryotic host systems can be used. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification or isolation of the polypeptides expressed in host systems can be accomplished by any method known in the art (e.g. partitioning exclusion, ion exchange chromatograph, gel filtration, etc.). Other controlling transcription or translation segments, such as signal sequences that direct the polypeptide to a specific cell compartment (i.e., for secretion), can also be used. Examples of prokaryotic host cells are known in the art and include, for example, *E. coli* and *B. subtilis*. Examples of eukaryotic host cells are known in the art and include yeast, avian, insect, plant, and animal cells such as COS7, HeLa, CHO, HEK-293 and other mammalian cells.

Alternatively, in vitro expression systems may also be used to produce polypeptides involved in olfactory sensation. A plasmid containing a polynucleotide encoding polypeptides involved in olfactory sensation, under the control of an appropriate promoter, can be transcribed and the resultant RNA translated in vitro through the use of commercially available reagents. Such methods can be used to produce relatively pure samples of the polypeptide and are known in the art.

Preferably, the polypeptides are at least partially purified from other cellular constituents. In one embodiment, the polypeptides are at least 70%, more preferably at least 80%, even more preferably at least 90% or most preferably at least 95% pure. In this context, purity can be calculated as a weight percent of the total protein content of the preparation. More highly purified polypeptides may also be obtained and are encompassed by the present invention. Methods of protein purification are known in the art and are not described in detail herein. For membrane-bound proteins, the lipid content of the preparation, which is required to maintain the structure and function of the protein, is excluded from the purity calculation. That is, if a preparation weighing 10 mg has 5 mg lipid, 4 mg of desired protein, and 1 mg of undesired proteins, the purity is calculated as 80% (desired protein content divided by total protein content). Preparations of biological or synthetic molecules suitable for maintaining structure and function of membrane proteins are described in Etemadi AH (1985) *Adv Lipid*

Res 1985;21:281-428; Villalobo A (1990) *Biochimica Et Biophysica Acta*, 1017(1):1-48; Montal M (1987) *Journal Of Membrane Biology* 98(2):101-115; Scotto AW et al. (1987) *Biochemistry* 26(3): 833-839; Jain MK and Zakim D (1987) *Biochimica Et Biophysica Acta* 906(1): 33-68; Czerski L and Sanders CR (2000) *Anal Biochem* 284(2):327-33 (lipid-detergent mixtures or "bicelles"); Hrafnisdottir S and Menon AK (2000) *J Bacteriol* 182(15):4198-206 (proteoliposomes); Puu G et al. (2000) *Biosens Bioelectron* 15(1-2):31-41 (protein-lipid preparations on solid surfaces); Schafmeister CE et al. (1993) *Science* 262(5134):734-8 ("peptitergents").

10. *Uses of polypeptides involved in olfactory sensation*

The polypeptides of this invention have a variety of uses. They can be used, for example, to screen odorant ligands in order to determine the scent representations, scent profiles or scent fingerprints of particular odorant molecules and further to characterize the effect of functional groups and chemical characteristics on perceived smell. Methods for screening odorant compounds using odorant receptors in neuronal cells are known in the art (Firestein et al., WO 98/50081; Duchamp-Viret et al., *Science* 1999, 284 2171-2174; Sato et al., *J. Neurophys.* 1994 72 2980-2989; Malnic et al, *Cell* 1999 96 713-723; Zhao et al., *Science* 1998 279, 237-242). There are also methods which can be employed to screen odorant compounds which do not require neuronal cells and are known in the art (Kauvar et al., U. S. Pat. No. 5,798,275; Kiefer et al., *Biochemistry* 1996 35 16077-16084; Krautwurst et al., *Cell* 1998 95 917-926),

Analysis of the scent can be performed in a number of ways. Various embodiments of the scent analysis system are presented. Examples of how these embodiments might operate are also presented, although it should be emphasized that the invention is not limited by any particular theory of olfactory perception or scent analysis.

Olfactory Space

The sensory subsystem comprises a series of olfactory receptors, which selectively bind with the chemical component(s) making up the scent. The scent can be characterized in terms of which of the approximately 1,000 olfactory receptors the scent component(s) bind to, and the strength of the interaction of the component(s) with those receptors. Each olfactory receptor can be considered an orthogonal basis vector; the entire set of olfactory receptors can be considered a set of basis vectors spanning "olfactory space." This is analogous to vectors

pointing along the x, y, and z directions in three-dimensional space, where any point in space can be represented by a combination of the x, y, and z basis vectors (with each of the x, y, and z vectors multiplied by the appropriate scalar quantity). The intensity of interaction of a scent with an olfactory receptor determines the magnitude of the vector along that particular "axis" in olfactory space. Thus, every scent can be uniquely described by a vector representation in olfactory space.

A representation of a scent in such a manner that the scent can later be re-created is defined as scent profiling. The aforementioned vector representation is one example of a scent profile.

Primary Scents

For the purposes of this invention, a receptor primary scent component is defined as a chemical that interacts with one and only one scent receptor. A receptor complex scent component is defined as a chemical that interacts with more than one scent receptor; the receptor complex scent component can interact with each of the scent receptors to different degrees, to equal degrees, or can interact with some receptors to the same degree and others to different degrees.

Olfactory receptors are proteins which fall in the class of seven transmembrane domain G protein-coupled receptors, and are found in olfactory neurons *in vivo*. Binding of an odorant to an olfactory receptor causes second messenger systems to become activated or inhibited in the cell, leading to increased cellular production of second messenger molecules such as cyclic AMP. These second messenger systems in turn lead to the depolarization of the olfactory neuron, or other changes in the state of the neuron, which provides the signal to the nervous system that the odorant has been detected.

With a complete set of receptor primary scent components, any scent can be re-created with the knowledge to the degree to which it interacts with each olfactory receptor. The instant invention encompasses such complete sets of receptor primary scent components. Other embodiments of the invention encompass sets of receptor primary scent component chemicals which provide the ability to re-create a particularly desired subset of scents, but not necessarily all possible scents. Still more embodiments encompass sets of receptor primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

In some cases, a receptor complex scent will be an acceptable approximation to a receptor-primary scent. That is, if a given receptor complex scent interacts with a first scent receptor strongly, but interacts with other scent receptors less strongly, it can be considered an approximation to a receptor primary scent component for the first receptor. Such a receptor complex scent component is described by the term receptor quasi-primary scent component. One embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating all scents. Another embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating a particularly desired subset of scents, but not necessarily all possible scents. Yet another embodiment encompasses sets of receptor quasi-primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

The identification of receptor primary or quasi-primary scent component chemicals provides the most conceptually straightforward method of re-creating scents. However, another embodiment of the invention encompasses the use of receptor complex scent components for re-creating scents. An example of such an embodiment would be re-creation of a scent that activates olfactory receptors designated OR1, OR2, OR3, OR4, OR5 and OR6 (for the sake of illustration, it is assumed that the olfactory receptors are stimulated to an equal extent). If one is in possession of two receptor complex scent component chemicals (RCSC's) where RCSC1 activates OR1 and OR5, and RCSC2 activates OR2, OR3, OR4, and OR6, then one can reproduce the original scent by mixing RCSC1 and RCSC2 to re-create the original olfactory receptor activation profile. In practice, the profiles of various receptor complex scent components will be much more complicated than the foregoing example, and components which inhibit olfactory activation as well as stimulate activation can be included in the sets. However, once receptor activation profiles of sufficient receptor complex scent components are known, computer algorithms can be utilized to create the appropriate combination of receptor complex scent components. Using vector representations of the olfactory receptor activation profiles for a set of receptor complex scent components, one can create linear combinations of such receptor complex scent components in order to represent a particular scent. For the example given above, such a vector representation would look like (1, 0, 0, 0, 1, 0) for the first receptor complex scent component and (0, 1, 1, 1, 0, 1) for the second receptor

complex scent component, while the vector representation of the scent to be re-created is (1, 1, 1, 1, 1, 1). If x_1 and x_2 are the relative proportions of the first receptor complex scent component and the second receptor complex scent component, respectively, to be combined to re-create the scent, then the problem can be represented as a series of linear equations:

$$\begin{array}{rclcl}
 1x_1 & + & 0x_2 & = & 1 \\
 0x_1 & + & 1x_2 & = & 1 \\
 0x_1 & + & 1x_2 & = & 1 \\
 0x_1 & + & 1x_2 & = & 1 \\
 1x_1 & + & 0x_2 & = & 1 \\
 0x_1 & + & 1x_2 & = & 1
 \end{array}$$

and the solutions for x_1 and x_2 are $x_1 = 1$, $x_2 = 1$. Solutions to systems of linear equations have been thoroughly studied and many algorithms are available for implementation on computers, including algorithms which evaluate the accuracy of an approximate solution when an exact solution cannot be determined. (See, e.g., Dettman, J.W., *Introduction to Linear Algebra and Differential Equations*, Dover Pubs., 1986; Press W.H. et al., *Numerical Recipes in C: The Art of Scientific Computing*, 2nd ed., Cambridge University Press, 1993; Vetterling (ed.) *Numerical Recipes in C: The Art of Scientific Computing/Disk V 2.02*, Cambridge University Press, 1997.) These methods can also be used to determine whether a set of receptor complex scent components is suitable for re-creating a given scent. For example, if the scent to be recreated is represented by the vector (1, 1, 1, 1, 1, 2), there will be no solution to the resulting system of linear equations using the two receptor complex scent components in the illustration above. In this instance, one or more additional receptor scent components will need to be identified in order to be able to re-create the scent in terms of the receptor primary scent components. Alternatively, the scent represented by (1, 1, 1, 1, 1, 1) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2). Integers are used in this example for clarity, but the vectors can contain any real number representing a measured intensity; for example, (1.1, 0.997, 1.08, 1.2, 0.88888..., 2.00001) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2).

It will be readily appreciated that the choice of a complete set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating all scents) versus a partial set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating, exactly or approximately, a subset of scents) depends on the application for which scent re-creation is desired.

A special category of receptor scent components are chemicals which bind to a receptor without activating it. If these non-activating chemicals prevent chemicals which do activate the receptors from binding, the non-activating chemicals act to "turn off" those receptors. These non-activating chemicals, or receptor binding antagonists, are particularly useful in editing scents, as they can be added to a scent to attenuate or eliminate particular aspects of the scent. In the vector example above, if a particular receptor antagonist blocks OR2, OR3, and OR4, but not OR1, OR5 or OR6, then it can be represented in vector format as (0, -1, -1, -1, 0, 0). In the reproduction of (1, 1, 1, 1, 1, 2) from the vectors (1, 0, 0, 0, 1, 0) and (0, 1, 1, 1, 0, 1), the following combination can be used:

$1 \times (1, 0, 0, 0, 1, 0) + 2 \times (0, 1, 1, 1, 0, 1) + 1 \times (0, -1, -1, -1, 0, 0)$ to yield the vector (1, 1, 1, 1, 1, 2). In some instances, enough of a particular receptor binding antagonist is used to eliminate any possibility of activation by a receptor scent component, in which case the vector entry for the receptor(s) which are blocked by that antagonist contains 0 in the vector position corresponding to that receptor(s).

Perceptive primary scents are defined as scents that give a single scent perception, for example, the scent "lemon" as perceived by a human. A perceptive primary scent can be composed of one or more receptor primary scent components, one or more receptor complex scent components, or a mixture of one or more receptor primary scent components and one or more receptor complex scent components. Since perceptive primary scents are to some extent subjective, identification of perceptive primary scents can be performed by using a panel of subjects who evaluate and describe scents. A perceptive complex scent is made up of more than one perceptive primary scent. The boundaries between a perceptive primary scent and a perceptive complex scent are also to some extent subjective; for example, one person may describe a scent as "pizza," while another person may describe the same scent as "sausage, cheese and tomato sauce." That is, one person may perceive a scent as a perceptive primary scent for "pizza," while another person may perceive the same scent as a perceptive complex scent made up of several individual perceptive primary scents. In order to standardize perceptive scents, a panel of five or more, preferably ten or more, more preferably fifty or

more, still more preferably one hundred or more, people can be surveyed to label various perceptive scents. When a plurality, preferably a majority, more preferably 66 2/3 % or greater, still more preferably 95 % or greater, even more preferably 99% or greater, of the panel identifies a scent as the same scent (e.g., of a panel of 100 people, 95 describe a scent as
5 "pizza," while the other 5 describe the scent otherwise), the scent can be labeled as a perceptive scent (the perceptive scent can be primary or complex, depending on whether the panel identifies it as a single scent or a mixture of scents).

In fields where existing classification schemes already exist, the perceptive primary and complex scents can be indexed according to those schemes. For example, the SFP (Société
10 Française des Parfumeurs) has drawn up a classification system based on 5 main groups, subdivided into classes. Such a classification can be used for selecting perceptive primary scents and used as guides for combining the scents.

Selecting Chemicals for Scent Re-creation

15 A scent which has been represented as a set of basis vectors in olfactory space can in principle be re-created simply by mixing the receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components needed to interact the olfactory receptors in the same pattern as the original scent. Such an approach requires 1) a method to generate a representation of the original scent in olfactory space, and 2) suitable
20 receptor primary scent component chemicals which can be mixed in the appropriate manner.

Identification of receptor scent components can be performed by various methods. One such method assays the interaction of candidate components with each olfactory receptor. The receptors can be expressed *in vitro* and assays can be set up to monitor the interaction of various candidate components with each individual receptor. Chemicals which interact with
25 one and only one olfactory receptor are receptor primary scent components, while chemicals which interact with more than one olfactory receptor are receptor complex scent components (and can possibly be receptor quasi-primary scent components, depending on the interaction profile it displays with the olfactory receptors). Such an approach can use methods known in the art, for example those of Breer *et al.*, Ann. N. Y. Acad. Sci. (1998) 855:175-81 or Malnic *et al.*,
30 *Cell* (1999) 96(5):713-23. Breer *et al.* expressed olfactory receptors in Sf9 cells and evaluated the second-messenger response to various odorants. Malnic *et al.* isolated olfactory neurons from mice and utilized calcium imaging to study the response of the neurons to different odorants, while using RT-PCR to determine which olfactory receptor was expressed

in the neuron under study. U.S. Patent No. 5,798,275 describes a method for evaluating interaction of compounds with members of a reference panel of proteins. WO 98/50081 discloses methods for detecting particular odorant ligand specificity for particular odorant receptors in nasal epithelium tissue of mammals such as rats and mice.

5

Selection of Receptor Primary Scents by in silico Methods

An alternative method utilizes *in silico* screening techniques--that is, computer simulation methods--for selecting candidate components. Protein-ligand screening can be used to select compounds which bind to particular receptors in order to identify receptor primary
10 scent components. Examples of such programs are DOCK, AutoDock, GOLD, FlexX, LUDI, GROWMOL, and HOOK. (See Wang, J., Kollman, P.A., Kuntz I.D., "Flexible ligand docking: a multistep strategy approach," *Proteins* 36(1):1-19 (1999) and references therein.) These programs function by taking a protein structure and either matching compounds of known structure to the protein structure to determine the protein-ligand interaction, or by
15 "growing" a molecule in the active site or binding site of a protein to determine what molecule will best interact with the protein.

Olfactory receptor proteins are membrane proteins, and experimental determination of the three-dimensional structures of membrane proteins has lagged the corresponding structural determination of water-soluble proteins for various reasons. However, alternative methods for
20 constructing the three-dimensional structures of proteins are available. The primary (amino acid) sequences of many olfactory receptors are known. This information can be used to model a three-dimensional structure of a receptor protein using various algorithms and computer programs known in the art. The resulting model structure can then be used as the basis for evaluating interaction of candidate components with the receptor.

25 Alternatively, given known chemical structures which give rise to a particular odor, analysis of the structures can indicate the particular portion of the chemical structure which is responsible for the odor. This is analogous to "pharmacore analysis" used in medicinal chemistry to determine the important portion of drugs.

Methods for developing compounds which bind to receptors and other proteins of
30 known structure, and determining interactions between ligands and receptors, are described in various references. The DOCK program evaluates the fit of a ligand into a protein molecule of known structure (see Gschwend, D.A., Good, A.C. and Kuntz, I.D., "Molecular Docking Towards Drug Discovery", *J. Mol. Recognition* 9, 175-86 (1996); Kuntz, I.D., Meng, E.C., and

B.K. Shoichet, "Structure-Based Strategies For Drug Design and Discovery", *Acc. Chem. Res.* 27, 117-123 (1994); and Kuntz, I.D., "Structure-based strategies for drug design and discovery", *Science* 257, 1078-1082 (1992); see also

<http://www.cmp Pharm.ucsf.edu/kuntz/dock.html>). Using a known (or modeled) structure of an

5 olfactory receptor, DOCK can be used to screen for compounds which bind to the receptor.

The program AMBER (see Cornell, WD, Cieplak P, Bayly CI, Gould IR, Merz KM Jr, Ferguson DM, Spellmeyer DC, Fox T, Caldwell JW and Kollman PA. "A second generation force field for the simulation of proteins and nucleic acids," *Journal of the American Chemical Society* 117, 5179-5197 (1995); Computer Simulation of Biomolecular Systems, A. Wilkinson, 10 P. Weiner, W. Van Gunsteren, eds. Volume 3, p. 83-96, P. Kollman, R. Dixon, W. Cornell, T. Fox, C. Chipot and A. Pohorille; Bayly CI, Cieplak P, Cornell WD and Kollman PA. "A well-behaved electrostatic potential based method using charge restraints for deriving atomic charges - the RESP model," *Journal of Physical Chemistry* 97(40), 10269-10280 (1993);

Cornell WD, Cieplak P, Bayly CI and Kollman PA. "Application of RESP charges to calculate 15 conformational energies, hydrogen bond energies, and free energies of solvation," *Journal of the American Chemical Society* 115(21), 9620-9631 (1993); see also

<http://www.amber.ucsf.edu/amber/amber.html>) can be used to calculate more precise interaction energies between candidate ligands. Other examples of such methods are described in, for example, U.S. Patent No. 5,866,343, directed to determining the energetically favorable 20 binding site between two molecules; U.S. Patent No. 5,854,992, a system and method for structure-based drug design which takes into account binding free energy as it "grows" candidate molecules into a receptor binding site; and U.S. Patent No. 5,495,423, which describes a method for ligand design (principally applicable to peptidic ligands).

The foregoing methods typically depend on a known three-dimensional structure for the 25 receptor. When such a structure cannot or has not been determined experimentally, a structure can be modeled using computer algorithms. Blundell TL, Sibanda BL, Sternberg MJ, Thornton JM, "Knowledge-based prediction of protein structures and the design of novel molecules," *Nature* 326(6111):347-52 (1987); Shortle D, "Structure prediction: The state of the art," *Curr Biol* 9(6):R205-9 (1999), Morea V, Leplae R, Tramontano A, "Protein structure prediction and design," *Biotechnol Annu Rev* 4:177-214 (1998) and Onuchic JN, Luthey-Schulten Z, Wolynes 30 PG, "Theory of protein folding: the energy landscape perspective," *Annu Rev Phys Chem* 48:545-600 (1997) address various methods of predicting protein structure from sequence data.

Various implementations for predicting protein structure from amino acid sequences are discussed in U.S. Patent Nos. 5,878,373 and 5,884,230.

If the structure, or even the identity, of the targeted receptor cannot be determined, alternative computational techniques can be used to generate information regarding possible ligands which will interact with the receptor. Quantitative structure-activity relationships (QSAR; see Green, S.M. and Marshall, G.R., "3-D QSAR: A current perspective," *Trends Pharmacol Sci* 16:285 (1995); and 3D QSAR in Drug Design: Theory, Methods and Applications, Kubinyi, H. Ed.; Escom, Leiden.), including QSAR refinements such as comparative molecular field analysis (ComFA) (Cramer, R. D. et al. "Comparative Molecular Field Analysis ComFA 1. Effect Of Shape On Binding Of Steroids To Carrier Proteins," *J. Am. Chem. Soc.* 110: 5959 (1988)); and pharmacophore mapping (Martin YC, Bures MG, Danaher EA, DeLazzer J, Lico I, Pavlik PA, "A fast new approach to pharmacophore mapping and its application to dopaminergic and benzodiazepine agonists," *J Comput Aided Mol Des* 7(1):83-102 (1993)) have been used to design pharmacophores that can interact with the receptor. U.S. Patent No. 5,699,268 provides a method for producing computer-simulated receptors which functionally mimic biological receptors; the simulated receptors are essentially abstractions of structurally useful information from compounds which are known to interact with a receptor. U.S. Patent No. 5,901,069 describes a method of automatically refining a set of chemicals using structure/activity data. U.S. Patent No. 5,862,514 describes a method of simulating synthesis of compounds of desired biological activity and evaluating their activity via further simulations.

Application of structure-function relationships to classification of odors has been described by Chastrette M., Rallet E. "Structure-minty odour relationships: Suggestion of an interaction pattern," *Flavour and Fragrance Journal*, 13(1):5-18 (1998); Chastrette M., De Saint Laumer J.Y., Peyraud J.F., "Adapting the structure of a neural network to extract chemical information. Application to structure-odour relationships," *SAR QSAR Environ Res* 1 (2-3):221-231 (1993), Chastrette M., "Trends in structure-odor relationships," *SAR QSAR Environ Res* 6(3-4):215-254 (1997) and Jain et al., "A shape-based machine learning tool for drug design," *J Comput Aided Mol Des* 8(6):635-652 (1994). These methods can be useful in determining the "chemical distance" between odors. For example, isoamyl acetate is typically experienced as a banana-like odor, while octyl acetate is typically experienced as an orange-like odor, which gives a measure of how the chain length of the alkoxy portion of the ester influences perception.

Olfactory Receptors and Libraries of Olfactory Receptors

The olfactory receptors of the invention can be used to analyze and describe the interaction of scent odorant molecules with each receptor. This can be done individually, receptor-by-receptor and odorant molecule by odorant molecule. However, a combinatorial approach provides a much more powerful method of analyzing and describing the interaction of scent odorant molecules with olfactory receptors.

In one embodiment, the invention comprises libraries of olfactory receptors. These libraries are used to screen compositions for interaction with receptors. A composition can be a single compound (essentially a pure chemical), or a mixture of two or more compounds or chemicals. The compositions can be presented to the library in vapor form, or in solutions, typically aqueous solutions.

The method for determining the binding pattern of a composition with olfactory receptors comprises the steps of: exposing the composition to an olfactory receptor library; and determining whether the composition binds to each olfactory receptor of the library, thereby determining the overall binding pattern of the composition. While it is desirable to determine whether the composition binds to each of the olfactory receptors, in certain cases, determining the binding pattern to a subset of the receptors is suitable. Such a situation can arise if the complete pattern is not needed, or if the experiment cannot determine binding to a receptor for a particular reason. (Determining the binding to a subset is equivalent to reducing the olfactory receptor library to that subset of receptors.)

Typically, the libraries are prepared as arrays, where the position of each olfactory receptor is known on the array. The arrays can take the form of multiwell plates, solid substrates such as chips or wafers, or any other form allowing identification of the receptor location. The arrays can be prepared in order to simply assess binding, or can be prepared in order to assess degree of activation as described above, using, for example, the technique of Malnic *et al.*, *Cell* 1999 96, 713-723. Alternatively, an *in silico* array of structures can be prepared, using the known primary structure of the receptors and the modeling techniques described above.

The libraries contain at least two olfactory receptors. In increasing order of preference, the libraries contain at least 5, 10, 20, 30, 40, 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1500, 1600, 1800, or 2000 olfactory receptors. The

receptors are presented as ordered arrays. For example, a 96-well plate can contain 96 receptor preparations. Upon exposure to a composition, the plate can be scanned, and the response of each receptor in each well can be evaluated. This leads to a 96-element vector description of the composition in terms of those 96 olfactory receptors.

- 5 In one embodiment, binding to the olfactory receptors is assessed. In another embodiment, the approximate binding constant of the composition to the olfactory receptors is determined. In yet another embodiment, the degree of activation of the olfactory receptor by the composition is determined. For receptor antagonists, binding will occur, but no activation will occur; the invention embraces the identification of such
- 10 antagonists.

- The compositions for use are varied. A set of all volatile compounds can be used. A standard set of perfumes or odorants can be used. A set of commercially used scents can be used. Sets of compounds particularly useful in the invention are disclosed in co-pending United States Patent Application Serial No. 09/620,753. However, it must be emphasized
- 15 that the invention is not limited to any one set or classification of compounds.

 Preferred subsets of olfactory receptor polynucleotide sequences include:

 SEQ ID NOS: 163, 331, 414, 425, 672, 762, 919, and 1027;

 SEQ ID NOS: 809 and 1067;

 SEQ ID NO: 744;

- 20 SEQ ID NOS: 207, 336, 441, and 615;

 SEQ ID NOS: 157, 168, 197, 221, 250, 334, 340, 412, 413, 459, 491, 618, 690, 694, 759, 760, 761, 767, 819, 860, 872, 873, 917, 936, 939, 940, 947, 952, 958, 959, 1023, 1034, 1038, 1043, and 1044;

 SEQ ID NOS: 783, 785, 882, 888, 922, and 925;

- 25 SEQ ID NOS: 707, 748, 752, 755, 756, 790, and 997;

 SEQ ID NOS: 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, and 1084;

 SEQ ID NOS: 163, 239, 331, 335, 368, 381, 385, 414, 425, 514, 572, 596, 603, 628, 638, 642, 672, 674, 689, 744, 762, 809, 835, 885, 896, 919, 920, 938, 948, 972, 999, 1007, 1014, and 1027;

- 30 SEQ ID NOS: 164, 173, 176, 180, 182, 184, 185, 188, 190, 194, 207, 210, 213, 214, 215, 217, 219, 220, 223, 226, 227, 229, 230, 234, 235, 240, 249, 255, 265, 270, 273, 274,

276, 277, 279, 281, 289, 291, 293, 294, 298, 302, 307, 311, 318, 319, 321, 330, 336, 339,
341, 342, 343, 348, 351, 356, 359, 361, 365, 366, 367, 368, 370, 372, 373, 374, 375, 376,
378, 379, 380, 382, 383, 384, 385, 388, 391, 392, 393, 398, 400, 401, 403, 408, 420, 423,
427, 428, 431, 434, 435, 438, 439, 440, 441, 447, 448, 450, 455, 458, 464, 465, 468, 471,
5 473, 474, 475, 478, 479, 481, 482, 484, 485, 492, 494, 499, 502, 508, 511, 512, 513, 515,
526, 532, 534, 541, 543, 545, 546, 550, 552, 553, 557, 558, 560, 563, 564, 568, 572, 576,
582, 583, 584, 585, 586, 588, 599, 600, 605, 606, 607, 608, 609, 610, 615, 620, 621, 631,
632, 636, 638, 640, 642, 645, 648, 650, 651, 652, 654, 656, 657, 661, 662, 664, 668, 679,
680, 686, 687, 689, 691, 696, 699, 700, 702, 706, 713, 720, 721, 723, 729, 734, 738, 745,
10 768, 772, 773, 775, 791, 798, 799, 823, 857, 898, 900, 901, 903, 914, 931, 933, 937, 941,
945, 948, 956, 965, 969, 983, 992, 993, 994, 999, 1003, 1005, 1009, 1010, 1011, 1019,
1028, 1035, 1037, 1052, 1061, 1062, and 1063

SEQ ID NOS: 157, 161, 163, 168, 197, 200, 205, 218, 221, 242, 250, 331, 334,
340, 412, 413, 414, 419, 425, 452, 453, 454, 456, 459, 462, 491, 591, 618, 622, 663, 665,
15 667, 670, 672, 690, 694, 695, 709, 759, 760, 761, 762, 767, 819, 820, 822, 826, 832, 846,
847, 860, 872, 873, 877, 881, 887, 908, 911, 913, 917, 919, 921, 936, 939, 940, 942, 944,
947, 951, 952, 955, 958, 959, 960, 964, 975, 977, 979, 986, 1023, 1027, 1034, 1038, 1043,
1044, 1049, and 1051;

SEQ ID NOS: 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 164, 165, 166,
20 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184,
185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220,
221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238,
240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257,
25 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275,
276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293,
294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311,
312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329,
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30 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367,
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427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444,
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536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553,
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10 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590,
591, 592, 593, 594, 595, 597, 598, 599, 600, 601, 602, 604, 605, 606, 607, 608, 609, 610,
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15 668, 669, 670, 671, 673, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687,
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707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724,
725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742,
743, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761,
20 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780,
781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798,
799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 810, 811, 812, 813, 814, 815, 816, 817,
818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 836,
837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854,
25 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872,
873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 886, 887, 888, 889, 890, 891,
892, 893, 894, 895, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910,
911, 912, 913, 914, 915, 916, 917, 918, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930,
931, 932, 933, 934, 935, 936, 937, 939, 940, 941, 942, 943, 944, 945, 946, 947, 949, 950,
30 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968,
969, 970, 971, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987,
988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1002, 1003, 1004, 1005,

1006, 1008, 1009, 1010, 1011, 1012, 1013, 1015, 1016, 1017, 1018, 1019, 1020, 1021,
1022, 1023, 1024, 1025, 1026, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036,
1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050,
1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, and 1064;

5 and any and all combinations of the foregoing sets.

The polypeptide translation products of those polynucleotide sequences form sets of preferred olfactory receptor polypeptides, as well as any and all combinations of those polypeptide sets. The preferred sets of polypeptide translation products, and any and all combinations thereof, are also preferred sets for use as libraries of olfactory receptors for
10 scent analysis.

Scent Fingerprinting

It will be appreciated that in many instances, analysis of a scent (whether in terms of
15 receptor primary scent components, receptor quasi-primary scent components, receptor complex scent components, or other scent representations) is of great utility in and of itself, in addition to the utility of that analysis in scent re-creation. Thus, another embodiment of the invention encompasses "scent fingerprinting," which comprises analysis of a scent profile when re-creation of that scent may not be necessary or desirable. The distinction between scent
20 profiling, as defined above, and scent fingerprinting, as defined here, is that scent profiling is a representation of a scent relative to a mammalian olfactory system in such a manner as to provide useful information about the interaction of the scent with that olfactory system, such as sufficient information to enable re-creation of the scent from receptor primary scent components. In contrast, scent fingerprinting can, but does not necessarily, provide such
25 information.

Various applications and examples of scent fingerprinting can include, but are not limited to, the following illustrative situations. Natural gas is widely used as a heating and fuel supply, but is in itself odorless. Utility companies routinely add small amounts of odorants such as mercaptans to allow detection of natural gas leaks in households. Should a leak occur
30 at an unattended site, however, potentially dangerous quantities of natural gas can accumulate. In such areas, a device which can recognize odorants would be useful.

Another use of scent fingerprinting is quality control of a manufacturing process. Many food items, such as freshly-baked bread and pastries, sauces, and cheeses, have distinct

odors. A manufacturer can record a scent fingerprint for a given food item, e.g. spaghetti sauce for packaging in jars. The quality of the product can then be monitored at various stages in manufacture and storage, and deviations from the established scent fingerprint can be used to alert the manufacturer to problems in manufacture or storage. Quality control scent fingerprints are not limited to food items, but can be used in any circumstance where a volatile component of an item of manufacture can be used as a quality control indicator, e.g., perfume, deodorants, solvent mixtures, etc.

While scent fingerprints need not be meaningful in terms of a mammalian olfactory system, it will be readily appreciated that a scent profile, which does represent a scent in a manner relevant to an olfactory system, is a special type of scent fingerprint. Additionally, the response of a device which yields a scent fingerprint of an odor (such as the "artificial nose" described in U.S. Pat. Nos. 5,571,401, 5,698,089, 5,788,833, 5,891,398 and 5,911,872) can be calibrated against the response of a mammalian olfactory system in order to transform the scent fingerprint generated by the device into a true scent profile which can be utilized to re-create an odor using receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components. The invention encompasses such data transformations.

Scent Editing

Representation of a scent as a scent profile provides the capability of editing the scent. A scent profile which represents a scent in terms of perceptive primary scent components is the most straightforward representation to edit. An example is the perceptive complex primary scent of "burned pizza" comprised of perceptive primary scent components of sausage, cheese, tomato sauce, and burned dough. In order to edit the scent to provide a more pleasant re-creation, the perceptive primary scent component of burned dough would simply be eliminated.

Other scent profiles can be edited using a knowledge of the perception of a particular components. Using our six-receptor example, suppose that the (1, 0, 0, 0, 1, 0) receptor complex scent component is known to provide an unpleasant aspect of the scent, while the (0, 1, 1, 1, 0, 1) component is known to provide the pleasant aspect of the scent. The first complex scent component can be omitted from the edited scent profile, leaving (0, 1, 1, 1, 0, 1) as the edited scent profile. (This would also alter the index values for scent re-creation, from 1 and 1, to 0 and 1.) More complex editing situations can be manipulated using computer algorithms as discussed above.

Individual scent components can be omitted, added, weakened, or intensified, and different scent components can be adjusted in different manners or degrees, depending on the desired result. The editing can be done interactively, with each edited scent emitted by the emitter module for evaluation by the user, or can be done automatically, with
 5 removal/weakening or addition/intensifying of particular components specified in advance, on either an absolute scale or relative to other components.

The following examples are presented to illustrate, but not to limit, the invention.

EXAMPLES

10 **Example 1: Isolation of human olfactory receptor cDNAs**

Total RNA was extracted from human olfactory epithelium and polyA⁺ RNA was obtained by oligo-dT selection. This RNA served as template for cDNA synthesis using reagents from the SMART cDNA Library construction kit (Clontech K1051-1; Palo Alto, CA). The Superscript IITM reverse transcriptase (Life Technologies, Gaithersburg, MD)
 15 was used for first-strand synthesis.

Double-stranded cDNA was passed through a Chroma-Spin⁺ STE-100 column (Clontech) to remove unreacted primers and cDNA fragments shorter than 100 nucleotides. The olfactory epithelial cDNA population was then subjected to amplification using primers homologous to conserved regions in GPCRs. The first primer set was homologous
 20 to transmembrane segment 2 (TM2) and the second set was homologous to TM 7.5. The TM2 primer set contained 32 oligonucleotides, representing all possible nucleotide sequences capable of encoding the TM2 amino acid sequence motif P-M-Y-F/L-F/Y-F/L, and designed to be non-degenerate at their 3' ends. Sequences of the TM2 primers are as follows:

25

	CCN ATG TAY TTN CTC CTA	SEQ ID NO: 74
	CCN ATG TAY TTN CTC CTC	SEQ ID NO: 75
	CCN ATG TAY TTN CTC CTG	SEQ ID NO: 76
	CCN ATG TAY TTN CTC CTT	SEQ ID NO: 77
30	CCN ATG TAY TTN CTC TTA	SEQ ID NO: 78
	CCN ATG TAY TTN CTC TTC	SEQ ID NO: 79
	CCN ATG TAY TTN CTC TTG	SEQ ID NO: 80
	CCN ATG TAY TTN CTC TTT	SEQ ID NO: 81
	CCN ATG TAY TTN CTT CTA	SEQ ID NO: 82
35	CCN ATG TAY TTN CTT CTC	SEQ ID NO: 83
	CCN ATG TAY TTN CTT CTG	SEQ ID NO: 84

	CCN ATG TAY TTN CTT CTT	SEQ ID NO: 85
	CCN ATG TAY TTN CTT TTA	SEQ ID NO: 86
	CCN ATG TAY TTN CTT TTC	SEQ ID NO: 87
	CCN ATG TAY TTN CTT TTG	SEQ ID NO: 88
5	CCN ATG TAY TTN CTT TTT	SEQ ID NO: 89
	CCN ATG TAY TIN TTC CTA	SEQ ID NO: 90
	CCN ATG TAY TTN TTC CTC	SEQ ID NO: 91
	CCN ATG TAY TTN TTC CTG	SEQ ID NO: 92
	CCN ATG TAY TTN TTC CTT	SEQ ID NO: 93
10	CCN ATG TAY TTN TTC TTA	SEQ ID NO: 94
	CCN ATG TAY TTN TTC TTC	SEQ ID NO: 95
	CCN ATG TAY TTN TTC TTG	SEQ ID NO: 96
	CCN ATG TAY TTN TTC TTT	SEQ ID NO: 97
	CCN ATG TAY TTN TTT CTA	SEQ ID NO: 98
15	CCN ATG TAY TTN TTT CTC	SEQ ID NO: 99
	CCN ATG TAY TTN TTT CTG	SEQ ID NO: 100
	CCN ATG TAY TTN TTT CTT	SEQ ID NO: 101
	CCN ATG TAY TTN TTT TTA	SEQ ID NO: 102
	CCN ATG TAY TTN TTT TTC	SEQ ID NO: 103
20	CCN ATG TAY TTN TTT TTG	SEQ ID NO: 104
	CCN ATG TAY TTN TTT TTT	SEQ ID NO: 105

The TM7.5 primer set was designed to contain the reverse complement of all sequences capable of encoding the TM7.5 amino acid sequence motif P-F/L/I/V-I/V-F/Y-S/T-L. The sequences of the TM7.5 primers are as follows:

	YYTNGTNYTNRYNCYGATANATNATNGGRTT	SEQ ID NO: 106
	YTRTTNCKNAGNWRTANATRAANGGRTT	SEQ ID NO: 107
	TCYTTRTTNCKNAGNGWRTANAYNASNGGRTT	SEQ ID NO: 108
30	TCNTSRTTNCKNARNsARTANATNATNGGRTT	SEQ ID NO: 109
	RTTNCKNARNsWRTANATRAANGGRTT	SEQ ID NO: 110

Reagents and enzymes for amplification were from the Advantage cDNA amplification kit (Clontech). A primary amplification reaction was constructed as follows:

35	5 µl olfactory epithelial cDNA (10-20 µg/ml)
	5 µl 10X PCR reaction buffer (Clontech)
	1 µl TM2 primer set (10 µM)
	1 µl TM7.5 primer set (10 µM)
	1 µl dNTP mix (10 mM each dATP, dCTP, dGTP, dTTP)
40	36 µl PCR-grade H ₂ O
	1 µl Advantage polymerase mix (Clontech)

Amplification was conducted in a PE 480 thermal cycler, using 28 cycles of 95°C for 15 sec, 45°C for 45 sec and 72°C for 2 min. After cycling, the amplification mixture was treated for 1 hour at 37°C with 10 Units of BspEI and 10 Units of PstI restriction enzymes, to degrade non-specific amplification products.

5 The primary amplification products were size-fractionated by agarose gel electrophoresis, and amplification products having a length between 600 and 800 base pairs were selected for secondary amplification.

10 The secondary amplification reaction was conducted identically to the primary amplification reaction, except that the size-selected primary amplification product was used as template. Secondary amplification reactions containing products which generated a specific gel band of between 600 and 800 base pairs were extracted once with phenol/chloroform and once with chloroform, and nucleic acids were precipitated from the reactions by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and
15 resuspended in 15 µl distilled water. After the precipitate dissolved, 3 µl loading dye was added, and the sample was subjected to electrophoresis on a 1.0% low-melting agarose gel containing ethidium bromide. Electrophoresis was conducted at 60V for approximately 40 min, with a 1 kb marker in adjoining lanes.

20 Following electrophoresis, the gel was illuminated with long-wavelength ultraviolet light, and the band was excised from the gel. The gel slice was placed in a 0.5 ml tube, and the tube was heated at 68°C for 15 min. The temperature of the tube was then equilibrated at 45°C. (This is conveniently accomplished in a thermal cycler.) AgarACE™ (Promega) was then added to the tubes, according to the manufacturer's instructions, and incubation at 45°C was continued for 15 min. As a general rule, 2 µl of enzyme per 50 µl of gel slice is
25 adequate. Following AgarACE™ digestion, the digestion mixture was extracted with phenol/chloroform according to the manufacturer's instructions, and nucleic acids were precipitated by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and resuspended in 5 µl distilled water.

30 Gel-purified amplification products were cloned using the TOPO XL PCR Cloning Kit (Invitrogen) according to the manufacturer's instructions. After cloning, individual

colonies were selected at random for nucleotide sequence analysis of the inserts, using procedures for sequence determination that are well-known to those of skill in the art.

Example 2: Use of olfactory receptor polypeptides for screening

5 Components of a scent are identified by determining the interaction between one or more potential odorant molecules and one or more OR polypeptides. For example, if a known original scent involves binding to a particular set of ORs, any subsequent set of molecules which bind to that same set of ORs and stimulate or inhibit the response of the ORs to the same extent as the original scent is capable of re-creating that original scent. If
10 each of the subsequent set of molecules interacts with one and only one OR, then the set of molecules is composed of receptor primary scent components. In similar fashion, scents which involve binding of multiple ORs can be recreated by identifying a molecule, or combination of molecules, which binds to that particular set of ORs.

 Binding of molecules to ORs is determined by a number of methods that are well-
15 known in the art including, but not limited to, in vitro and in silico methods as described herein. Binding of molecules to ORs can also be determined or approximated by using quantitative structure-activity relationships as described herein.

Example 3: Identification of agonists and antagonists of olfactory receptors

20 Interaction of an odorant with a particular OR embedded in the membrane of an olfactory neuron will activate a signaling cascade within the neuron, ultimately resulting in the perception of a particular smell. A molecule, produced for example by combinatorial chemistry, which activates a similar or identical signaling cascade, will induce the perception of the same smell. Such a molecule would be considered a OR agonist. An OR
25 agonist, once identified, can be used as a probe to identify additional agonists, as well as antagonists, of that particular OR.

 Assays for the activation and the end product(s) of signaling cascades are known in the art. For example, direct Ca^{++} imaging can be employed, using either dye -labeled Ca^{++} or dyes that are sensitive to Ca^{++} concentration. Such dyes, and techniques for their use,
30 are available from, for example, Molecular Dynamics (Sunnyvale, CA) and Molecular Probes (Eugene, OR).

Because ORs are transmembrane proteins, identification of agonists and/or antagonists for a particular OR require that the OR is present either in a living cell or in a membrane preparation.

In one embodiment of a method for the determination of OR agonists or antagonists, a known OR agonist is labeled *in situ*, or is resynthesized with an attached label, and is bound to an OR. The effect of various test molecules on the binding of the labeled OR agonist is then determined. Labeling of an OR agonist is accomplished by any of a number of methods that are known to those of skill in the art including, but not limited to, various fluorescent labels (for example, chemical fluorochromes or green fluorescent protein). Binding of the OR agonist is measured by any of a number of competitive binding assays, as are known in the art. A test molecule that displaces the agonist from the OR (*i.e.*, reduces the binding of the agonist) is identified as a candidate agonist or antagonist of the particular OR. In a subsequent experiment, the candidate molecule is bound to the OR, and the effect on the signaling cascade induced by the original agonist is determined. A similar or higher level of activation is indicative of an agonist; while a reduced level of activation of the signaling cascade reflects the action of an antagonist.

In additional embodiments of the displacement assay, an unlabeled agonist is used, and its degree of binding is determined by mass spectrometry. *See*, for example, U.S. Patent No. 5,894,063; U.S. Patent No. 5,719,060; and Wei *et al.* (1999) *Nature* 399:243-246.

In another embodiment, fluorescent microparticles ("beads"), which can be separated by flow cytometry, are used to identify OR agonists and antagonists. Such beads are available, for example, from Luminex (Austin, TX). Multiple different ORs are attached to the beads, wherein each distinct color of bead is associated with a particular OR. The collection of beads, containing different ORs, is exposed to a test molecule or a collection of test molecules, such as can be synthesized by combinatorial chemistry, and binding of the test molecule(s) is determined, for example, by use of a labeled ligand of the test molecule(s). The beads are sorted according to their color by flow cytometry. Correlation of test molecule binding with bead color allows the determination of test molecules capable of binding to the OR. Agonist or antagonist function of an OR binding molecule is determined by methods described *supra*.

Example 4: Summary of search parameters for homology searches

Step 1: (masking) rempolyatmask raw sequence on -NONE- [?] with remAT_moderate (15) . Continue to step 2.

Step 2: (masking) mask masked sequence from step 1 on RepBase [N] with

5 mask_moderate (85) . Continue to step 3.

Step 3: (masking) mask masked sequence from step 2 on VecBase [N] with

mask_moderate (85) . Continue to step 4.

Step 4: blastn masked sequence from step 3 on NR-Nuc [N] with blastn_10_hits (V=10

B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 5. Otherwise, stop.

10 Step 5: blastx masked sequence from step 3 on NR-Pro [P] with blastx_10_hits (V=10

B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 6. Otherwise, stop.

Step 6: blastn masked sequence from step 3 on GB_CurAwareness-Nuc [N] with

blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step

7. Otherwise, stop.

15 Step 7: blastx masked sequence from step 3 on GB_CurAwareness-Pro [P] with

blastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step

8. Otherwise, stop.

Step 8: tblastx masked sequence from step 3 on NR-Nuc [N] with tblastx_10_hits (V=10

B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 9. Otherwise, stop.

20 Step 9: blastn masked sequence from step 3 on EST [N] with blastn_10_hits (V=10 B=10) .

If the P/Z score is $> 1.0E-50$, or no hits are found go to step 10. Otherwise, stop.

Step 10: blastn masked sequence from step 3 on STS [N] with blastn_10_hits (V=10 B=10)

. Stop.

25

Example 5: Summary of search results

Step	Program	Database	Score	Sequences By Best Hit's Score				No Hits	Run	Not Finished	Not Run
1	rempolyat mask	-NONE-[P]	P/Z/E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0
2	mask	RepBase[N]	P/Z/E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0
3	mask	VecBase[N]	P/Z/E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0
4	blastn	NR-Nuc[N]	P/Z/E	46	< 1.0E-20 <=	28		0	74	0	0
5	blastx	NR-Pro[P]	P/Z/E	16	< 1.0E-20 <=	34		0	50	0	24
6	blastn	GB_CurAwareness-Nuc[N]	P/Z/E	17	< 1.0E-20 <=	31		0	48	0	26
7	blastx	GB_CurAwareness-Pro[P]	P/Z/E	13	< 1.0E-20 <=	28		2	43	0	31
8	tblastx	NR-Nuc[N]	P/Z/E	14	< 1.0E-20 <=	29		0	43	0	31
9	blastn	EST[N]	P/Z/E	10	< 1.0E-20 <=	33		0	43	0	31
10	blastn	STS[N]	P/Z/E	5	< 1.0E-20 <=	33		0	38		

5

Example 6. Datamining and analysis from GenBank

Datamining. A datamining pipeline was built to detect all available OR-like sequences in the public databases and to update the results as new database versions are released. tblastn (Altschul et al., 1997) was used to compare amino acid query sequences to the non-redundant version of GenBank (partitions nt, htg and est_human, all updated to August 6th, 2000), with a non-stringent expectation value cutoff of 1e-4. The queries used included 96 curated OR sequences representing all known families (SEQ ID NO:2651 through SEQ ID NO:2747) and 249 additional HORDE entries (SEQ ID NO:2402 through SEQ ID NO:2650). In a second round 105 newly mined mouse genes (SEQ ID NO:2296 through SEQ ID NO:2401) and 344 newly mined human genes (SEQ ID NO:2009 through SEQ ID NO:2295) were used as additional queries (all datasets are available

electronically). All resulting database entries were catalogued by species and subdivided into four types: mRNA, EST, DNA and genomic, the latter including entries annotated with keyword HTGS_PHASE1-3, or with length at least 10 kb. Low-pass genomic sampling sequences were ignored (keyword HTGS_PHASE0). In addition, a set of 132 olfactory sequence tag (OST) sequences was used. All sequences used were split into contigs according to annotation or, where unavailable, according to runs of at least 50 Ns. All resulting contigs were analyzed for interspersed repeats using RepeatMasker (Smit and Green, 1997). Subcontigs were defined as segments between interspersed repeats, ignoring simple repeats and low-complexity regions.

10. *Localization of genomic clones.* The University of Santa Cruz (UCSC) Working Draft Sequence ("golden path", <http://genome.ucsc.edu>) presents a first tentative assembly of the finished and draft human genomic sequence based on the WUSTL clone map (<http://genome.wustl.edu/gsc>). The "golden path" data was used to assign a coordinate to each finished or unfinished genomic clone, in Mb from the p telomere. In parallel, the
15 Unified DataBase (UDB) was used to assign similar Mb coordinates to the clones, based on their marker contents (Chalifa-Caspi et al., 1998). The two maps are largely colinear, and were integrated based on the coordinates of clones that could be localized in both. Clones for which no coordinate could be obtained by either method were assigned a chromosome according to UDB, by sequence similarity to another mapped clone, by annotation, or by e-
20 PCR (Schuler, 1997).

Detection of OR sequences. Each subcontig was compared using FASTY (Pearson et al., 1997) to a curated set of OR protein sequences from several species, yielding a conceptual translation product. The possibility of a pseudogene being disrupted by the insertion of interspersed repeats was taken into account, with the two or more resulting
25 parts being therefore located in different subcontigs. Such compatible candidate sequences were automatically joined into a combined reconstructed pseudogene. Whenever possible, all resulting sequences were trimmed or extended to use a suitable ATG codon for initiation and to end at a stop codon, but avoiding those stop codons that yield products shorter than 275 amino acids. The sequences were finally split into OR or non-OR by comparing them
30 to previously recognized OR sequences and to a non-redundant database of non-OR GPCRs which we extracted from Swiss-Prot. To be automatically classified as an OR, a

new sequence has to be at least 40% identical over at least 100 amino acids to another OR. A more stringent cutoff (50%) was required for shorter sequences.

Definition of OR genes. A given gene could be represented in more than one overlapping genomic clone. Such redundancy was removed by considering two sequences as representing the same gene, if they are in the same chromosome, located in clones less than 300 kb apart and at least 99% identical at the nucleotide level. An exception to this rule is when two genes coappear in the same clone, in which case they were considered to be distinct genes. Sequences localized to a chromosome but without a coordinate were only compared to other sequences within that chromosome, and finally those sequences lacking a chromosomal assignment were compared to the rest, applying only the criterion of sequence similarity. For each resulting gene with more than one constituent sequence, a consensus nucleotide sequence was created after multiple alignment by ClustalW (Higgins et al., 1996) using the fast comparison parameter. This was followed by conceptual translation and end trimming to suitable start and stop codons, as above. Genes with length at least 275 amino acids without frame disruptions (frameshifts, in-frame stop codons or disrupting interspersed repeats) were considered to be full-length and apparently intact. For partial sequences without frame disruptions no statement could be made on their apparent functionality, except when the partial sequences were observed in the genome as such, in which case they were considered to be pseudogenes. Finally, each OR gene was assigned a family and subfamily by amino acid sequence similarity to previously classified OR genes.

The references cited in this example are: Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D. J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25: 3389-402; Chalifa-Caspi, V., Prilusky, J. and Lancet, D. (1998) The Unified Database. Weizmann Institute of Science, Bioinformatics Unit and Genome Center (Rehovot, Israel). World Wide Web URL: bioinformatics.weizmann.ac.il/udb; Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol* 266: 383-402; Pearson, W. R., Wood, T., Zhang, Z. and Miller, W. (1997) Comparison of DNA sequences with protein sequences. *Genomics* 46: 24-36; Schuler, G. D. (1997) Sequence mapping by electronic PCR. *Genome Res* 7: 541-50; and Smit, A. F.

A. and Green, P. (1997) RepeatMasker at URL: repeatmasker.genome.washington.edu/cgi-bin/RM2_req.pl.

5 Tables 1 and 2 contain additional information regarding SEQ ID NO. 153 to SEQ ID NO. 1085. The explanation of the entries in Tables 1 and 2 is as follows:

Symbol: The Human Genome Organization gene symbol, as allotted by a procedure to be published soon. OR = Olfactory Receptor, numeral to the immediate right - family designation, capital letters - subfamily designation, rightmost numeral - individual gene within subfamily, n appearing when such number is not assigned yet; P = Pseudogene.

10 All ORs within a family share at least 40% protein sequence identity.

All ORs within a subfamily share at least 60% protein sequence identity.

HORDE: The H serial number within the Human Olfactory Receptor Data Exploratorium (URL bioinfo.weizmann.ac.il/HORDE). The numeral 38 represents the HORDE build (version), gxxx is the individual gene number.

15 Digi: Appearance of a DSnn serial number here means that the sequence has been PCR-amplified from human olfactory epithelial cDNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. See separate page for explanations on the analysis of the DS entries.

OST: OSTnnn is the serial number of the sequence in the Olfactory Sequence Tag collection in the Lancet laboratory (URL bioinfo.weizmann.ac.il/HORDE). Appearance here means that the sequence has been PCR-amplified from human genomic DNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. There are a total of 112 OST sequences.

25 Trivial name: One or more aliases given to the same gene by different laboratories. Many of the trivial names are of the form ORnn-xx, whereby nn is a chromosome number and xx is an arbitrary numerical identifier.

Tran: (transcribed) Plus appears if the entry was sequenced from cDNA, or was found in the Expressed Sequence Tags (EST) databases. Plus also appears if in the public databases the gene was annotated as mRNA.

30 Int.: (intact) "Yes" indicates that the gene may be intact, as there are no obvious sequence frame disruptions. "Put" (putative) indicates the same, except that the known sequence is short, hence there may be disruptions in the unsequenced segments. "Pol"

indicates a polymorphism between intact and pseudogenic alleles. When no word appears, this indicates a pseudogene.

E: (Extent) FL indicates that the Full Length sequence is known (typically 310 ± 30 amino acids).

5 D: The number of sequence disruptions in the known sequence of a pseudogene.

C: The human chromosomal location of the OR gene, assigned as described under Mb coord.

Mb coord: The location of the OR gene within a human chromosome, in megabase units, beginning at the p-telomere and ending at the q-telomere, computed based on integrating information from Unified Database (URL is bioinfo.weizmann.ac.il/udb) and the University of California Santa Cruz (URL is genome.ucsc.edu).

CDR: The 17 amino acids suggested to line the odorant ligand binding pocket, delineated by the extracellular 2/3 of transmembrane helices 3,4 and 5. The assignment is based on an algorithm at URL bioinformatics.weizman.ac.il/HORDE/humanGenes/CDR.html.

%: (% id) The percent protein identity between the human sequence in the current line and the known rodent (rat or mouse) OR sequence to which it bears the highest similarity.

S: (Species) Rat (R) or mouse (M).

20 Acc: The Genbank accession number of the clone that contains the rodent sequence.

Range: The positions x ... y of the first and last bases within the rodent which constitute the OR coding region. If $x > y$ then the OR is on the reverse strand.

Table 1

25

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
153	OR10D3	H38g001			HSHTPCR09			
154	OR7EnP	H38g002						FL
155	OR1D5	H38g003		OST901	OR17-31	+	pol	FL
156	OR10NnP	H38g00						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
157	OR2F1	H38g00 5		OST902	OLF3;OR7-139;OR7-140	+	yes	FL
158	OR7EnP	H38g00 6						FL
159	OR8FnP	H38g00 7						FL
160	OR2Q1P	H38g00 8			DJ0669B10;OR7-2			FL
161	OR2W1	H38g00 9			AL035402- B;dJ88J8.1;hs6M1-15		yes	FL
162	OR7EnP	H38g01 0				+		FL
163	OR6B1	H38g01 1	DS119		OR7- 3;WUGSC:H_DJ0669B10. 3	+	yes	FL
164	OR10Kn	H38g01 2					yes	FL
165	ORnP	H38g01 3				+		FL
166	OR4F2P	H38g01 4			HS191N21;dJ191N21.4; hs6M1-11			FL
167	OR7EnP	H38g01 5						FL
168	OR1F2P	H38g01 6			OLFMF2	+	yes	FL
169	OR2P1P	H38g01 7			AL035402- A;dJ88J8.2;hs6M1-26			
170	OR7E43P	H38g01 8		OST903	OR4-116			FL
171	OR4F1	H38g01 9			HSDJ0609N19			FL
172	OR7E55P	H38g02 0		OST904	OR2DG;OR3.2			FL
173	OR13Dn	H38g02 1					yes	FL
174	OR4CnP	H38g02 2						FL
175	OR10D1P	H38g02 3		OST074	HSHTPCR03	+		FL
176	OR4Cn	H38g02					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
177	OR8GnP	H38g02 5						
178	OR13CnP	H38g02 6						FL
179	OR4CnP	H38g02 7						FL
180	OR13Cn	H38g02 8					yes	FL
181	OR4CnP	H38g02 9						
182	OR51Bn	H38g03 0					yes	FL
183	OR7E5P	H38g03 1		OST905	OR11-12			FL
184	OR13Cn	H38g03 2					yes	FL
185	OR4Sn	H38g03 3					yes	FL
186	OR51BnP	H38g03 4						FL
187	OR6JnP	H38g03 5						FL
188	OR51Bn	H38g03 6					yes	FL
189	OR7EnP	H38g03 7						FL
190	OR2An	H38g03 8					yes	FL
191	OR7E22P	H38g03 9			OR3.6;OR6DG			FL
192	OR7E4P	H38g04 0			OR11-11a			FL
193	OR7E66P	H38g04 1		OST906	OR3.3;OR3DG;hg630			FL
194	OR6Mn	H38g04 2					yes	FL
195	OR2ALnP	H38g04 3						
196	OR6MnP	H38g04 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
197	OR4D1	H38g04 5			AC005962-A;HSTPCR16	+	yes	FL
198	OR5D2P	H38g04 6		OST907	OR11-7a;OR912-91			FL
199	OR7E38P	H38g04 7		OST127	AC004967	+		FL
200	OR4D2	H38g04 8			AC005962-B		yes	FL
201	OR7E7P	H38g04 9			AC004967-A			FL
202	OR5AHnP	H38g05 0						
203	OR2U2P	H38g05 1			AL050339- B;dJ974I11.2;hs6M1- 23			FL
204	OR2U1P	H38g05 2			974I11;AL050339- C;dJ974I11.3;hs6M1- 24			FL
205	OR2H2	H38g05 3			AC006137- A;dJ271M21.2;hs6M1- 12		yes	FL
206	OR2H5P	H38g05 4		OST616	HS271M21;hs6M1-13			FL
207	OR2In	H38g05 5				+	yes	FL
208	OR11HnP	H38g05 6						FL
209	OR7EnP	H38g05 7				+		
210	OR9In	H38g05 8					yes	FL
211	OR2AFnP	H38g05 9						FL
212	OR13KnP	H38g06 1						FL
213	OR13Cn	H38g06 2					yes	FL
214	OR13Fn	H38g06 3					yes	FL
215	OR9Qn	H38g06 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
216	OR2TnP	H38g06 5						FL
217	OR4Kn	H38g06 6					yes	FL
218	OR2B8P	H38g06 7			dJ313I6.4;hs6M1-29P		yes	FL
219	OR2Tn	H38g06 8					yes	FL
220	OR4Kn	H38g06 9					yes	FL
221	OR2A4	H38g07 0			WUGSC:H_DJ0988G15.2	+	yes	FL
222	OR7EnP	H38g07 1						FL
223	OR4Kn	H38g07 2					yes	FL
224	OR13InP	H38g07 3						FL
225	OR7EnP	H38g07 4						FL
226	OR6Jn	H38g07 5					yes	FL
227	OR4Mn	H38g07 6					yes	FL
228	OR4VnP	H38g07 7						FL
229	OR6Xn	H38g07 8					yes	FL
230	OR51Gn	H38g07 9					yes	FL
231	OR6EnP	H38g08 0						FL
232	OR4NnP	H38g08 1						FL
233	OR6MnP	H38g08 2						FL
234	OR4Nn	H38g08 3					yes	FL
235	OR4Cn	H38g08 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
236	OR4KnP	H38g08 5						FL
237	ORnP	H38g08 6						
238	OR5D3	H38g08 7		OST908	OR11-8b;OR11-8c			
239	OR2G1P	H38g08 8	DS13;D S16	OST619	dJ974I11.4;hs6M1-25	+		FL
240	OR4Kn	H38g08 9					yes	FL
241	OR8BnP	H38g09 0						FL
242	OR2B2	H38g09 1			OR6-1;dJ193B12.4		yes	FL
243	OR7EnP	H38g09 2						FL
244	OR4KnP	H38g09 3						FL
245	OR2AD1P	H38g09 4			dJ25J6.1;hs6M1-8P			FL
246	OR1AAnP	H38g09 5						FL
247	OR1E3P	H38g09 6			OR17-210			FL
248	OR8BnP	H38g09 7						FL
249	OR5Hn	H38g09 8					yes	FL
250	OR1G1	H38g09 9		OST909	OR17-130;OR17-209	+	yes	FL
251	OR5HnP	H38g10 0						FL
252	ORnP	H38g10 1						
253	ORnP	H38g10 2						
254	OR4PnP	H38g10 3						FL
255	OR13Hn	H38g10 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
256	OR7D1P	H38g10 5		OST910	CIT-B-440L2;OR19- 131;OR19-A			FL
257	OR4KnP	H38g10 6						FL
258	OR7E24	H38g10 7		OST911	CIT-B-440L2;OR19-8	+		FL
259	OR51NnP	H38g10 8						FL
260	OR7E18P	H38g10 9		OST912	OR19-14;TPCR26	+		FL
261	OR7E19P	H38g11 0		OST913	HSCIT-B-440L2;OR19- 7;TPCR110	+		FL
262	OR7E41P	H38g11 1		OST914	OR11-20;hg84			FL
263	OR2R1	H38g11 2		OST058				FL
264	OR10ACn P	H38g11 3						FL
265	OR51Ln	H38g11 4					yes	FL
266	OR52JnP	H38g11 5						FL
267	OR9LnP	H38g11 6						
268	OR51PnP	H38g11 7						FL
269	OR5HnP	H38g11 8						FL
270	OR51An	H38g11 9					yes	FL
271	OR5HnP	H38g12 0						FL
272	ORnP	H38g12 1						
273	OR52En	H38g12 2					yes	FL
274	OR5Hn	H38g12 3					yes	FL
275	OR4CnP	H38g12 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	B
276	OR52En	H38g12 5					yes	FL
277	OR10Dn	H38g12 6					yes	FL
278	OR5HnP	H38g12 7						FL
279	OR13An	H38g12 8					yes	FL
280	OR5HnP	H38g12 9						FL
281	OR5Kn	H38g13 0					yes	FL
282	OR7EnP	H38g13 1						FL
283	OR4DnP	H38g13 2						FL
284	OR2ARnP	H38g13 3						
285	OR7E29P	H38g13 4		OST032				FL
286	OR4CnP	H38g13 5						FL
287	OR5PnP	H38g13 6						FL
288	OR7EnP	H38g13 7						FL
289	OR56An	H38g13 8					yes	FL
290	OR56AnP	H38g13 9						
291	OR5Pn	H38g14 0					yes	FL
292	OR7E53P	H38g14 1		OST915	OR3-142;OR3-143			FL
293	OR5Pn	H38g14 2					yes	FL
294	OR52Ln	H38g14 3					yes	FL
295	OR5E1	H38g14 4			HSTPCR24	+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
296	OR56AnP	H38g14 5						
297	OR4KnP	H38g14 6						
298	OR52Ln	H38g14 7					yes	FL
299	OR7EnP	H38g14 8						
300	OR52XnP	H38g14 9						FL
301	ORnP	H38g15 0						
302	OR56An	H38g15 1					yes	FL
303	OR56AnP	H38g15 2						
304	OR1R1P	H38g15 3			OR17-1			FL
305	OR52EnP	H38g15 4						FL
306	OR51AnP	H38g15 5						FL
307	OR51An	H38g15 6					yes	FL
308	OR4CnP	H38g15 7						FL
309	OR52JnP	H38g15 8						FL
310	OR4RnP	H38g15 9						
311	OR52Jn	H38g16 0					yes	FL
312	OR4CnP	H38g16 1						FL
313	OR51AnP	H38g16 2						FL
314	OR7EnP	H38g16 3						FL
315	OR5MnP	H38g16 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
316	OR10ABn P	H38g16 5						FL
317	OR52SnP	H38g16 6						FL
318	OR5Mn	H38g16 7					yes	FL
319	OR10Sn	H38g16 8					yes	FL
320	OR5MnP	H38g16 9						FL
321	OR10Gn	H38g17 0					yes	FL
322	ORnP	H38g17 1						FL
323	OR5MnP	H38g17 2						FL
324	OR10GnP	H38g17 3						
325	OR10TnP	H38g17 4						FL
326	ORnP	H38g17 5						
327	OR10RnP	H38g17 6						FL
328	OR5MnP	H38g17 7						FL
329	OR7EnP	H38g17 8						FL
330	OR10Tn	H38g17 9					yes	FL
331	OR1E1	H38g18 0	DS37;D S43;DS 46	OST916	HGMP07I;OR17-2;OR17- 32	+	yes	FL
332	OR5BKnP	H38g18 1						
333	OR5MnP	H38g18 2						FL
334	OR3A3	H38g18 3		OST917	OR17-137;OR17- 16;OR17-201	+	yes	FL
335	OR10ADn P	H38g18 4	DS10			+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
336	OR10Rn	H38g18 5				+	yes	FL
337	OR5TnP	H38g18 6						FL
338	OR4GnP	H38g18 7						FL
339	OR6Yn	H38g18 8					yes	FL
340	OR1E2	H38g18 9		OST918	OR17-135;OR17-93	+	yes	FL
341	OR8Hn	H38g19 0					yes	FL
342	OR4Fn	H38g19 1					yes	FL
343	OR10Kn	H38g19 2					yes	FL
344	OR7LnP	H38g19 3						
345	OR8InP	H38g19 4						FL
346	OR10RnP	H38g19 5						
347	OR2AFnP	H38g19 6						FL
348	OR8Kn	H38g19 7					yes	FL
349	ORnP	H38g19 8						
350	OR8KnP	H38g19 9						FL
351	OR51Hn	H38g20 0					yes	FL
352	OR7EnP	H38g20 1						FL
353	ORnP	H38g20 2						
354	OR5BMnP	H38g20 3						FL
355	OR10GnP	H38g20 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
356	OR2Yn	H38g20 5					yes	FL
357	OR10DnP	H38g20 6						FL
358	OR3BnP	H38g20 7						FL
359	OR8Dn	H38g20 8					yes	FL
360	OR5RnP	H38g20 9						
361	OR10Gn	H38g21 0					yes	FL
362	OR5BDnP	H38g21 1						FL
363	OR5ALnP	H38g21 2						FL
364	OR52HnP	H38g21 3						
365	OR10Gn	H38g21 4					yes	FL
366	OR5Mn	H38g21 5					yes	FL
367	OR51Mn	H38g21 6					yes	FL
368	OR6Tn	H38g21 7	DS15;D S146;D S147			+	yes	FL
369	OR6DnP	H38g21 8						FL
370	OR4B1	H38g21 9		OST208			yes	FL
371	OR5ALnP	H38g22 0						FL
372	OR51Qn	H38g22 1					yes	FL
373	OR4Dn	H38g22 2					yes	FL
374	OR52Nn	H38g22 3					yes	FL
375	OR4Xn	H38g22 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
376	OR8Jn	H38g22 5					yes	FL
377	OR51JnP	H38g22 6						FL
378	OR10Gn	H38g22 7					yes	FL
379	OR52En	H38g22 8					yes	FL
380	OR4Xn	H38g22 9					yes	FL
381	OR10A2	H38g23 0	DS5;DS 53;DS5 6	OST363		+		FL
382	OR5Mn	H38g23 1					yes	FL
383	OR52En	H38g23 2					yes	FL
384	OR8Kn	H38g23 3					yes	FL
385	OR10An	H38g23 4	DS55			+	yes	FL
386	OR8LnP	H38g23 5						FL
387	OR5BPnP	H38g23 6						
388	OR52Nn	H38g23 7					yes	FL
389	ORnP	H38g23 8						
390	OR8JnP	H38g23 9						FL
391	OR5Mn	H38g24 0					yes	FL
392	OR52En	H38g24 1					yes	FL
393	OR5Tn	H38g24 2					yes	FL
394	OR52NnP	H38g24 3						FL
395	OR4B2P	H38g24 4		OST919	hg449			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
396	OR51KnP	H38g24 5						FL
397	OR52QnP	H38g24 6						FL
398	OR4Fn	H38g24 7					yes	FL
399	OR11MnP	H38g24 8						
400	OR52Nn	H38g24 9					yes	FL
401	OR56An	H38g25 0					yes	FL
402	OR5AWnP	H38g25 1						FL
403	OR52Nn	H38g25 2					yes	FL
404	ORnP	H38g25 3						
405	OR52EnP	H38g25 4						FL
406	OR5BHnP	H38g25 5						FL
407	OR4QnP	H38g25 6						FL
408	OR51En	H38g25 7					yes	FL
409	OR11KnP	H38g25 8						FL
410	OR12D1P	H38g25 9			AC004174- B;dJ994E9.7;hs6M1-19			FL
411	OR4NnP	H38g26 0				+		FL
412	OR11A1	H38g26 1			AC004174- A;dJ994E9.6;hs6M1-18	+	yes	FL
413	OR10C1	H38g26 2			AC004174;dJ994E9.5;h s6M1-17	+	yes	FL
414	OR2H1	H38g26 3	DS114		OLFR42A-9004-14;OR6- 2;dJ994E9.4;hs6M1-16	+	yes	FL
415	OR9RnP	H38g26 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
416	OR4FnP	H38g26 5						
417	OR7D4	H38g26 6		OST920	OR19-B;hg105			FL
418	OR7E25P	H38g26 7		OST921	CIT-B-440L2;OR19-C			FL
419	OR2D2	H38g26 8			OR11-610		yes	FL
420	OR10An	H38g26 9					yes	FL
421	OR2WnP	H38g27 0				+		
422	OR7E16P	H38g27 1		OST922	CIT-B-440L2;OR19-133;OR19-9			FL
423	OR52Pn	H38g27 2					yes	FL
424	OR6AnP	H38g27 3						FL
425	OR7D2	H38g27 4	DS70;D S73	OST923	HTPCRHO3;OR19-4	+	yes	FL
426	OR52UnP	H38g27 5						FL
427	OR2AGn	H38g27 6					yes	FL
428	OR7G3	H38g27 7		OST085			yes	FL
429	OR56BnP	H38g27 8						FL
430	OR2AGnP	H38g27 9						FL
431	OR56Bn	H38g28 0					yes	FL
432	OR6AnP	H38g28 1						FL
433	OR4FnP	H38g28 2						FL
434	OR6Wn	H38g28 3					yes	FL
435	OR4Mn	H38g28 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
436	OR52YnP	H38g28 5						
437	OR11HnP	H38g28 6						FL
438	OR9An	H38g28 7					yes	FL
439	OR5Mn	H38g28 8					yes	FL
440	OR6Vn	H38g28 9					yes	FL
441	OR4Nn	H38g29 0				+	yes	FL
442	OR51AnP	H38g29 1						FL
443	OR9PnP	H38g29 2						
444	OR4H6P	H38g29 3			OR15-71;OR15-82			FL
445	OR51FnP	H38g29 4						FL
446	OR7E1P	H38g29 5			AC004923			FL
447	OR51Tn	H38g29 6					yes	FL
448	OR2Vn	H38g29 7					yes	FL
449	OR51HnP	H38g29 8						FL
450	OR51An	H38g29 9					yes	FL
451	OR2AInP	H38g30 0						FL
452	OR2F2	H38g30 1			OR7- 1;WUGSC:H_DJ0669B10. 1		yes	FL
453	OR1F12	H38g30 2			dJ313I6.5;hs6M1-35P		yes	FL
454	OR7G1P	H38g30 3			OR19-15		yes	FL
455	OR7G2	H38g30 4		OST260			yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
456	OR1M1	H38g30 5		OST924	OR19-6		yes	FL
457	OR51UnP	H38g30 6						
458	OR52Hn	H38g30 7					yes	FL
459	OR1F1	H38g30 8		OST925	OLFMF; OR16-36; OR16- 37; OR16-88; OR16- 89; OR16-90	+	yes	FL
460	OR10PnP	H38g30 9						
461	OR4FnP	H38g31 0						FL
462	OR2T1	H38g31 1			OR1-25		yes	FL
463	OR7EnP	H38g31 2						FL
464	OR51Gn	H38g31 3					yes	FL
465	OR2Tn	H38g31 4					yes	FL
466	OR5BGnP	H38g31 5						
467	OR5WnP	H38g31 6						FL
468	OR51Sn	H38g31 7					yes	FL
469	OR5WnP	H38g31 8						
470	OR51AnP	H38g31 9						FL
471	OR5Dn	H38g32 0					yes	FL
472	OR7EnP	H38g32 1						FL
473	OR51Fn	H38g32 2					yes	FL
474	OR5Dn	H38g32 3					yes	FL
475	OR52Rn	H38g32 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
476	ORnP	H38g32 5						FL
477	OR7EnP	H38g32 6						FL
478	OR6Qn	H38g32 7					yes	FL
479	OR4Fn	H38g32 8					yes	FL
480	OR7EnP	H38g32 9						
481	OR7En	H38g33 0					yes	FL
482	OR4Nn	H38g33 1					yes	FL
483	OR2ASnP	H38g33 2						
484	OR11Hn	H38g33 3					yes	FL
485	OR2Tn	H38g33 4					yes	FL
486	OR2TnP	H38g33 5						
487	OR2AKnP	H38g33 6						FL
488	ORnP	H38g33 7						
489	OR5DnP	H38g33 8						FL
490	OR7EnP	H38g33 9						
491	OR5L2	H38g34 0			HSHTPCR16	+	yes	FL
492	OR5Dn	H38g34 1					yes	FL
493	ORnP	H38g34 2						
494	OR10Qn	H38g34 3					yes	FL
495	OR9MnP	H38g34 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
496	OR7E62P	H38g34 5		OST926	OR2-4;OR2-52;OR2- 53;OR2-75			FL
497	OR9LnP	H38g34 6						FL
498	OR7E46P	H38g34 7		OST379				FL
499	OR1S1	H38g34 8		OST034			yes	FL
500	OR5DnP	H38g34 9						
501	OR9InP	H38g35 0						FL
502	OR5Dn	H38g35 1					yes	FL
503	OR9QnP	H38g35 2						FL
504	OR51CnP	H38g35 3						
505	OR5WnP	H38g35 4						
506	OR9InP	H38g35 5						FL
507	OR51AnP	H38g35 6						FL
508	OR5L1	H38g35 7		OST262			yes	FL
509	OR7EnP	H38g35 8				+		
510	OR5BLnP	H38g35 9						
511	OR51En	H38g36 0					yes	FL
512	OR51Dn	H38g36 1					yes	FL
513	OR52In	H38g36 2					yes	FL
514	OR4KnP	H38g36 3	DS67			+		FL
515	OR52In	H38g36 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
516	OR4KnP	H38g36 5						FL
517	OR52MnP	H38g36 6						FL
518	ORnP	H38g36 7						
519	ORnP	H38g36 8						
520	ORnP	H38g36 9						FL
521	ORnP	H38g37 0						
522	ORnP	H38g37 1						
523	ORnP	H38g37 2						
524	ORnP	H38g37 3						
525	ORnP	H38g37 4						
526	OR6Pn	H38g37 5					yes	FL
527	OR7EnP	H38g37 6						FL
528	ORnP	H38g37 7						
529	OR7EnP	H38g37 8						FL
530	ORnP	H38g37 9						
531	OR10XnP	H38g38 0						FL
532	OR10Zn	H38g38 1					yes	FL
533	OR6KnP	H38g38 2						FL
534	OR6Kn	H38g38 3					yes	FL
535	OR1FnP	H38g38 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
536	OR1ABnP	H38g38 5						
537	OR52MnP	H38g38 6						FL
538	OR1XnP	H38g38 7						FL
539	OR4FnP	H38g38 8						
540	OR52MnP	H38g38 9						FL
541	OR2Vn	H38g39 0					yes	FL
542	OR2V1P	H38g39 1		OST265				FL
543	OR2Zn	H38g39 2					yes	FL
544	OR52KnP	H38g39 3				+		
545	OR10Hn	H38g39 4					yes	FL
546	OR2Dn	H38g39 5					yes	FL
547	OR7EnP	H38g39 6						
548	OR11GnP	H38g39 7						FL
549	ORnP	H38g39 8						
550	OR11Gn	H38g39 9					yes	FL
551	OR11HnP	H38g40 0						FL
552	OR6Kn	H38g40 1					yes	FL
553	OR11Hn	H38g40 2					yes	FL
554	OR6KnP	H38g40 3						
555	OR11HnP	H38g40 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	B
556	OR6KnP	H38g40 5						FL
557	OR6Kn	H38g40 6					yes	FL
558	OR2Ln	H38g40 7					yes	FL
559	OR4GnP	H38g40 8						
560	OR6Nn	H38g40 9					yes	FL
561	OR2LnP	H38g41 0						
562	OR9A1	H38g41 1			HSHTPCR06			
563	OR6Nn	H38g41 2					yes	FL
564	OR10Hn	H38g41 3					yes	FL
565	OR7EnP	H38g41 4						FL
566	OR2AQnP	H38g41 5						
567	OR2LnP	H38g41 6						FL
568	OR5ARn	H38g41 7					yes	FL
569	OR7EnP	H38g41 8						FL
570	OR10AA P	H38g41 9						FL
571	OR10JnP	H38g42 0						FL
572	OR5A1P	H38g42 1	DS69;D S71;DS 128;DS 129	OST181		+	yes	FL
573	OR2AHnP	H38g42 2						FL
574	OR10JnP	H38g42 3						FL
575	OR56BnP	H38g42						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
576	OR5M1	H38g42 5		OST050			yes	FL
577	OR52WnP	H38g42 6						
578	OR5AMnP	H38g42 7						FL
579	OR52BnP	H38g42 8						FL
580	OR5MnP	H38g42 9						FL
581	OR5APnP	H38g43 0						FL
582	OR56Bn	H38g43 1					yes	FL
583	OR5APn	H38g43 2					yes	FL
584	OR52Bn	H38g43 3					yes	FL
585	OR9Gn	H38g43 4					yes	FL
586	OR52Kn	H38g43 5					yes	FL
587	OR5MnP	H38g43 6						FL
588	OR52Kn	H38g43 7					yes	FL
589	OR52KnP	H38g43 8				+		FL
590	OR52BnP	H38g43 9						FL
591	OR2B6P	H38g44 0			OR6-31		yes	FL
592	OR2WnP	H38g44 1						FL
593	OR2AnP	H38g44 2						FL
594	ORnP	H38g44 3						
595	OR2LnP	H38g44 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
596	OR2W2P	H38g44 5	DS148		dJ313I6.2;hs6M1-30P	+		FL
597	OR2LnP	H38g44 6						
598	OR2B7P	H38g44 7			dJ313I6.3;hs6M1-31P			FL
599	OR2Ln	H38g44 8					yes	FL
600	OR5BFn	H38g44 9					yes	FL
601	OR2LnP	H38g45 0						FL
602	OR7EnP	H38g45 1						
603	OR1H1	H38g45 2	DS122	OST26		+		FL
604	ORnP	H38g45 3						
605	OR4Dn	H38g45 4					yes	FL
606	OR1Ln	H38g45 5					yes	FL
607	OR5AXn	H38g45 6					yes	FL
608	OR5An	H38g45 7					yes	FL
609	OR5AYn	H38g45 8					yes	FL
610	OR13Gn	H38g45 9					yes	FL
611	OR5BBnP	H38g46 0						
612	OR9GnP	H38g46 1						FL
613	OR2TnP	H38g46 2						FL
614	ORnP	H38g46 3						FL
615	OR1Jn	H38g46 4				+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
616	OR2CnP	H38g46 5						FL
617	OR9GnP	H38g46 6						FL
618	OR2C1	H38g46 7			OLFmf3	+	yes	FL
619	OR51AnP	H38g46 8						
620	OR9Gn	H38g46 9					yes	FL
621	OR52Bn	H38g47 0					yes	FL
622	OR1K1	H38g47 1			hg99		yes	FL
623	OR51RnP	H38g47 2						FL
624	OR7EnP	H38g47 3						FL
625	OR52PnP	H38g47 4						FL
626	OR7EnP	H38g47 5						FL
627	OR7EnP	H38g47 6						
628	OR4KnP	H38g47 7	DS66		OR21-1	+		FL
629	OR4KnP	H38g47 8			OR21-2			FL
630	OR7EnP	H38g47 9						
631	OR51In	H38g48 0					yes	FL
632	OR51In	H38g48 1					yes	FL
633	OR2AnP	H38g48 2						
634	OR2A2	H38g48 3		OST008				FL
635	OR2AnP	H38g48 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
636	OR2Gn	H38g48 5					yes	FL
637	OR2AnP	H38g48 6						
638	OR6Fn	H38g48 7	DS20;D S21;DS 23;DS2 7;DS28 ;DS39; DS40;D S113;D S126;D S135;D S137;D S138;D S139;D S140;D S141;D S145			+	yes	FL
639	OR2AnP	H38g48 8						
640	OR2Gn	H38g48 9					yes	FL
641	OR7E37P	H38g49 0			hg533	+		FL
642	OR5AVn	H38g49 1	DS4;DS 6;DS11			+	yes	FL
643	OR2AJnP	H38g49 2						FL
644	OR13EnP	H38g49 3						FL
645	OR2Cn	H38g49 4					yes	FL
646	OR2TnP	H38g49 5						
647	OR2WnP	H38g49 6						
648	OR13Jn	H38g49 7					yes	FL
649	OR6RnP	H38g49 8						FL
650	OR5ATn	H38g49 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
651	OR2Zn	H38g50 0					yes	FL
652	OR4Ln	H38g50 1					yes	FL
653	OR4UnP	H38g50 2						FL
654	OR4Fn	H38g50 3					yes	FL
655	OR4FnP	H38g50 4						FL
656	OR4Fn	H38g50 5					yes	FL
657	OR4Fn	H38g50 6					yes	FL
658	OR4AnP	H38g50 7						FL
659	OR4LnP	H38g50 8						FL
660	OR7E33P	H38g50 9		OST927	hg688			FL
661	OR2Cn	H38g51 0					yes	FL
662	OR4Kn	H38g51 1					yes	FL
663	OR5U1	H38g51 2			bA150A6.4;hs6M1-28		yes	FL
664	OR4Kn	H38g51 3					yes	FL
665	OR5V1	H38g51 4			bA150A6.2;hs6M1-21		yes	FL
666	OR4QnP	H38g51 5						FL
667	OR12D3	H38g51 6			bA150A6.1;hs6M1-27		yes	FL
668	OR4Kn	H38g51 7					yes	FL
669	OR51CnP	H38g51 8						
670	OR1J2	H38g51 9		OST044	hg152		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
671	OR5BJnP	H38g52 0						
672	OR1J1	H38g52 1	DS130	OST928	hg32	+	yes	FL
673	OR13En	H38g52 2					put	
674	OR4KnP	H38g52 3	DS1			+		FL
675	OR1LnP	H38g52 4						
676	OR2CnP	H38g52 5						
677	OR4TnP	H38g52 6						FL
678	OR5BnP	H38g52 7						
679	OR4Kn	H38g52 8					yes	FL
680	OR11Ln	H38g52 9					yes	FL
681	OR7E68P	H38g53 0		OST929	OR912-108;OR912- 109;OR912-110;OR912- 46;hg523;hg674			FL
682	OR7EnP	H38g53 1						FL
683	OR7E31P	H38g53 2		OST016;O ST205				FL
684	OR7EnP	H38g53 3						FL
685	OR5AKnP	H38g53 4						FL
686	OR5AKn	H38g53 5					yes	FL
687	OR5AKn	H38g53 6					yes	FL
688	OR5BQnP	H38g53 7						
689	OR1Nn	H38g53 8	DS136; DS142			+	yes	FL
690	OR1J4	H38g53 9		OST930	HSHTPCR01	+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
691	OR1Nn	H38g54 0					yes	FL
692	OR2AnP	H38g54 1						FL
693	OR2ANnP	H38g54 2						
694	OR5K1	H38g54 3			HSHTPCR10	+	yes	FL
695	OR2K2	H38g54 4			HSHTPCR06		yes	FL
696	OR8Hn	H38g54 5					yes	FL
697	ORnP	H38g54 6						
698	OR4AnP	H38g54 7						
699	OR4An	H38g54 8					yes	FL
700	OR6Sn	H38g54 9					yes	FL
701	OR4RnP	H38g55 0						
702	OR13Cn	H38g55 1					yes	FL
703	OR13DnP	H38g55 2						FL
704	OR7EnP	H38g55 3						FL
705	OR10PnP	H38g55 4						FL
706	OR8In	H38g55 5					yes	FL
707	OR8G1	H38g55 6			HSTPCR25	+	put	
708	ORnP	H38g55 7						
709	OR5F1	H38g55 8			OR11-10		yes	FL
710	OR5FnP	H38g55 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
711	OR6BnP	H38g56 0						FL
712	OR2D1	H38g56 1			hg27		put	
713	OR5ASn	H38g56 2					yes	FL
714	OR5SnP	H38g56 3						FL
715	OR5AQnP	H38g56 4						
716	OR6BnP	H38g56 5						FL
717	OR5JnP	H38g56 6						FL
718	OR9AnP	H38g56 7						FL
719	OR5BEnP	H38g56 8						FL
720	OR9An	H38g56 9					yes	FL
721	OR8Hn	H38g57 0					yes	FL
722	OR5BNnP	H38g57 1						
723	OR8Jn	H38g57 2					yes	FL
724	OR9NnP	H38g57 3						
725	OR7EnP	H38g57 4						FL
726	OR7E9P	H38g57 5		OST289				FL
727	OR8KnP	H38g57 6						
728	OR2AnP	H38g57 7						
729	OR8Kn	H38g57 8					yes	FL
730	OR7E39P	H38g57 9		OST931	hg611			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
731	OR7E27P	H38g58 0		OST932	hg616			
732	OR2Hn	H38g58 1					put	
733	OR13CnP	H38g58 2						FL
734	OR13Cn	H38g58 3					yes	FL
735	OR2S1P	H38g58 4		OST611				FL
736	OR2AMnP	H38g58 5						
737	OR1N1	H38g58 6		OST933	OR1-26		put	
738	OR2S2	H38g58 7		OST715			yes	FL
739	OR7E26P	H38g58 8			OR1-51; OR1-72; OR1-73; OR912-95			
740	OR1F11	H38g58 9			hg91		put	
741	OR5ACnP	H38g59 0						FL
742	OR5B10P	H38g59 1			OR13-34; OR13-64; OR13-67			
743	OR2AnP	H38g59 2						FL
744	OR1E5	H38g59 3	DS117; DS143		OR13-66	+	put	
745	OR4Fn	H38g59 4					yes	FL
746	OR5CnP	H38g59 5						
747	OR2WnP	H38g59 6						
748	OR2L2	H38g59 7			HSHTPCRHO7	+	put	
749	OR4H8P	H38g59 8			OR14-58			
750	OR5D10P	H38g59 9			OR912-94			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
751	OR7A12P	H38g60 0			OR14-11;OR14-59			
752	OR2L1	H38g60 1			HSHTPCR02	+	put	
753	OR2F3P	H38g60 2			OR14-60		put	
754	OR4H10P	H38g60 3		OST934	OR15-69;OR15- 80;OR15-81			
755	OR5H1	H38g60 4			HSHTPCR14	+	put	
756	OR2K1	H38g60 5			HSHTPCR17	+	put	
757	OR7E11P	H38g60 6			OR11-2			
758	OR7A3P	H38g60 7		OST935	OR11-7b			
759	OR6A1	H38g60 8			OR11-55	+	yes	FL
760	OR5I1	H38g60 9			OLF1	+	yes	FL
761	OR2H3	H38g61 0			HUMORLMHC	+	yes	FL
762	OR10J1	H38g61 1	DS3;DS 14		HSHGMP07J	+	yes	FL
763	OR7E3P	H38g61 2			OR11-9			
764	OR1D6P	H38g61 3			OR11-13;OR11-22			
765	OR5D10P	H38g61 4			OR18-17;OR18- 42;OR18-43;OR18-44			
766	OR5D5P	H38g61 5			OR18-79;OR912-47			
767	OR52A1	H38g61 6			HPFH1OR	+	yes	FL
768	OR2AEn	H38g61 7					yes	FL
769	OR6LnP	H38g61 8						FL
770	OR6LnP	H38g61 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
771	OR7MnP	H38g62 0						
772	OR13Cn	H38g62 1					yes	FL
773	OR13Cn	H38g62 2					yes	FL
774	OR2InP	H38g62 3				+		
775	OR4An	H38g62 4					yes	FL
776	OR2InP	H38g62 5				+		
777	OR4AnP	H38g62 6						FL
778	OR4AnP	H38g62 7						FL
779	OR8C1P	H38g62 8			OR11-175			
780	OR4AnP	H38g62 9						FL
781	OR7E15P	H38g63 0			OR11-392			
782	OR10A1	H38g63 2			OR11-403		put	
783	OR2An	H38g63 3				+	put	
784	OR7EnP	H38g63 4				+		FL
785	OR7En	H38g63 5				+	put	
786	OR51A1P	H38g63 6			HPFH6OR	+		FL
787	OR7E47P	H38g63 7			HSORBPL41;bpl41-16	+		FL
788	OR5B5P	H38g63 8			OR3-144;OR912-92			
789	OR1F10	H38g63 9			OR3-145		put	
790	OR8G2	H38g64 0			HSTPCR120	+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
791	OR1Sn	H38g64 1					yes	FL
792	OR4AnP	H38g64 2						FL
793	OR4AnP	H38g64 3						FL
794	OR4AnP	H38g64 4						FL
795	OR4AnP	H38g64 5						FL
796	OR4AnP	H38g64 6						FL
797	OR4AnP	H38g64 7						FL
798	OR4An	H38g64 8					yes	FL
799	OR4An	H38g64 9					yes	FL
800	OR7E42P	H38g65 0		OST001				
801	OR2M3P	H38g65 1		OST003				
802	OR4H11P	H38g65 2			OR4-114;OR4-115;OR4-119			
803	OR7E57P	H38g65 3		OST007				
804	OR2B1P	H38g65 4			OR5-40;OR5-41		put	
805	OR7E34P	H38g65 5		OST011				
806	OR7E56P	H38g65 6		OST013				
807	OR3AnP	H38g65 7						
808	OR4H5P	H38g65 8			OR5-39;OR5-84			
809	OR1En	H38g65 9	DS47;D S115;D S120;D S121;D S123;D			+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
			S125					
810	OR51CnP	H38g66 0						
811	OR2WnP	H38g66 1						FL
812	OR51B1P	H38g66 2			AF149710			FL
813	OR7E81P	H38g66 3		OST021				
814	OR7E44P	H38g66 4		OST022				
815	OR5B7P	H38g66 5			OR6-55;OR6-57			
816	OR7E36P	H38g66 6		OST024				
817	OR2A5	H38g66 7			OR7-138;OR7-141		put	
818	OR5B1P	H38g66 8		OST936	OR8-122;OR8-123			
819	OR8B8	H38g66 9			HSTPCR85	+	yes	FL
820	OR8B4P	H38g67 0			AC002556-D		yes	FL
821	ORnP	H38g67 1						FL
822	OR8B3	H38g67 2			AC002556-B		yes	FL
823	OR2Bn	H38g67 3					yes	FL
824	OR8B6P	H38g67 4			AC002556-G			FL
825	OR8B5P	H38g67 5			AC002556-A			FL
826	OR4E2	H38g67 6			AE000658-A		yes	FL
827	OR8B7P	H38g67 7			AC002556-F			FL
828	OR11JnP	H38g67 8						FL
829	OR4E1P	H38g67 9			AE000658			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
830	OR10DnP	H38g68 0						
831	ORnP	H38g68 1						
832	OR8D2	H38g68 2			AC002556-E		yes	FL
833	OR11InP	H38g68 3						FL
834	OR11JnP	H38g68 4						FL
835	OR10AnP	H38g68 5	DS12;D S65			+		FL
836	OR8C3P	H38g68 6			OR912-106;OR912- 45;pDJ9j14			FL
837	OR2DnP	H38g68 7						FL
838	OR4PnP	H38g68 8						
839	OR7E21P	H38g68 9		OST035	OR4DG			
840	OR2M1	H38g69 0		OST037			put	
841	OR7AnP	H38g69 1						
842	OR5D11P	H38g69 2			OR8-125;OR8-127			
843	OR7E50P	H38g69 3			OR8-126			
844	OR7E45P	H38g69 4		OST049				
845	OR7E77P	H38g69 5		OST060				
846	OR8B2	H38g69 6			AC002556-C		yes	FL
847	OR8D1	H38g69 7		OST004	pDJ9j14		yes	FL
848	OR8B1P	H38g69 8		OST937	OR11-561			FL
849	OR7A1P	H38g69 9		OST938	OLF4p;OR19-3;hg513			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
850	OR7E8P	H38g70 0			OR11-11a;pDJ392a17			FL
851	OR4DnP	H38g70 1						FL
852	OR7E80P	H38g70 2		OST939	pDJ392a17			FL
853	OR4DnP	H38g70 3						FL
854	OR7E10P	H38g70 4			AC000385-A			FL
855	OR10B1P	H38g70 5			AC003956-A;OR19-19			FL
856	OR2InP	H38g70 6				+		
857	OR4Dn	H38g70 7					yes	FL
858	OR5ACn	H38g70 8					put	
859	OR2I1	H38g70 9			AC004179- A;dJ271M21.7;hs6M1- 14	+		
860	OR10H1	H38g71 0			AC004510	+	yes	FL
861	OR7E59P	H38g71 1		OST119				
862	OR7E28P	H38g71 2		OST128				
863	OR5B3	H38g71 3		OST129			put	
864	OR2A6	H38g71 4		OST182			put	
865	OR6Cn	H38g71 5					put	
866	OR7E54P	H38g71 6		OST185				
867	OR7E48P	H38g71 7		OST193				
868	OR67AnP	H38g71 8						FL
869	OR4DnP	H38g71 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
870	OR4CnP	H38g72 0						FL
871	OR4DnP	H38g72 1						FL
872	OR10H2	H38g72 2			AC004597-A	+	yes	FL
873	OR10H3	H38g72 3			AC004597-B	+	yes	FL
874	OR55CnP	H38g72 4						
875	OR55BnP	H38g72 5						
876	OR52VnP	H38g72 6						FL
877	OR2B3	H38g72 7			OR6- 4;dJ80I19.1;hs6M1-1		yes	FL
878	OR52TnP	H38g72 8						FL
879	OR2J1P	H38g72 9			OR6- 5;dJ80I19.2;hs6M1-4			FL
880	OR52HnP	H38g73 0						FL
881	OR2J3	H38g73 1			OR6- 6;dJ80I19.7;hs6M1-3		yes	FL
882	OR52An	H38g73 2				+	put	
883	OR4Qn	H38g73 3					put	
884	OR52BnP	H38g73 4						FL
885	OR2N1P	H38g73 5	DS9		OR6- 7;dJ80I19.3;hs6M1-2	+		FL
886	OR51EnP	H38g73 6				+		
887	OR2J2	H38g73 7			OR6- 8;dJ80I19.4;hs6M1-6		yes	FL
888	OR2In	H38g73 8				+	put	
889	OR2J4P	H38g73 9			OR6- 9;dJ80I19.5;hs6M1-5			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
890	OR7E40P	H38g74 0		OST215				
891	OR2H4P	H38g74 1			OK6- 3;dJ80I19.6;hs6M1-7			FL
892	OR7E52P	H38g74 2		OST245				
893	OR2InP	H38g74 3				+		
894	OR6C1	H38g74 4		OST267			put	
895	OR7E30P	H38g74 5		OST339				
896	OR5BAnP	H38g74 6	DS132			+		
897	OR7H1P	H38g74 7		OST940	CIT-B-440L2			FL
898	OR5B2	H38g74 8		OST073			yes	FL
899	OR5AZnP	H38g74 9						FL
900	OR5Bn	H38g75 0					yes	FL
901	OR52Bn	H38g75 1					yes	FL
902	OR5BnP	H38g75 2						FL
903	OR52Dn	H38g75 3					yes	FL
904	OR7A11	H38g75 4		OST527	CIT-HSP-87m17			FL
905	OR5BnP	H38g75 5						FL
906	OR51AnP	H38g75 6						FL
907	OR7A15P	H38g75 7		OST941	CIT-HSP-87m17;OR19- 1;OR19-134;OR19-146			FL
908	OR7C2	H38g75 8			CIT-HSP-87m17;OR19- 18		yes	FL
909	OR7E23P	H38g75 9		OST942	OR21-3			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
910	OR2E1	H38g76 0			HS29K1;HSNH0569I24;h s6M1-9			
911	OR1I1	H38g76 1			F20569;OR19-20		yes	FL
912	OR1RnP	H38g76 2						FL
913	OR4F3	H38g76 3			AC004908		yes	FL
914	OR2AEn	H38g76 4					yes	FL
915	OR2InP	H38g76 5				+		
916	OR52AnP	H38g76 6				+		
917	OR7C1	H38g76 7		OST943	CIT-HSP-146e8;OR19- 5;TPCR86	+	yes	FL
918	OR2A3P	H38g76 8			AC004889-B			FL
919	OR7A5	H38g76 9	DS8;DS 19;DS6 1;DS68 ;DS112	OST944	HTPCR2	+	yes	FL
920	OR2InP	H38g77 0	DS72			+		
921	OR7A10	H38g77 1		OST027	CIT-HSP-146e8		yes	FL
922	OR2An	H38g77 2				+	put	
923	OR2M2	H38g77 3		OST423			put	
924	OR7A8P	H38g77 4		OST042	OR19-11;hg83			FL
925	OR2An	H38g77 5				+	put	
926	OR7E20P	H38g77 6		OST516				
927	OR2AnP	H38g77 7				+		
928	OR5BHnP	H38g77 8				+		
929	OR1En	H38g77					put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
930	OR1EnP	H38g78 0						
931	OR5Bn	H38g78 1					yes	FL
932	OR8RnP	H38g78 2						
933	OR5ANn	H38g78 3					yes	FL
934	OR5ANnP	H38g78 4						FL
935	OR5BRnP	H38g78 5						FL
936	OR2A1	H38g78 6			AC004889-A	+	yes	FL
937	OR10An	H38g78 7					yes	FL
938	OR2A9	H38g78 8	DS149		HSDJ0798C17	+		FL
939	OR2A7	H38g78 9			HSDJ0798C17	+	yes	FL
940	OR10A3	H38g79 0			HSHTPCR12	+	yes	FL
941	OR10Cn	H38g79 1					yes	FL
942	OR7A2P	H38g79 2			OLF4p;OR19-18;hg1003		yes	FL
943	OR10WnP	H38g79 3						FL
944	OR7A17	H38g79 4			HSHTPCR19		yes	FL
945	OR5Bn	H38g79 5					yes	FL
946	OR5BnP	H38g79 6						FL
947	OR1Q1	H38g79 7		OST226	HSTPCR106;OR9- A;hrPK-465_F_21	+	yes	FL
948	OR2Hn	H38g79 8	DS133; DS144; DS150			+	yes	FL
949	OR7EnP	H38g79						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
950	OR7A14	H38g80 0		OST945	OR19-12			
951	OR1B1	H38g80 1			OR9-B;hRPK-465_F_21		yes	FL
952	OR12D2	H38g80 2			AC004171;dJ994E9.8;h s6M1-20	+	yes	FL
953	OR7EnP	H38g80 3						FL
954	OR8BnP	H38g80 4						FL
955	OR1L1	H38g80 5			OR9-C;hRPK- 465_F_21;hg23		yes	FL
956	OR11An	H38g80 6					yes	FL
957	OR7AnP	H38g80 7						
958	OR1C1	H38g80 8			HSTPCR27	+	yes	FL
959	OR1D2	H38g80 9		OST946	OR17-4	+	yes	FL
960	OR1L3	H38g81 0			OR9-D;hRPK-465_F_21		yes	FL
961	OR12DnP	H38g81 1						FL
962	OR4G1P	H38g81 2			OLB			FL
963	OR2B4P	H38g81 3			AL050339- A;dJ974I11.1;hs6M1- 22			
964	OR11H1	H38g81 4			OR22-1		yes	FL
965	OR4Fn	H38g81 5					yes	FL
966	OR56AnP	H38g81 6						FL
967	OR8NnP	H38g81 7						FL
968	OR7EnP	H38g81 8						
969	OR4Pn	H38g81					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
970	OR6Cn	H38g82 0					put	
971	OR5BCnP	H38g82 1						
972	OR10QnP	H38g82 2	DS64			+		FL
973	OR5BnP	H38g82 3						FL
974	OR10PnP	H38g82 4						FL
975	OR1L4	H38g82 5		OST046	OR9-E;hRPK-465_F_21		yes	FL
976	OR2APnP	H38g82 6						
977	OR1L6	H38g82 7		OST947	HShRPK-465_F_21;hg16		yes	FL
978	OR6UnP	H38g82 8						FL
979	OR5C1	H38g82 9			OR9-F;hRPK-465_F_21		yes	FL
980	OR11InP	H38g83 0						FL
981	OR4AnP	H38g83 1						FL
982	OR4GnP	H38g83 2						FL
983	OR10Vn	H38g83 3					yes	FL
984	OR4G2P	H38g83 4			HS14a-1-B			FL
985	OR10VnP	H38g83 5				+		
986	OR4F4	H38g83 6			HS14a-1-A		yes	FL
987	OR4G3P	H38g83 7			OLC-7501			FL
988	OR5AKnP	H38g83 8						FL
989	OR10YnP	H38g83 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
990	OR4GnP	H38g84 0						FL
991	ORnP	H38g84 1						
992	OR4Fn	H38g84 2					yes	FL
993	OR8A1	H38g84 3		OST025			yes	FL
994	OR8Bn	H38g84 4					yes	FL
995	OR6DnP	H38g84 5						
996	OR7E14P	H38g84 6		OST948	OR11-5	+		FL
997	OR2M4	H38g84 7		OST710	HSHTPCRX18	+	put	
998	OR4WnP	H38g84 8						
999	OR4Fn	H38g84 9	DS36			+	yes	FL
1000	OR7EnP	H38g85 0						
1001	OR4GnP	H38g85 1						FL
1002	OR10JnP	H38g85 2						
1003	OR52En	H38g85 3					yes	FL
1004	OR4RnP	H38g85 4						FL
1005	OR4Cn	H38g85 5					yes	FL
1006	OR4AnP	H38g85 6						
1007	OR4AnP	H38g85 7	DS54			+		
1008	OR4AnP	H38g85 8						FL
1009	OR9Gn	H38g85 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1010	OR10An	H38g86 0					yes	FL
1011	OR4Cn	H38g86 1					yes	FL
1012	OR10VnP	H38g86 2						
1013	OR10UnP	H38g86 3						FL
1014	OR7E2P	H38g86 4	DS127		OR11-6;hg94	+		FL
1015	OR7E35P	H38g86 5		OST018				FL
1016	OR9KnP	H38g86 6						
1017	OR7E13P	H38g86 7		OST949	OR11-4			FL
1018	OR7EnP	H38g86 8						FL
1019	OR9Kn	H38g86 9					yes	FL
1020	ORnP	H38g87 0						FL
1021	OR7EnP	H38g87 1		OST950	OR11-1;hg500	+		FL
1022	OR7EnP	H38g87 2						FL
1023	OR3A4P	H38g87 3		OST951	OR17-24;OR17-25	+	yes	FL
1024	OR8QnP	H38g87 4						
1025	OR7EnP	H38g87 5						FL
1026	OR7EnP	H38g87 6						FL
1027	OR3A1	H38g87 7	DS2		OLFRA03;OR17- 40;hg138	+	yes	FL
1028	OR5Gn	H38g87 8					yes	FL
1029	OR5MnP	H38g87 9						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1030	OR7EnP	H38g880						FL
1031	OR5G1P	H38g881		OST952	OR11-104;OR93;OR93Hum			FL
1032	OR5PnP	H38g882						FL
1033	OR10AEnP	H38g883						
1034	OR3A2	H38g884		OST953	OR17-228	+	yes	FL
1035	OR10Jn	H38g885					yes	FL
1036	OR1D3P	H38g886		OST954	OR17-23			FL
1037	OR10Jn	H38g887					yes	FL
1038	OR1D4	H38g888			OR17-30	+	yes	FL
1039	OR5GnP	H38g889						FL
1040	OR4SnP	H38g890						FL
1041	OR5GnP	H38g891						FL
1042	OR9HnP	H38g892						FL
1043	OR1A1	H38g893			OR17-7	+	yes	FL
1044	OR1A2	H38g894			OR17-6	+	yes	FL
1045	OR8AnP	H38g895						FL
1046	OR1P1P	H38g896			OR17-208	+		FL
1047	OR7E12P	H38g897		OST955	AC000378-A;OR11-3;hg1058	+		FL
1048	OR4A1P	H38g898			OR11-30			FL
1049	OR10G3	H38g899			AE000658-D		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1050	OR10G1P	H38g90 0			AE000658-C			FL
1051	OR10G2	H38g90 1			AE000658-B		yes	FL
1052	OR5Tn	H38g90 2					yes	FL
1053	OR7EnP	H38g90 3						FL
1054	OR7EnP	H38g90 4						FL
1055	OR4AnP	H38g90 5						FL
1056	OR4C1	H38g90 6			HSHTPCR11	+		FL
1057	OR1EnP	H38g90 7						
1058	OR7KnP	H38g90 8						FL
1059	OR4CnP	H38g90 9						FL
1060	OR1RnP	H38g91 0						FL
1061	OR5AUn	H38g91 1					yes	FL
1062	OR4Cn	H38g91 2					yes	FL
1063	OR4Cn	H38g91 3					yes	FL
1064	OR13DnP	H38g91 4						FL
1065	OR5n	H38g91 5	DSU116			+		
1066	OR2Hn	H38g91 6	DSU150			+		
1067	ORn	H38g91 7	DSU151			+	put	
1068	ORn	H38g91 8	DSU17			+		
1069	ORn	H38g91 9	DSU18			+		

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	B
1070	ORn	H38g92 0	DSU35			+		
1071	OR6Fn	H38g92 1	DSU41			+		
1072	ORn	H38g92 2	DSU49			+		
1073	ORn	H38g92 3	DSU50			+		
1074	OR10An	H38g92 4	DSU57			+		
1075	ORn	H38g92 5	DSU58			+		
1076	OR2Ln	H38g92 6	DSU59			+		
1077	OR10Jn	H38g92 7	DSU60			+		
1078	OR1Kn	H38g92 8	DSU63			+		
1079	OR10Dn	H38g92 9	DSU7			+		
1080	ORn	H38g93 0	DSU32			+		
1081	OR2Ln	H38g93 1	DSU38			+		
1082	ORn	H38g93 2	DSU62			+		
1083	ORn	H38g93 3	DSU48			+		
1084	OR2n	H38g93 4	DSU111			+		

Table 2

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SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
153	OR10D3	0	11	137.96SDVISV	69	M	AC074177.4	12106 ... 13038
154	OR7EnP	4	4	11.58	MVACGVLDLHIIDSFAL	53	R	AF091580.1	7 ... 663
155	OR1D5	0	17	3.75	LVVTNLLYLLLLTGIFT	49	M	AF073967.1	2 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
156	OR10Nn P	4	11	138.02	LQSGSVVHILFGNVLAT	82	M	AC074177.4	159287 ... 158526
157	OR2F1	0	7	148.62	LLGGFTSSVQI ISSLLT	56	M	AF073974.1	41 ... 649
158	OR7EnP	7	4	11.58	MAGGELLDLHILPALGL	54	M	AF073989.1	547 ... 1515
159	OR8FnP	6	11	137.96	LLVICEMGAHCVC SNIF	75	M	AC069561.1 0	51687 ... 50743
160	OR2Q1P	2	7	148.62	LLCGFSANMEIVSGVIL	49	M	AC020865.3	190954 ... 189954
161	OR2W1	0	6	33.74	LMGSCMINVLLVLGIVT	88	M	AF102516.1	52 ... 669
162	OR7EnP	7	4	11.58	MVACGVLDLHITHSFGL	53	R	AF091580.1	7 ... 663
163	OR6B1	0	7	148.62	LIMCCGIIAKFDLAIFF	61	M	NM_010983. 1	178 ... 975
164	OR10Kn	0	1	154.34	MLGSSACVVTILGALI	79	M	AC073778.1	168744 ... 167803
165	ORnP	13	11	138.02	VPYCIGGHLICLSLSS	33	M	AC074177.4	12106 ... 13038
166	OR4F2P	4	6	186.49	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
167	OR7EnP	3	4	11.58	MVACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
168	OR1F2P	0	16	6.15	MSADNGVNLHLIEAVTT	72	R	M64377.1	1 ... 939
169	OR2P1P	7	6	33.74	FGGSCMSNQSALVRXSV	48	M	NM_008762. 1	1 ... 936
170	OR7E43 P	5	4	5.57	MAGGELFDLHIMPAFGL	54	M	AF102536.1	22 ... 669
171	OR4F1	4	6	0.23	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
172	OR7E55 P	5	3	89.94	MAGDEFDLHILPAFGL	53	M	AF073989.1	547 ... 1515
173	OR13Dn	0	9	86.89	MLGSCWITLQLMTNSLI	61	M	AC023789.5	371264 ... 372220
174	OR4CnP	3	16		AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
175	OR10D1 P	1	11	137.96	LHGCCGFQFLGSMPS	83	M	AC074177.4	128803 ... 129726
176	OR4Cn	0	16		LHGGIVGHVQLVNSICL	86	M	AB030895.1	1 ... 924

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
177	OR8GnP	0	11	137.96	LSAICGLGIHFVLSNIM	73	M	AC074177.4	106297 ... 105361
178	OR13CnP	2	9	86.85	MFGACGGNLQLMASFLG	82	M	AJ251154.1	2703 ... 1747
179	OR4CnP	5	16		LHEAIVLHIQFINSCL	61	M	AF102522.1	40 ... 660
180	OR13Cn	0	9	86.81	MLGTCGINVQFMATFIT	69	M	AJ133425.1	61 ... 1014
181	OR4CnP	0	16		LHGGIMGHIQLVNSMCL	63	M	AB030895.1	1 ... 924
182	OR51Bn	0	11		AHSVSGRSPVRPLITIL	76	M	AF071080.2	15931 ... 16851
183	OR7E5P	2	11	51.76	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
184	OR13Cn	0	9	86.77	MFGSCVSNVQLMSNLL	71	M	AJ251154.1	2703 ... 1747
185	OR4Sn	0	16		LHGGIAAHLQLVNSISA	56	M	AB030895.1	1 ... 924
186	OR51BnP	4	11		VHYPEWRSPPPPLVIFL	72	M	AF071080.2	15931 ... 16851
187	OR6JnP	1	14	2.72	CFGTFFGSFPLDLSVIC	50	R	M64378.1	1 ... 933
188	OR51Bn	0	11		SHAISGRSPISPQTTVL	76	M	AF071080.2	26330 ... 27262
189	OR7EnP	2	11	71.8	MFACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
190	OR2An	0	6	144.32	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
191	OR7E22P	3	3	89.94	MVACDVLDLHIIDSFGL	56	M	AF073989.1	547 ... 1515
192	OR7E4P	2	11	71.8	IVACDVLDLHIMHSFGL	55	M	AF102536.1	22 ... 669
193	OR7E66P	9	3	89.94	MAGGELLFLHIMPAFGL	55	M	AF073989.1	547 ... 1515
194	OR6Mn	0	11	138.18	TFGTFGGSPVNLSVIS	50	M	NM_010991.1	1 ... 939
195	OR2ALnP	11	11	112.69	ILGTCASNFDFFNHLL	32	M	AL359352.1	85325 ... 86251
196	OR6MnP	2	11	138.18	TGGTFGGSCPVNLSILT	50	M	NM_010991.1	1 ... 939
197	OR4D1	0	17	60.7	IHGGVAGHVQLMNSLVI	90	M	AC019272.4	62255 ... 61317
198	OR5D2P	3	11	51.09	LCVVTTWCTLFTSANES	48	M	AC073947.3	29192 ... 30115

SEQ ID #	Symbol	D	C	Mb coord	CDR	#	S	Acc	Range
199	OR7E38 P	7	7	95.91	MAGGELFHLHIMPAFGL	55	R	AF091580.1	7 ... 663
200	OR4D2	0	17	60.7	IHGGVAGHVQLKNSLDV	89	M	AC012272.4	183633 ... 182701
201	OR7E7P	4	7	95.91	MIACGVLDLHIIDSFGL	56	R	AF091580.1	7 ... 663
202	OR5AHn P	0	19	68.97RSGIMC	77	M	AC020957.2	48184 ... 49107
203	OR2U2P	5	6	33.53	LVYSCIVNIPYTMCIIV	49	M	AC044846.2	105668 ... 104736
204	OR2U1P	2	6	33.53	LVCTCMINILCCVVIFA	54	M	AF102516.1	52 ... 669
205	OR2H2	0	6	33.19	ILGTCVIEVQSVASILV	89	M	AL078630.1	41097 ... 40165
206	OR2H5P	7	6	33.19	FLGTCVIEVQSMASILV	84	M	AL078630.1	41097 ... 40165
207	OR2In	0	6	33.19	LLGSCASNAQLMARILL	74	M	AL078630.1	151152 ... 150391
208	OR11Hn P	5	13		IFNTCLCWIPLCLSVIG	60	M	AF121972.1	171 ... 1109
209	OR7EnP	6			AAACDVIDLHITHSFGL	56	M	AF073964.1	41 ... 649
210	OR9In	0	11	54.06	FTAGCGCGLRCIFGVIA	50	R	AF091579.1	7 ... 663
211	OR2AFn P	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
212	OR13Kn P	5	X	140.17	MFGMCVIIHIGIGTLL	43	R	L34074.1	73 ... 1011
213	OR13Cn	0	9	86.77	MFGSCVSNVQLLSNFL	68	M	AJ251154.1	2703 ... 1747
214	OR13Fn	0	9	86.77	MLGSCGTTVESMISLLM	55	M	AJ133428.1	61 ... 1017
215	OR9Qn	0	11	54.08	FTGSCGASVRSIFAVIA	47	M	AF146372.1	509 ... 1456
216	OR2TnP	1	1	254.77	ILIGFGDMLVMCCMLI	71	M	AF102527.1	22 ... 669
217	OR4Kn	0	14	0.08	IHVGMIVHSHFTNSISS	56	M	AF259072.1	104176 ... 105099
218	OR2B8P	0	6	31.6	LLGSCTINLQLLVSVILV	62	R	L34074.1	73 ... 1011

SEQ ID #	Symbol	D	C	Mb coord	CDR	#	S	Acc	Range
219	OR2Tn	0	1	254.77	MLAGVALDLLITCCMLT	57	M	AF102527.1	22 ... 669
220	OR4Kn	0	14	0.08	IHTGIAMHSQFMTSIAS	53	M	AF259072.1	104176 ... 105099
221	OR2A4	0	6	144.76	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
222	OR7EnP	6	2	161.53	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
223	OR4Kn	0	14	0.08	MHGGILVHSQFMTSIAV	57	M	AF259072.1	104176 ... 105099
224	OR13InP	6	9	86.85	MYGSCVLNNVIGKTLL	41	M	AJ251155.1	15491 ... 16423
225	OR7EnP	8	2	161.53	MVACDVLDLHIFFDFGL	54	M	AF073989.1	547 ... 1515
226	OR6Jn	0	14	2.72	CFGTFFGSFPLDLVIC	50	R	M64378.1	1 ... 933
227	OR4Mn	0	14	0.08	LHGAMLGHIQLMSSISV	54	M	AC019272.4	183633 ... 182701
228	OR4VnP	10	11	51.09	IHGIIVLHFQMVNSFAV	50	M	AB030896.1	1 ... 906
229	OR6Xn	0	11	138.36	AFGTFSVICQLGATVIG	46	M	AF106007.1	178 ... 975
230	OR51Gn	0	11	3.7	LHSSSSRLPLLGVVTVV	55	M	NM_013617.1	1 ... 921
231	OR6EnP	3	14	2.72	SFGTFCTLIPLGIASLG	82	M	NM_010991.1	1 ... 939
232	OR4NnP	2	14	0.08	LHGGGAGHIQLMNSMTL	54	M	AC019272.4	62255 ... 61317
233	OR6MnP	7	11	138.18	IFGTFGGARLVXSMTV	37	R	M64378.1	1 ... 933
234	OR4Nn	0	14	0.08	LHGGGAGHIQLMNSMTL	57	M	AC019272.4	62255 ... 61317
235	OR4Cn	0	11	51.09	LHGGIGGHIQFVNSMCA	65	M	AF102522.1	40 ... 660
236	OR4KnP	4	14	0.08	IHAGMGTHSQFMDSMGT	51	M	AF259072.1	104176 ... 105099
237	ORnP	8	11	137.59	AIAITVVVAHAAAGVVA	35	M	AC069559.8	73704 ... 74636
238	OR5D3	0	11	51.15	FCVVTAWCTYFISANES	46	R	U50948.1	34 ... 978
239	OR2G1P	6	6	33.53	LLGSCVSNIQVLASLLL	84	M	AL359352.1	85325 ... 86251

SEQ ID.#	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
240	OR4Kn	0	14	0.08	IHTGMIVHSQFINSLS	51	M	AF259072.1	104176 ... 105099
241	OR8BnP	2	11	137.59	LCVFSGMGAHNIVVGIV	68	M	AC069559.8	120212 ... 119283
242	OR2B2	0	6	31.47	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
243	OR7EnP	3	2	73.87	MVACDVLDLRIIDSFGL	54	M	AF073989.1	547 ... 1515
244	OR4KnP	3	14	0.08	IHTGIVVHSQFMTSIAI	57	M	AB030896.1	1 ... 906
245	OR2AD1P	6	6	33.87	FLGACTSSIVLVFGFLV	51	M	AL136158.1 4	162423 ... 161461
246	OR1AAnP	8	X	140.17	MIVDNTIVLHLIIGVII	48	M	AC068902.1 1	144125 ... 143193
247	OR1E3P	1	17	2.99	MLGVSLHLHLMMGILI	74	R	M64392.1	1 ... 942
248	OR8BnP	3	11	137.59	FCVFSGMGAHNIVVGIV	63	M	AC069561.1 0	96653 ... 95690
249	OR5Hn	0	3	104.18	FAGTCFGHIHLVLSIQF	55	R	AF091575.1	52 ... 663
250	OR1G1	0	17	2.99	LMVMAAMHLHLITGTGI	56	R	M64392.1	1 ... 942
251	OR5HnP	2	3	104.18	FAVTCGGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
252	ORnP	5	X	140.17	MLVTCSHHFLSFTGIWS	36	R	U50948.1	34 ... 978
253	ORnP	11	X	140.17	LIVTFAKITTTQDHHHH	29	M	AC069561.1 0	127636 ... 126698
254	OR4PnP	2	11	51.09	LHGDIAGHSQLVNSISL	51	M	AB030895.1	1 ... 924
255	OR13Hn	0	X	140.17	TLATCTTVAMLITSTLL	47	M	AJ251154.1	35662 ... 36615
256	OR7D1P	5	19	11.38	VMAGTAIFVHLLATLGF	64	R	AF091580.1	7 ... 663
257	OR4KnP	2	18	47.77	IHNIGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
258	OR7E24	1	19	11.38	MVACDLIDLHIIMGFGL	60	R	AF091580.1	7 ... 663
259	OR51NnP	2	11	3.6	LHGFSARSPSLGVLTV	49	R	AF079864.1	632 ... 1576
260	OR7E18P	6	19	11.38	VAGCDLLDLHIMLAFGL	59	M	AF102536.1	22 ... 669

SEQ ID #	Symbol	D	C	Mb coprd	CDR	%	S	Acc	Range
261	OR7E19P	2	19	11.38	MYVCDVLNLHIMDSFGL	58	M	AF073989.1	547 ... 1515
262	OR7E41P	7	11	14.36	IVVCDMLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
263	OR2R1	3	7	148.69	LLGGFVVNMELISSVLV	77	M	AF073974.1	41 ... 649
264	OR10ACnP	7	7	148.69	MVGGCGRVGLLLACLLL	46	M	AC073778.1	168744 ... 167803
265	OR51Ln	0	11	3.79	LHTFSARVPTLGVVTLV	54	R	AF079864.1	632 ... 1576
266	OR52JnP	3	11	3.79	MHTGSSRLPILGVALDA	57	M	AF121979.1	53 ... 1106
267	OR9LnP	9	8	45.22	TVVNNFFFFFFFFFDLIA	37	M	AC069561.1 0	147203 ... 146274
268	OR51PnP	4	11	3.79	MHSISARLPALGVVSML	48	M	AF071080.2	2641 ... 1697
269	OR5HnP	4	3	104.18	FAVTCLGHIHFFFSIQL	50	R	AF091575.1	52 ... 663
270	OR51An	0	11	3.79	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
271	OR5HnP	6	3	104.18	FAVTCLGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
272	ORnP	11	17	17.43	LLPCILSIIALYYYYYY	27	M	AL359352.1	9138 ... 8177
273	OR52En	0	11	3.79	MHTGSARFPFFYCAILF	57	M	AF121979.1	53 ... 1106
274	OR5Hn	0	3	104.18	FVVTCLGHIHFVFAVQF	53	R	AF091575.1	52 ... 663
275	OR4CnP	3	11	50.21	VHRGVVGHIQFVNSICL	73	M	AF102522.1	40 ... 660
276	OR52En	0	11	3.79	MHTLSGRFPSLYCANLF	60	M	AF121979.1	53 ... 1106
277	OR10Dn	0	11	138	LHGCCGIHILLGNVLSI	86	M	AC074177.4	12106 ... 13038
278	OR5HnP	2	3	104.18	FVVTCLGHIHFVFAIQF	54	R	AF091575.1	52 ... 663
279	OR13An	0	10	47.91	LTASLALNIHLIADYGV	67	M	AF102520.1	16 ... 669
280	OR5HnP	2	3	104.18	FGGTCLGHIHILLSIQF	57	R	AF091575.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
281	OR5Kn	0	3	104.47	FCETCGAHIHLLFSVQF	45	M	AC069559.8	36251 ... 35322
282	OR7EnP	9	21	17.99	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
283	OR4DnP	6	8	77.48	IHGGVAGHVQVMNSLVI	87	M	AC019272.4	62255 ... 61317
284	OR2ARnP	0	3	30.89	MLGSC.....	71	M	AJ251154.1	56533 ... 57369
285	OR7E29P	4	3	136.03	MAGGELLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
286	OR4CnP	3	11	51.12	AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
287	OR5PnP	2	11	6.93	LVGTCVGNTFCPSSIIV	74	M	AF121977.1	262 ... 1197
288	OR7EnP	5	3	136.04	MVACGVLDLHIIGSFGL	52	R	AF091580.1	7 ... 663
289	OR56An	0	11	4.73	MNLPSFRLPILQAGLLS	41	M	AF121975.1	50 ... 1012
290	OR56AnP	9	11	4.73	KNQAFFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
291	OR5Pn	0	11	6.89	LAATCVAISYSLSSIIV	63	M	AF121977.1	262 ... 1197
292	OR7E53P	5	3	136.04	MAGGEFPDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
293	OR5Pn	0	11	6.89	LVGTCMGNTFCPSSIIA	83	M	AF121977.1	262 ... 1197
294	OR52Ln	0	11	4.73	MHSSSVRLPFLGMAVIL	59	M	AF121976.2	474 ... 1307
295	OR5E1	3	11	6.89	LGATXGYNIQLLFSNLG	51	R	U50948.1	34 ... 978
296	OR56AnP	3	11	4.73	MNLASFRMAILPPPPPP	39	M	AF121976.2	474 ... 1307
297	OR4KnP	2	8	88.25	IHTGMIVHSQFIDS...	57	M	AB030896.1	1 ... 906
298	OR52Ln	0	11	4.73	MHSSSVRLPFLGVAVVL	59	M	AF121976.2	474 ... 1307
299	OR7EnP	1	4	74.82	MVF.....	55	R	AF091580.1	7 ... 663
300	OR52XnP	5	11	4.73	MHSASLXLSFLAVALGG	51	M	AF121976.2	474 ... 1307
301	ORnP	13	4	74.82	STGCKGRKXKLKLRDFQ	24	R	M64386.1	130 ... 975
302	OR56An	0	11	4.73	MNLTSFRVPVLQAGLLS	84	M	AF121981.1	89 ... 475

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
303	OR56An P	10	11	4.73	LI...GMMXNL...KKK	60	M	AF121981.1	89 ... 475
304	OR1R1P	5	17	3	MVGISAVKHLIEGVVA	48	M	AF073967.1	2 ... 649
305	OR52En P	2	11	3.79	MHTGSGRSPFLYGAILF	64	M	AF121979.1	53 ... 1106
306	OR51An P	4	11	3.7	EHTVALKLPLLGAGSTL	46	R	AF079864.1	632 ... 1576
307	OR51An	0	11	3.7	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
308	OR4CnP	1	11	51.12	VHGGVVGHVQFVNSICL	75	M	AF102522.1	40 ... 660
309	OR52Jn P	9	11	3.79	MHTGACRFPI LGVVYLN	58	M	AF121979.1	53 ... 1106
310	OR4RnP	9	11	51.12GGGVXSVNGNYL	66	M	AF102522.1	40 ... 660
311	OR52Jn	0	11	3.79	MHTGACRLPMLGVVFN	58	M	AF121976.2	474 ... 1307
312	OR4CnP	3	11	51.12	VHGGGVGHIQFINSICL	76	M	AF102522.1	40 ... 660
313	OR51An P	2	11	3.79	EHSASAKLPFTYFVTGL	83	M	AF121985.1	2 ... 478
314	OR7EnP	15	12	93.55	IVVCDLLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
315	OR5MnP	2	11	52.17	CIVLHVYLMERMVASNQ	54	M	AF102528.1	52 ... 669
316	OR10AB nP	1	11	6.93	MLASCAVFCITILSVLG	47	M	AC073778.1	168744 ... 167803
317	OR52Sn P	2	11	3.79	MHSTSARLPHLSVATGV	54	M	AF121976.2	474 ... 1307
318	OR5Mn	0	11	52.14	CIVHIFYTAAWMLANFY	49	R	AF091579.1	7 ... 663
319	OR10Sn	0	11	138.1	LHASCIIHIHLSIVAG	61	M	AF259072.1	32953 ... 32000
320	OR5MnP	4	11	52.14	CIVHIFYTTAWMLANFY	48	R	AF091579.1	7 ... 663
321	OR10Gn	0	11	138.1	LHGSCGSHVQLIDIVAG	61	M	AF259072.1	55611 ... 54658
322	ORnP	20	11	29.15	ILGIYEGSAHYFIILFL	33	M	AL365337.1	192661 ... 191711
323	OR5MnP	2	11	52.19	CIVIIYGYSMEWMVANLS	54	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb Record	CDR	%	S	Acc	Range
324	OR10Gn P	10	11	138.1	LYGSCWGHLPYIVIKFT	30	M	L14567.1	17 ... 667
325	OR10Tn P	1	1	154.34	LVACCACTIVLILSVLV	57	M	X92969.1	8035 ... 8961
326	ORnP	16	11	52.17	LAAPLLLVLFLAAAAAA	33	R	M64376.1	1 ... 999
327	OR10Rn P	11	1	154.5	MLAVFTICVFLIGGALV	47	M	AC023611.2	108224 ... 107271
328	OR5MnP	2	11	52.16	CIVHLVYTMWVMVANFY	49	R	AF091579.1	7 ... 663
329	OR7EnP	4	8	6.68	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
330	OR10Tn	0	1	154.27	LLACCLTIVALLLSVIV	58	M	AC012302.5	54283 ... 55224
331	OR1E1	0	17	3.04	MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
332	OR5BK nP	4	12	42.11	STGGAIAIMDFLSQWGL	46	M	AF073965.1	2 ... 643
333	OR5MnP	3	11	52.17	CIVHIVYTMWVMVANLF	48	R	AF091579.1	7 ... 663
334	OR3A3	0	17	3.06	LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
335	OR10AD nP	1	12	42.11	TFGVCTFNFLIIDAVIS	44	M	AF247657.1	1 ... 945
336	OR10Rn	0	1	154.5	MLAICAGATVLCIGVLV	56	M	AC073778.1	168744 ... 167803
337	OR5TnP	4	11	51.94	MCGTCAAHIAFFVIEV	51	M	AF121977.1	262 ... 1197
338	OR4GnP	15	7	0.23	ICRKMVHVSQFVNSISA	42	M	AB030892.1	1 ... 939
339	OR6Yn	0	1	154.5	LVVCYGCTIKFDLAVII	61	M	NM_010983. 1	178 ... 975
340	OR1E2	0	17	3.15	MLSDSLLHLHLIMGILI	80	R	Y07557.1	1 ... 942
341	OR8Hn	0	11	51.94	MVGACGINVNWILATLV	51	M	NM_013728. 1	1 ... 948
342	OR4Fn	0	7	0.23	IHGGMVHVSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
343	OR10Kn	0	1	154.27	MLGCSACVILILCVLI	83	M	AC073778.1	168744 ... 167803
344	OR7LnP	11	X	140.17	MLGVCGHGTNLXFFFFI	32	M	AL133160.1	63932 ... 64759
345	OR8InP	7	11	51.94	MVCCMINVSVSLATLG	44	R	M64386.1	130 ... 975

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
346	OR10Rn P	0	1	154.5	MLAVCTSIVGFIFGVLV	54	M	AC073778.1	168744 ... 167803
347	OR2AFn P	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
348	OR8Kn	0	11	51.94	LEIILVYVFLKIFSNLF	55	M	AF102528.1	52 ... 669
349	ORnP	7	10	127.57	S.CCCLLTYYIIHHHHH	31	M	AC020958.1	164590 ... 163746
350	OR8KnP	10	11	51.94	MIIILYQMVKIFSNLF	35	M	AC073945.4	152209 ... 153150
351	OR51Hn	0	11	3.6	MHGSSRPVPLGVVTLL	49	R	AF079864.1	632 ... 1576
352	OR7EnP	5	3	136.03	MVACGVLDLHIIDSFGL	51	M	AF073989.1	547 ... 1515
353	ORnP	8	3	56.17	LLLLFLIIEQH.....I	32	R	M64376.1	1 ... 999
354	OR5BMn P	20	3	103.93	KXNKCTLSSSLMVFIQF	30	M	AF146372.1	509 ... 1456
355	OR10Gn P	0	11	138.1	LHGCGGHHFQFTDILAT	63	M	AF259072.1	55611 ... 54658
356	OR2Yn	0	5	209.23	LLGSCAANIQLMARVVV	74	M	AC044846.2	139468 ... 138536
357	OR10Dn P	1	11	138.1	LHGCGGHHVLLSNVAM	66	M	AC074177.4	128803 ... 129726
358	OR3BnP	7	X	158.48	IHAPSILNTYLLSFVAA	37	M	AL136158.1 4	29455 ... 30402
359	OR8Dn	0	11	138.1	LCVICAVDIHCIGNMA	62	R	X80671.1	203 ... 1129
360	OR5RnP	0	11	52.13	LLMICVYVFHIIFADMS	68	M	AF102528.1	52 ... 669
361	OR10Gn	0	11	138.1	LHGSCGSHVQLINIVAG	58	M	AF259072.1	55611 ... 54658
362	OR5BDn P	12	11	53.74	MTGTCVVIHRALSSITP	39	M	NM_013728. 1	1 ... 948
363	OR5ALn P	1	11	52.13	VIVVLSYVVQALIANTC	52	M	AC073947.3	29192 ... 30115
364	OR52Hn P	3	11	4.15	LHFVSGRVPCLGVPVT	59	M	AF121975.1	50 ... 1012
365	OR10Gn	0	11	138.1	LHGGCSSHVQLITVVAG	56	M	AF259072.1	55611 ... 54658

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
366	OR5Mn	0	11	52.17	CIVHIVYTMWVMVANLF	52	M	AF146372.1	509 ... 1456
367	OR51Mn	0	11	4.15	MHSFSIRAPILGvVTVL	50	M	NM_013617.1	1 ... 921
368	OR6Tn	0	11	138.1	SFGTFAAWCPLALSVLG	52	M	NM_010991.1	1 ... 939
369	OR6DnP	5	10		SLGSFVVLGLKALVVLT	69	R	AF034903.1	85 ... 1053
370	OR4B1	0	11	45.36	IHGVIGGHIQVVSFSF	62	M	AF102522.1	40 ... 660
371	OR5ALn P	4	11	52.13	VISVVGMIQALIANVC	50	M	AF146372.1	509 ... 1456
372	OR51Qn	0	11	4.15	FHSFSACAPSLGLAIIV	49	M	NM_013617.1	1 ... 921
373	OR4Dn	0	11	138.1	LHGGIAGHVQLMNNVTM	63	M	AC019272.4	62255 ... 61317
374	OR52Nn	0	11	4.58	MHTGSLRLPSLGVAIGF	52	M	NM_013619.1	118 ... 969
375	OR4Xn	0	11	45.36	MHGGGAIGHGQLINGISV	58	M	AB030896.1	1 ... 906
376	OR8Jn	0	11	52.03	LLIVVLYTVVYVSANVG	77	M	X89682.1	2 ... 472
377	OR51Jn P	2	11	4.15	MHSMSIKLPLLGIVTFL	46	M	AF071080.2	15931 ... 16851
378	OR10Gn	0	11	138.1	LHGSCSSHVQLIDIVAG	60	M	AF259072.1	55611 ... 54658
379	OR52En	0	11	4.58	MHTGTVRLPFLGVIIID	66	M	AF121979.1	53 ... 1106
380	OR4Xn	0	11	45.36	LHGGIIGHAQLINGLSI	64	M	AB030895.1	1 ... 924
381	OR10A2	1	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
382	OR5Mn	0	11	52.14	CIVHVYVICWMIANFY	49	R	AF091579.1	7 ... 663
383	OR52En	0	11	4.58	MHTGSRFPFLISVVGI	59	M	AF121979.1	53 ... 1106
384	OR8Kn	0	11	51.94	LLIGLIYILVKIFADLS	53	M	AF146372.1	509 ... 1456
385	OR10An	0	11	5.66	MFGACASVVQWAATFIF	89	M	AF247657.1	1 ... 945
386	OR8LnP	3	11	52.13	LIVMSYVLQLLLANTF	51	M	AF102528.1	52 ... 669
387	OR5BPn P	8	11	52.82	VVVVVGGSIVPPVGLHL	43	R	U50948.1	34 ... 978
388	OR52Nn	0	11	4.58	MHTGSARLPFLGVAIGF	54	M	AF121976.2	474 ... 1307

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
389	ORnP	7	11	45.36	WWWIALLR.AAAAAK	28	M	X89686.1	32 ... 472
390	OR8JnP	1	11	51.94	LLIVILQTTVCVFSNLF	99	M	X89682.1	2 ... 472
391	OR5Mn	0	11	52.24	CIVIFVYNSQLMVATLS	50	R	AF091579.1	7 ... 663
392	OR52En	0	11	4.58	MHTVSIRMPPLGSIILL	66	M	AF121979.1	53 ... 1106
393	OR5Tn	0	11	51.94	VCGTCAAHIHALFVIEV	52	M	AF146372.1	509 ... 1456
394	OR52NnP	5	11	4.58	MHTGSVQLPFLGAAIGF	51	M	NM_013619.1	118 ... 969
395	OR4B2P	6	11	45.36	IFGIIGRHVQVNSELS	53	M	AB030896.1	1 ... 906
396	OR51KnP	6	11	4.15	MHSCSGKLPPLGIVNFL	51	M	NM_013617.1	1 ... 921
397	OR52QnP	10	11	4.58	MYTGSVRFPFLFVAVGI	45	M	AF121979.1	53 ... 1106
398	OR4Fn	0	15	86.21	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
399	OR11MnP	1	12	41.92	FSAACGSSTL.....	48	M	AL359381.1	175785 ... 176720
400	OR52NnP	0	11	4.44	MHTGSARLPFLGVAIGF	57	M	NM_013619.1	118 ... 969
401	OR56An	0	11	4.58	MNLASFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
402	OR5AWnP	14	X		LXADFTSNLPTTSSNVV	39	R	X80671.1	203 ... 1129
403	OR52NnP	0	11	4.51	MHTGSARLPFLGVAIGF	55	M	AF121976.2	474 ... 1307
404	ORnP	15	X		ISCIFELTLPLPSNVV	31	M	AC073947.3	29192 ... 30115
405	OR52EnP	6	11	4.58	VHSVSVRMPILGNIILL	62	M	AF121979.1	53 ... 1106
406	OR5BHnP	9	X		MVASC GGKTVSLCGTLT	40	M	NM_013728.1	1 ... 948
407	OR4QnP	1	15	1.66	IHGAMAGHMQLMNSLSV	60	M	AC019272.4	62255 ... 61317
408	OR51En	0	11	3.04	MHSGSARLPFLGVIAIL	60	R	AF079864.1	632 ... 1576
409	OR11KnP	2	15	1.66	FSGYGFCITLLITFVFI	53	M	AF121972.1	171 ... 1109
410	OR12D1P	1	6	33.02	LHGSATIHLMSTGIAG	76	M	AL133159.4	16108 ... 15185

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
411	OR4NnP	3	15	1.61	LHGGGAGHIQLMNSMTM	55	M	AC019272.4	62255 ... 61317
412	OR11A1	0	6	33.02	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
413	OR10C1	0	6	33.02	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
414	OR2H1	0	6	33.02	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
415	OR9RnP	8	12	59.71	LAVGGGCNIQFLLSITT	54	R	AF091579.1	7 ... 663
416	OR4FnP	0	7	0.53VLHFQFVNSICG	50	M	AB030896.1	1 ... 906
417	OR7D4	3	19	11.31	VMAGTAIFVHLLATLGF	67	R	AF091580.1	7 ... 663
418	OR7E25 P	3	19	11.31	MIACSVLDLHIVIGFGL	61	R	AF091580.1	7 ... 663
419	OR2D2	0	11	5.69	LLGCCGSVDFITGILI	65	M	AF073987.1	2 ... 649
420	OR10An	0	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
421	OR2WnP	3	1	254.49	LLGGCVCQGHWWLAVVS	54	R	L34074.1	73 ... 1011
422	OR7E16 P	8	19	11.31	IAGCDLLDLHIMLALGL	60	M	AF102536.1	22 ... 669
423	OR52Pn	0	11	4.44	MHCMSARLPCLGAAVIV	59	M	AF121976.2	474 ... 1307
424	OR6AnP	4	11	5.66	LLGCCGGIVKLDLAILG	94	R	M64386.1	130 ... 975
425	OR7D2	0	19	11.24	VMPITVITLHLIMTLGF	61	R	AF091580.1	7 ... 663
426	OR52Un P	3	11	4.44	LHSASVRFPMLGVAVAY	52	M	AF121976.2	474 ... 1307
427	OR2AGn	0	11	5.6	MLGGDTLSIYYVMGFLP	55	M	AF102527.1	22 ... 669
428	OR7G3	0	19	11.24	ILVGNLVDLHMVVTLG	64	R	AF091580.1	7 ... 663
429	OR56Bn P	3	11	4.44	IHVGSFRFPVLQLAGMS	41	M	AF133300.1	25713 ... 26573
430	OR2AGn P	1	11	5.51	MLGSDTLIGHYITGFL	55	M	AF102527.1	22 ... 669
431	OR56Bn	0	11	4.44	MHVASFRCSVLQALMS	39	M	NM_013619. 1	118 ... 969
432	OR6AnP	5	11	5.51	LLGCCGGIVKLDLAILG	93	R	M64386.1	130 ... 975
433	OR4FnP	4	19	63.23	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
434	OR6Wn	0	7	148.04	SFGSFAVSSPQDLSEVT	47	M	NM_010991.1	1 ... 939
435	OR4Mn	0	15	1.59	LHGAMLGHIQLMSSISV	52	M	AF259072.1	104176 ... 105099
436	OR52Yn P	13	11	3.6	VVVVVLQWPVMGMAVDF	29	M	AF133300.1	46551 ... 47498
437	OR11Hn P	2	15	1.78	FFGTCLCWIPLCLSVIG	61	M	AF121972.1	171 ... 1109
438	OR9An	0	7	148.04	LSGTFVFSWPALMAILG	46	M	NM_010991.1	1 ... 939
439	OR5Mn	0	11	52.19	CILLFFYDFQLMSANLS	50	M	AC069563.9	129775 ... 130725
440	OR6Vn	0	7	148.04	FFGSFAAAPTSDMAFVS	45	M	NM_010991.1	1 ... 939
441	OR4Nn	0	15	1.61	LHGGGAGHIQLMNSMTL	53	M	AC019272.4	62255 ... 61317
442	OR51An P	4	11	3.6	EHTDSLILPFTGLACMS	43	M	NM_013617.1	1 ... 921
443	OR9Pn P	10	7	148.04	FGSNSFEHLVFIHSLLM	39	M	NM_010983.1	178 ... 975
444	OR4H6P	3	15	1.66	MHGCI LGHVQLVNSISG	59	M	AF259072.1	104176 ... 105099
445	OR51Fn P	2	11	3.6	MHTFSLRLPLLGDLTII	48	R	AF079864.1	632 ... 1576
446	OR7E1P	3	11	68.1	MVACGVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
447	OR51Tn	0	11	3.6	MHSLSVRFPLAGLQNT	44	R	AF079864.1	632 ... 1576
448	OR2Vn	0	13	104.15	IVVGGSFDIQVICMLF	84	M	AF102535.1	16 ... 669
449	OR51Hn P	7	11	3.6	MHGGSARAPVLGAVIIL	51	R	AF079864.1	632 ... 1576
450	OR51An	0	11	3.6	EHTVSIRLPFTGIAC TL	48	M	AF071080.2	26330 ... 27262
451	OR2AIn P	2	5	209.13	YLGSCLSNFHLMARILL	55	M	AC044846.2	112743 ... 113748
452	OR2F2	0	7	148.74	LLGGFTSNVQIISSLLT	54	M	AF073974.1	41 ... 649
453	OR1F12	0	6	31.61	MMANNAINLHMVTIVFV	58	M	AC023167.7	60743 ... 61663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Rang
454	OR7G1P	0	19	11.24	ILAGSLMDVQMIASFGI	60	R	AF091580.1	7 ... 663
455	OR7G2	0	19	11.24	ILAGNLTNLLMIAAFGV	61	R	AF091580.1	7 ... 663
456	OR1M1	0	19	11.24	MHGISAFITHLIVAVIT	89	M	X89689.1	32 ... 472
457	OR51UnP	1	11	2.89	VTDDN.....	48	R	AF079864.1	632 ... 1576
458	OR52Hn	0	11	4.19	MHFVSGRIPDLGVPTVS	59	M	AF121975.1	50 ... 1012
459	OR1F1	0	16	6.15	MFVDNGVNLHLIEGVM	75	R	M64377.1	1 ... 939
460	OR10PnP	0	16	87.09	MIGICTTTTHLVATFII	48	M	AF247657.1	1 ... 945
461	OR4FnP	4	19	7.9	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906
462	OR2T1	0	1	254.77	HLVGFGDLLIMCCMLI	92	M	AF102527.1	22 ... 669
463	OR7EnP	9	19	22.8	VAGCDLLDLHIMLAFGL	60	M	AF102536.1	22 ... 669
464	OR51Gn	0	11	3.6	LHSFSVRLPLMGVITVI	57	M	NM_013617.1	1 ... 921
465	OR2Tn	0	1	254.77	MVAGFGLDTFIMCCMLI	67	M	AF102527.1	22 ... 669
466	OR5BGnP	2	11	51.27	AAAAAGGSIHNLFAVEI	52	R	U50948.1	34 ... 978
467	OR5WnP	3	11	51.27	MGADCLVDIHCMFVVAC	51	M	AF146372.1	509 ... 1456
468	OR51Sn	0	11	3.6	MHSVSARLPLLLVLMGD	42	M	AF071080.2	26330 ... 27262
469	OR5WnP	1	11	51.27LVFIES	55	M	AC074177.4	107189 ... 107708
470	OR51AnP	3	11	3.6	EHTDSLILLPTGVAMMD	46	M	NM_013617.1	1 ... 921
471	OR5Dn	0	11	51.21	FCGVTGWCILFCIANES	46	M	AF146372.1	509 ... 1456
472	OR7EnP	4	4	5.55	MVACGVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
473	OR51Fn	0	11	3.6	MHTFSSRPVVFALTTF	53	R	AF079864.1	632 ... 1576
474	OR5Dn	0	11	51.21	YCVVSGWGVLYLFANEC	48	M	NM_013728.1	1 ... 948
475	OR52Rn	0	11	3.6	VHSSSIRWPFMGVAVAF	58	M	AF121976.2	474 ... 1307
476	ORnP	27	11	51.21	FCFAAGQSPGFLCFFFF	23	M	AB030893.1	37 ... 930

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
477	OR7EnP	6	3	121.47	MVACDVLDLHIIDSFSL	57	M	AF073989.1	547 ... 1515
478	OR6Qn	0	11	54.04	LTGACAVTLPLDVSFLA	52	M	NM_010983.1	178 ... 975
479	OR4Fn	0	6	185.89	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
480	OR7EnP	3	13	40.31	FFSP.AAALHIMPAFGL	65	M	X89686.1	32 ... 472
481	OR7En	0	2	95.17	MVACDVLDLHIIDSFGL	57	M	AF073989.1	547 ... 1515
482	OR4Nn	0	14	0.27	LHGAMVGHVQLMNSLSL	58	M	AC019272.4	62255 ... 61317
483	OR2ASn P	7	1	254.77GGGGGMICLLP	43	M	AF102535.1	16 ... 669
484	OR11Hn	0	14	0.33	FFGTCTFIGIPYFQSVLF	90	M	AF121972.1	171 ... 1109
485	OR2Tn	0	1	254.77	MLAGFGLDMLIMCCMLI	69	M	AF102527.1	22 ... 669
486	OR2TnP	1	1	254.77	CMMGFSGDLLIMCCMLI	77	M	AF102527.1	22 ... 669
487	OR2AKn P	3	1	254.55	TLGGACSNIHVSGILL	50	M	AF102533.1	16 ... 669
488	ORnP	16	12	4.38	VLKSKCWQLPFYMPLLM	25	R	Y07557.1	1 ... 942
489	OR5DnP	4	11	51.21	FCAVTGWSTLFCIANES	48	R	U50948.1	34 ... 978
490	OR7EnP	1	4	5.55	FVACDVLDLHIIDNFG	54	M	AF102536.1	22 ... 669
491	OR5L2	0	11	51.27	FCGVVCCCIHLLVANEV	53	M	AF146372.1	509 ... 1456
492	OR5Dn	0	11	51.27	FCVVLVWCTLSLVANES	48	M	NM_013728.1	1 ... 948
493	ORnP	4	9	81.99	..CCCLFFQSIASGTI	23	M	AL359381.1	82137 ... 81544
494	OR10Qn	0	11	54.08	MVGSCGLPQLLLVSVLI	50	M	AL365336.1	123248 ... 124093
495	OR9MnP	1	11	51.27	LCVDSGGSIHNLFAVEI	54	M	AC069559.8	73704 ... 74636
496	OR7E62 P	5	2	73.96	MAACDVLDLHTIDSFRL	56	M	AF073989.1	547 ... 1515
497	OR9LnP	13	11	54.06	MFVGCTLVAYGILTMIA	32	M	AC069561.1 0	147203 ... 146274

SEQ ID #	Symbol	D	C	Mb coord	CDR	#	S	Acc	Range
498	OR7E46 P	10	2	73.96	MAGVEFCDLHIMPAFGL	54	M	AF102536.1	22 ... 669
499	OR1S1	0	11	54.08	MIVVNILITHLLVGIVF	56	M	AC073769.1	133488 ... 132556
500	OR5DnP	0	11	51.21	FCVIMGWCTLSCISSEC	45	M	AC069563.9	111696 ... 112671
501	OR9InP	4	11	54.06	FTASCGGNICCSAVIT	46	R	AF091579.1	7 ... 663
502	OR5Dn	0	11	51.21	FCVVSGWCELSLLANES	53	M	AF146372.1	509 ... 1456
503	OR9QnP	4	11	54.08	FTASCGASVRTIFAVMA	47	M	AL365337.1	192661 ... 191711
504	OR51Cn P	0	11	3.04	MKTVSARMPMLGAMTVV	51	R	AF079864.1	632 ... 1576
505	OR5WnP	1	11	51.27	FCADCGVDIHL.....	53	M	AC069561.1 0	127636 ... 126698
506	OR9InP	2	11	54.06	FTAGCSCGLHCICAMFA	46	M	AC074177.4	106297 ... 105361
507	OR51An P	4	11	3.04	MHSVSARVPVPGVVTGL	72	M	X89685.1	2 ... 481
508	OR5L1	0	11	51.21	FCVVVCCCIHLLVANEV	55	M	AF146372.1	509 ... 1456
509	OR7EnP	5	13	50.42VVDLHIMPAFGL	66	M	X89686.1	32 ... 472
510	OR5BLn P	18	11	54.08	ILGNXLENQCFIFAMIT	29	R	M64392.1	1 ... 942
511	OR51En	0	11	3.04	MHSASVRFPPLGAIVMV	95	R	AF079864.1	632 ... 1576
512	OR51Dn	0	11	3.04	MHSASSRFPLIGIIVMV	61	R	AF079864.1	632 ... 1576
513	OR52In	0	11	3.04	MHTATARFPLMSGSMVS	46	M	AF121975.1	50 ... 1012
514	OR4KnP	2	18	19.04	IHTGMIVHSQFIDSLSS	56	M	AB030896.1	1 ... 906
515	OR52In	0	11	2.99	MHTATARAPLMSGSMVS	47	M	AF121975.1	50 ... 1012
516	OR4KnP	2	18	19.04	IHNIGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
517	OR52Mn P	1	11	3.04	MHATSVRYLPIGIGVLL	51	R	AF079864.1	632 ... 1576

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Rang
518	ORnP	7	6	31.58	FLVSCLLLLLLLEGIHW	30	M	AF073964.1	41 ... 649
519	ORnP	9	8	88.25	IXVVVLNIVNMTTIIFL	24	M	AC074177.4	149899 ... 148964
520	ORnP	9	10	70.63	YSIVMFYHAHFICELLN	26	M	AC068902.1 1	144125 ... 143193
521	ORnP	9	9	70.7	WWWWSWYGNFDD SITX	26	R	AF091563.1	7 ... 669
522	ORnP	9	5	202.43	FFFFFF.PPPPP.....	27	R	AF034902.1	4197 ... 5177
523	ORnP	10	11	137.77	LLLLWSQFXQFLAVVVV	29	R	M64376.1	1 ... 999
524	ORnP	3	11	16.31	NNNNNLLXMNILTLLAI	27	M	AL136158.1 4	29455 ... 30402
525	ORnP	17	11	55.6	LAGNNIYCYHM..LLLL	26	R	M64377.1	1 ... 939
526	OR6Pn	0	1	154.6	LIACCASSMKFDLAMIL	60	M	NM_010983. 1	178 ... 975
527	OR7EnP	3	14	33.48	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
528	ORnP	12	11	138.51	LMCHS.FFFFFFFMMMMM	29	R	AF091573.1	7 ... 663
529	OR7EnP	5	14	33.48	MAGGDFLDLYILPDFGL	55	M	AF073989.1	547 ... 1515
530	ORnP	7	10	127.4	S.CCCLLTYYIIHHHHH	31	M	AC020958.1	164590 ... 163746
531	OR10XnP	2	1	154.6	MLGGCSAITELIISGLG	49	M	AC073778.1	168744 ... 167803
532	OR10Zn	0	1	154.71	MAACCTTFGMVILSVLV	56	M	AC025913.3	108128 ... 109067
533	OR6KnP	2	1	154.73	MYGIVGCTPEWVVEIT	40	R	M64386.1	130 ... 975
534	OR6Kn	0	1	154.73	MHGIVSCTPEWVIHEIT	44	M	AC027184.3	54955 ... 54017
535	OR1FnP	1	4	97.57IEGVMT	73	R	M64377.1	1 ... 939
536	OR1ABnP	3	19	19.44	MIGISAFNTHLV.....	64	M	AC073769.1	133488 ... 132556
537	OR52MnP	1	11	2.89	MHATSARYLPIGIGVLL	49	M	AF121975.1	50 ... 1012
538	OR1XnP	6	5	202.43	MIANTLGIVHIFAALFA	71	M	AF102530.1	1 ... 666

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
539	OR4FnP	8	16	83.04	QQQQQVIHSQFVNSLTC	46	M	AC019272.4	62255 ... 61317
540	OR52Mn P	5	11	2.89	MHATSVRYLPIGIGVLM	45	R	AF079864.1	632 ... 1576
541	OR2Vn	0	5	209.61	IVVGGSFDIQVICMLF	83	M	AF102535.1	16 ... 669
542	OR2V1P	4	5	209.61	IVVGGSFDIQALCCMLL	90	M	AF102537.1	16 ... 669
543	OR2Zn	0	19	65.55	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
544	OR52Kn P	5	11	2.89AMFIEL	52	M	AF121975.1	50 ... 1012
545	OR10Hn	0	19	19.7	MFGFSWGMVIGLVTAI	75	M	AC023604.2	214343 ... 213396
546	OR2Dn	0	11	5.77	ILGCCRSVVDFIMGILA	85	M	AF073987.1	2 ... 649
547	OR7EnP	6	2	161.49	VVGGCSSLHIMPAPGL	64	M	X89686.1	32 ... 472
548	OR11Gn P	4	14	0.27	FFGSCSLWIPVLSLLI	68	M	AC027184.3	54955 ... 54017
549	ORn P	12	14	0.27	GSCGNSLHHYLMVNIIL	28	M	AF121972.1	171 ... 1109
550	OR11Gn	0	14	0.33	FFGSCNLWIPNLSFVPM	67	M	AF121972.1	171 ... 1109
551	OR11Hn P	5	14	0.33	FTGTAFFSVSQFLSIIL	68	M	AF121972.1	171 ... 1109
552	OR6Kn	0	1	154.73	MHENGGFIPMDHATII	46	R	AF034897.1	354 ... 1199
553	OR11Hn	0	14	0.33	FFGTCVGCVPFCFNIIG	71	M	AF121972.1	171 ... 1109
554	OR6KnP	0	1	154.73	MHGNGGFVPEWDHAAIF	46	M	AL365336.1	122764 ... 121784
555	OR11Hn P	2	14	0.33	FFGTCLIGISFFVSFIL	70	M	AF121972.1	171 ... 1109
556	OR6KnP	2	1	154.82	MHGVAGFMPECDRASIT	43	M	AC027184.3	54955 ... 54017
557	OR6Kn	0	1	154.84	MHGISGCLPEWVIHEIA	45	R	AF034900.1	1 ... 963
558	OR2Ln	0	1	254.55	SSGGAGINAHYVSTFLF	53	M	AF102527.1	22 ... 669
559	OR4GnP	8	16	83.04	ICRKMAVHSQFVNSISA	45	M	AB030892.1	1 ... 939

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
560	OR6Nn	0	1	154.84	IHGACGGGVELDINKIA	50	R	M64386.1	130 ... 975
561	OR2LnP	2	1	254.55	SLAVGGINAHY.....W	52	M	AF102535.1	16 ... 669
562	OR9A1	0	7	146.91	LLGTLVLSPALMAIIG	45	M	L14567.1	17 ... 667
563	OR6Nn	0	1	155.69	THGACACCSELDINIII	51	M	AL136158.1 4	29455 ... 30402
564	OR10Hn	0	19		MFGFSCGMVVAGLVLTAL	86	M	AC023604.2	245345 ... 246298
565	OR7EnP	4	9	71.72	MVACDVLDLHIMNSFGL	57	M	AF073989.1	547 ... 1515
566	OR2AQn P	5	1	155.69	FCHSCLLLLSLLPFFFF	31	M	AL359352.1	55588 ... 56546
567	OR2LnP	3	1	254.55	SMAGAGINAHYVSSFLF	50	M	AF102537.1	16 ... 669
568	OR5ARn	0	11	52.46	FVVDGCGASAHLLLCIES	53	R	AF091579.1	7 ... 663
569	OR7EnP	4	9	71.79	TAGGETLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
570	OR10AA nP	2	1	155.69	THGMCAAAPLHVIAATC	84	M	AC005992.1 5	9114 ... 8173
571	OR10Jn P	4	1	157.7	MIAICGVVVQSNVSVIV	72	M	X92969.1	8035 ... 8961
572	OR5A1P	0	11	55.81	FVGLCGGSIQSNVVVGT	81	M	Y15525.1	1 ... 705
573	OR2AHn P	5	11	52.46	MLGSCISSVILVFSIVI	51	M	AF247657.1	1 ... 945
574	OR10Jn P	4	1	157.7	LLGICGIMVQSNVSVLL	68	M	X92969.1	8035 ... 8961
575	OR56Bn P	2	11	4.93	IHMCSSRLPVLQLVVVS	39	M	AF121975.1	50 ... 1012
576	OR5M1	0	11	52.35	CIVIFIYSSQLMVANLS	49	R	AF091579.1	7 ... 663
577	OR52Wn P	0	11	4.93	MHTASLLAVPLGLSISM	48	M	AF121976.2	474 ... 1307
578	OR5AMn P	5	11	52.35	FIVIYAYNVQLMVANLC	35	M	AC068904.1 5	113793 ... 114719
579	OR52Bn P	3	11	4.93	MHFVSTQTPVLGVPSVV	89	M	AF121975.1	50 ... 1012
580	OR5MnP	1	11	52.35	CVLLYFWVMQLLSANLV	48	R	X80671.1	203 ... 1129

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
581	OR5APn P	6	11	52.35	FGAGGALNIHFIFANES	55	R	X80671.1	203 ... 1129
582	OR56Bn	0	11	4.95	IHFCSFRLPVLQALVS	41	M	AF121975.1	50 ... 1012
583	OR5APn	0	11	52.35	FGLGCTANIHMIFSIVS	55	M	AF121977.1	262 ... 1197
584	OR52Bn	0	11	4.93	GHFVSARIPVLGVPMVL	73	M	AF121975.1	50 ... 1012
585	OR9Gn	0	11	52.5	FAAYCVGNIKMLLNVC	45	M	AC074177.4	106297 ... 105361
586	OR52Kn	0	11	2.86	MHSISARLPLLGVASVL	53	M	NM_013619. 1	118 ... 969
587	OR5MnP	1	11	52.35	FIVIIYAYNSQLMVANLC	51	M	AC074177.4	106297 ... 105361
588	OR52Kn	0	11	2.86	MHSISARLPLLGVAIVL	52	M	NM_013619. 1	118 ... 969
589	OR52Kn P	3	11	2.82	MHSISARLPLLGVAIGL	53	M	NM_013619. 1	118 969
590	OR52Bn P	4	11	2.78	IHFISARVPDLGVLTVL	57	M	AF121975.1	50 ... 1012
591	OR2B6P	0	6	31.62	LLGAYATNWLLLVSFHI	79	R	L34074.1	73 ... 1011
592	OR2WnP	7	6	31.61	LLRGCASNVMLAFAIVL	58	M	AF102516.1	52 ... 669
593	OR2AnP	5	7	148.83	TMAHCTCLVHLISSILG	72	M	AF102521.1	22 ... 669
594	ORnP	16	6	31.61	FLVSCMDFMIVLNNVI	39	M	AF102516.1	52 ... 669
595	OR2LnP	0	1	254.55	STAVAGINAHYVSAFLF	50	M	AF102527.1	22 ... 669
596	OR2W2P	5	6	31.61	LLGGCVCQSYWVLSIVM	55	R	L34074.1	73 ... 1011
597	OR2LnP	1	1	254.55	SLAGA.....	61	M	AF102535.1	16 ... 669
598	OR2B7P	1	6	31.61	LLGGCTTNIQLIVSFLV	59	M	AC044846.2	105668 ... 104736
599	OR2Ln	0	1	254.43	SLGGAGINAHYVSAFLF	53	M	AF102527.1	22 ... 669
600	OR5BFn	0	1	254.77	VVVYLASYMHSISAVGG	46	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
601	OR2LnP	4	1	254.55	SVAGMSMDAHYVSTFLF	47	M	AF102527.1	22 ... 669
602	OR7EnP	3	10	17.14	MVACCVLDLHI.....	51	R	AF091580.1	7 ... 663
603	OR1H1	2	9	106.04	LGADNVIHVHLLVALLA	57	M	AC073769.1	133488 ... 132556
604	ORnP	14	1	254.49	TTTKKSERIYIVSSFLI	24	M	AF102527.1	22 ... 669
605	OR4Dn	0	11	55.81	IHGGIASHIQLMNNVTL	64	M	AC019272.4	183633 ... 182701
606	OR1Ln	0	9	106.04	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
607	OR5AXn	0	1	254.2	L TSAIVIFAYGGVGLSS	47	M	AL136158.1 4	154973 ... 155908
608	OR5An	0	11	55.77	YCGLCGGSIESTVSVG	64	M	Y15525.1	1 ... 705
609	OR5AYn	0	1	254.2	LVAGILNLLYGSIGYAS	50	M	AL359352.1	126933 ... 127889
610	OR13Gn	0	1	255.42	LTLGMMINVHLVADLAG	59	M	AF102540.1	16 ... 669
611	OR5BBn P	0	11	55.77	YASLCGGSVHPLEAVGG	54	M	Y15525.1	1 ... 705
612	OR9GnP	6	11	52.49	FVXNCAGNIIELMLNIT	47	M	AF121977.1	262 ... 1197
613	OR2TnP	4	1	254.77	HLAGFAGNLLVMCCMLI	75	M	AF102527.1	22 ... 669
614	ORnP	7	1	255.42	PVAGKGAFLHSVESLGS	38	M	AL365337.1	192661 ... 191711
615	OR1Jn	0	9	95.9	MITDSVLSSHLMVGIL	66	M	AF102524.1	52 ... 669
616	OR2CnP	1	16	6.47	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
617	OR9GnP	2	11	52.49	FAAYCYGNILNLLNVS	49	M	AL365337.1	192661 ... 191711
618	OR2C1	0	16	6.4	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
619	OR51An P	2	11	4.22	52	M	AF071080.2	26330 ... 27262
620	OR9Gn	0	11	52.49	LCAYCGGNAHNLVVTVS	53	M	AC068904.1 5	165039 ... 165965

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
621	OR52Bn	0	11	2.78	LHFISTRTPILGILTVL	61	M	AF121975.1	50 ... 1012
622	OR1K1	0	9	105.89	MFGVSMVHLYLIEGVVT	58	R	M64377.1	1 ... 939
623	OR51Rn P	3	11	2.78	MHTYSARLPGLGSISLL	47	R	AF079864.1	632 ... 1576
624	OR7EnP	2	13	54.83	MVACDVLDLHILDSFGL	57	M	AF073989.1	547 ... 1515
625	OR52Pn P	3	11	2.82	MHSASARLP LLGAAVVT	55	M	AF121975.1	50 ... 1012
626	OR7EnP	5	9	70.7	MVACDVQYVHSMDSFGL	48	M	AF102536.1	22 ... 669
627	OR7EnP	5	9	70.7	TAGGD.CCCCC.....	43	M	AF073989.1	547 ... 1515
628	OR4KnP	1	21	8.12	IHTGMIVHSQFIDSLSS	57	M	AF259072.1	104176 ... 105099
629	OR4KnP	2	21	8.12	IHNIGIVVHSQFMTSTAT	54	M	AB030896.1	1 ... 906
630	OR7EnP	6	9	70.7VFLVHVPAPFGL	58	M	X89686.1	32 ... 472
631	OR51In	0	11	4.15	MHSFSGKTPFVGVITYM	51	R	AF079864.1	632 ... 1576
632	OR51In	0	11	4.15	MHSMSGRTPLLGVLTFM	56	R	AF079864.1	632 ... 1576
633	OR2AnP	1	7	148.83	TLAICTFL.....	63	M	AF102521.1	22 ... 669
634	OR2A2	2	7	148.83	TLAVCTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
635	OR2AnP	8	7	148.83	TFAACTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
636	OR2Gn	0	1	256.63	LHGSCMSTVQLLASFLV	59	M	NM_008762.1	1 ... 936
637	OR2AnP	0	7	148.83	TLAHCAFFFFL.....	57	M	AF102521.1	22 ... 669
638	OR6Fn	0	1	254.2	MFGCYGCAVPLAIAVIS	71	R	M64378.1	1 ... 933
639	OR2AnP	4	7	148.83	TLAHCAFLVHLISCILG	68	M	AF102521.1	22 ... 669
640	OR2Gn	0	1	256.02	LLGSCISSIHFLVSFVI	63	M	M84005.1	1 ... 936
641	OR7E37 P	5	13	26.5	MAGGEFLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
642	OR5AVn	0	1	256.02	AMATVMSCMHAVFGLVI	51	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
643	OR2AJnP	7	1	254.43	VLLGCGINVHYVSAFLI	55	M	AF102527.1	22 ... 669
644	OR13EnP	1	9	39.89	MLGSCLTNLQLLATLTA	79	M	AJ251155.1	15491 ... 16423
645	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
646	OR2TnP	0	1	254.43	IPGGCSLDLQAMCCMLV	59	M	AF102537.1	16 ... 669
647	OR2WnP	2			LMGSCVCNIMQTLGLLV	56	M	M84005.1	1 ... 936
648	OR13Jn	0	9	39.89	MLGSCALKTEILGSLLV	82	M	AJ251155.1	6062 ... 6997
649	OR6RnP	2	1	254.39	SFGCFLGLPSLDSSLIS	45	M	NM_010983.1	178 ... 975
650	OR5ATn	0	1	254.39	VLASLVYIMHGLINLDC	50	M	AL359352.1	111313 ... 112242
651	OR2Zn	0	19	10.64	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
652	OR4Ln	0	14	0.08	MHGGMLIHSQLVDSLST	53	M	AB030893.1	37 ... 930
653	OR4UnP	14	14	0.15	RHSGMAMHSQLVDSLST	46	M	AB030895.1	1 ... 924
654	OR4Fn	0	6	185.98	IHGGMIHIHQFVNSISA	50	M	AF102522.1	40 ... 660
655	OR4FnP	2	6	185.98	IHGGMAIHVQFVNSISS	50	M	AB030896.1	1 ... 906
656	OR4Fn	0	6	185.98	IHGGMATHVQFVNSISG	50	M	AB030896.1	1 ... 906
657	OR4Fn	0	6	185.98	IHGGMTIHVQFVNSISG	50	M	AB030896.1	1 ... 906
658	OR4AnP	5	11	50.28	IHGGILGHVQFVNDICV	65	M	AF102522.1	40 ... 660
659	OR4LnP	1	14	0.21	KHGSMLIHSQLVDSLST	53	M	AB030893.1	37 ... 930
660	OR7E33P	6	13	54.79	MAGGEFLDLRILPAFGL	56	M	AF073989.1	547 ... 1515
661	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
662	OR4Kn	0	14	0.15	MHGGMSVHSQFVDSLVS	53	M	AF259072.1	104176 ... 105099
663	OR5U1	0	6	33.45	VIASVAASMHILFTAAI	84	M	AL359352.1	111313 ... 112242
664	OR4Kn	0	14	0.08	IHGGMAVHSQFMDSLSS	58	M	AF259072.1	104176 ... 105099

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
665	OR5V1	0	6	33.45	LVVGCSANVHLLTGIGT	84	M	AL365337.1	192661 ... 191711
666	OR4QnP	1	14	0.08	LHGAMAGHVQLMNSISI	62	M	AF259072.1	104176 ... 105099
667	OR12D3	0	6	33.45	LHGSAAIYMHMLVTISG	70	M	AL359381.1	128169 ... 127234
668	OR4Kn	0	14	0.08	IHTGMIVHSQFIDSLSS	59	M	AF259072.1	104176 ... 105099
669	OR51CnP	3			MKTVSARMPMLGAMTVV	53	R	AF079864.1	632 ... 1576
670	OR1J2	0	9	105.94	MITDSVLSSHLMVGVL	66	M	AF102524.1	52 ... 669
671	OR5BJnP	3			SIGSAAVNTKFPSC LGV	46	M	AF073965.1	2 ... 643
672	OR1J1	0	9	105.82	TIADSGICLHLIAAAIL	63	M	AF102524.1	52 ... 669
673	OR13En	0			MLGSCLTNLQLLATLTA	83	M	AJ251155.1	15491 ... 16423
674	OR4KnP	5	14	0.08	IHGGMVIHTHFVNSLSM	53	M	AB030893.1	37 ... 930
675	OR1LnP	5	9	105.84	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
676	OR2CnP	2			FHGACAGTVGLMASFVL	59	M	M84005.1	1 ... 936
677	OR4TnP	9	14	0.21	MLSELLSHSQFVKSLSI	47	M	AC019272.4	62255 ... 61317
678	OR5BnP	1			FVITSGCNIHNIVVNDF	51	M	AF121977.1	262 ... 1197
679	OR4Kn	0	14	0.21	IHGGMTLHFQFINSISS	53	M	AB030896.1	1 ... 906
680	OR11Ln	0	1	254.43	LVGACVTTLHMILSVLI	50	M	AF121972.1	171 ... 1109
681	OR7E68P	5	10	17.21	MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
682	OR7EnP	2	10	17.21	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
683	OR7E31P	6	9	70.71	TAGGELLDLHIMPAFGL	55	M	AF073989.1	547 ... 1515
684	OR7EnP	3	9	70.71	MVACDVLDLHIMDSFGL	58	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
685	OR5AKn P	3	11	52.82	LAATCGMNVHFLFVNLF	79	R	U50948.1	34 ... 978
686	OR5AKn	0	11	52.83	FAATCGMNVQFLFVNLF	79	R	U50948.1	34 ... 978
687	OR5AKn	0	11	52.83	FAATCGINVHFDVDFDLF	79	R	U50948.1	34 ... 978
688	OR5BQn P	9	11	52.82	TTTTTLLLLLMLTFFFF	42	R	U50948.1	34 ... 978
689	OR1Nn	0	9	105.94	LLGGNVLPMLHIMGFLV	56	R	AF091566.1	1 ... 663
690	OR1J4	0	9	105.94	MITDNVLNSHLIVGVIL	69	M	AF102524.1	52 ... 669
691	OR1Nn	0	9	105.94	MLGDSLLVTHLVLGVLV	85	R	AB038167.1	1 ... 933
692	OR2AnP	4	3	94.41	TLAVCTIMVHHLGSIVG	65	M	AF102521.1	22 ... 669
693	OR2ANn P	17	9	93.78VVVLEFMVNLLI	23	M	AC074177.4	128803 ... 129726
694	OR5K1	0	3	104.47	FCETCGAHIHLLFSVQF	51	R	AF091575.1	52 ... 663
695	OR2K2	0	9	93.78	MLGSCVTTLEFMVSLLI	60	M	AJ251154.1	35662 ... 36615
696	OR8Hn	0	11	51.76	MAGTCGIDVNSIIVTLV	51	M	AC069559.8	36251 ... 35322
697	ORnP	15	11	51.76	LIFKNLFSPLXXHYIL	28	M	X89682.1	2 ... 472
698	OR4AnP	14	11	50.28	FGRRVVGHIQLYGHNYV	38	M	AB030895.1	1 ... 924
699	OR4An	0	11	50.28	LHGGVVQGQFQIVNGSCI	59	M	AB030895.1	1 ... 924
700	OR6Sn	0	14	0.58	FFGAFAGPGPADLAVIS	50	R	M64378.1	1 ... 933
701	OR4RnP	16	11	50.28	NLGAIMEHVXSVNGNYL	52	M	AF102522.1	40 ... 660
702	OR13Cn	0	9	86.77	MLGTCGINVQFLTTFLT	65	M	AJ133425.1	61 ... 1014
703	OR13Dn P	4	9	86.77	MYGSCVLNTELIGNFLS	64	M	AC023789.5	371264 ... 372220
704	OR7EnP	3	11	2.13	MIACGVLDLHIINSFGL	54	R	AF091580.1	7 ... 663
705	OR10Pn P	1	12	59.88	MIGICTTTTHLVATFII	49	M	AF247657.1	1 ... 945
706	OR8In	0	11	51.76	MVVCCMISISVSLATLS	50	M	AC069559.8	137090 ... 138039
707	OR8G1	0			..IIIGICVHCIVGNIV	75	R	AF091576.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
708	ORnP	7	12	59.88	CFPGEAFFTLL.....	34	M	AL359352.1	145887 ... 145042
709	OR5F1	0	11	51.76	MIATCGANVNHSLANIG	50	M	Y15525.1	1 ... 705
710	OR5FnP	1	11	51.76	MIATCGANVNYFFANKG	52	M	Y15525.1	1 ... 705
711	OR6BnP	6	2	251.7	LSVCCFSIIKFDLAILF	70	M	L14567.1	17 ... 667
712	OR2D1	0			LLGCCASVVD FITGILI	64	M	AF073987.1	2 ... 649
713	OR5ASn	0	11	51.76	MAADCLSTVHLLLCIQS	52	M	AC068904.1 5	165039 ... 165965
714	OR5SnP	8	2	251.7	FSSTTGRSVQLKLCMMN	64	R	AF091579.1	7 ... 663
715	OR5AQn P	0	11	51.76	SAVTDAGNTHGPF SIAF	51	R	X80671.1	203 ... 1129
716	OR6BnP	3	2	251.7	LSVCCFSIIKFDLAILF	67	M	L14567.1	17 ... 667
717	OR5JnP	2	11	51.76	YVLTGGGNTHGLFSIAL	52	R	X80671.1	203 ... 1129
718	OR9AnP	4	7	146.91	QLGTLVFFFWPALMAIIG	44	M	NM_010991. 1	1 ... 939
719	OR5BEn P	2	11	51.76	YSLTCVLNTHSFLSTST	45	R	AF091564.1	7 ... 663
720	OR9An	0	7	146.91	LLGTFVFFFWPVLMAVLG	47	M	NM_010991. 1	1 ... 939
721	OR8Hn	0	11	51.76	MVGTCGIDVNSIIATLV	51	M	AC069559.8	36251 ... 35322
722	OR5BNn P	14	11	51.76	LLMTCAYMSHS.....P	54	M	AF102528.1	52 ... 669
723	OR8Jn	0	11	51.76	LLIVVLYTVVCVSANLF	80	M	X89682.1	2 ... 472
724	OR9NnP	9	7	146.91	LFGTFIIIIIL.AAAAA	36	M	NM_010991. 1	1 ... 939
725	OR7EnP	4	7		MVACGMLDLHITHSFAL	51	R	AF091580.1	7 ... 663
726	OR7E9P	3	7		MVACDVLDLHVIDSFGL	51	M	AF073989.1	547 ... 1515
727	OR8KnP	8	11	51.76	MMITLICQIIDILTNP	36	M	AC069563.9	28460 ... 29383
728	OR2AnP	1	7	148.97	ILAHC.....	44	M	AF102521.1	22 ... 669
729	OR8Kn	0	11	51.76	LLIIFIYQMFKSFSNLS	56	M	AF102528.1	52 ... 669
730	OR7E39 P	4			MVGGEFLHLHIMPAFGL	55	R	AF091580.1	7 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Rang
731	OR7E27P	3			MAGGELLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
732	OR2Hn	0	6		FLGTCVTEVQSLASILV	81	M	AL078630.1	41097 ... 40165
733	OR13Cn P	2	9	40.16	MLGACGATVQLMANFLV	87	M	AJ133428.1	61 ... 1017
734	OR13Cn	0	9	40.16	MFGACGAAVQLMTNFLV	89	M	AJ133424.1	61 ... 1017
735	OR2S1P	4	9	40.16	MFGACGANVQLMTNELL	89	M	AJ251154.1	2703 ... 1747
736	OR2AMn P	1	9	40.16RRRRRV.MMMM	63	M	AJ251154.1	2703 ... 1747
737	OR1N1	0	1		MLGDSLLVTHLVGLVLV	85	R	AB038167.1	1 ... 933
738	OR2S2	0	9	40.13	MFAGCSIAVHLMTNFLV	83	M	AJ251154.1	2703 ... 1747
739	OR7E26P	4	1		MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
740	OR1F11	0			LAGNNGVNLHLIEGVMT	99	R	M64377.1	1 ... 939
741	OR5ACn P	3	3	103.97	FGATCIIHHLIFSIOF	66	R	AF091575.1	52 ... 663
742	OR5B10P	2	13		MVATNGCNLRDLMSNVL	46	M	AF102528.1	52 ... 669
743	OR2AnP	1	12	85.7	TLAVCAFLVHLIACILG	76	M	AF102521.1	22 ... 669
744	OR1E5	0	13		MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
745	OR4Fn	0	6	185.71	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
746	OR5CnP	0	9	40.53	MAADC.....	47	M	Y15525.1	1 ... 705
747	OR2WnP	0	6	31.62	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
748	OR2L2	0			..IIIGINAHYVSSFLL	48	M	AF102537.1	16 ... 669
749	OR4H8P	2	14		MHGCILGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
750	OR5D10P	5			LCVVTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
751	OR7A12P	1	14		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
752	OR2L1	0			..IIIGINAHYVSTFLF	48	M	AF102527.1	22 ... 669
753	OR2F3P	0	14		LLGGFTSSVQIISLLT	55	M	AF073974.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb Coord	CDR	%	S	Acc	Range
754	OR4H10 P	2	15		MHGCI LGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
755	OR5H1	0			..IIILGHIHFVFSIQF	56	R	AF091575.1	52 ... 663
756	OR2K1	0			..IIIIITTLVCMVSLLI	58	M	AJ133428.1	61 ... 1017
757	OR7E11 P	7	11		MAGGEFLDLHILPAFGL	52	M	AF073989.1	547 ... 1515
758	OR7A3P	1	11		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
759	OR6A1	0	11		LLGCCGGIVKLDLAILG	91	R	M64386.1	130 ... 975
760	OR5I1	0	11		FCADSLGSVHFLYGVEI	52	M	Y15525.1	1 ... 705
761	OR2H3	0	6		ILGTCVIGVQSVASILV	86	M	AL078630.1	41097 ... 40165
762	OR10J1	0			MVGICGIVTQSTISVLV	73	M	X92969.1	8035 ... 8961
763	OR7E3P	3	11		MFACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
764	OR1D6P	1	11		LVVANLFYIHLTGIFI	48	R	Y07557.1	1 ... 942
765	OR5D10 P	2	18		LCVVTTWCTLFTSASES	45	R	U50948.1	34 ... 978
766	OR5D5P	2	18		LCVVTTWCTLFTSANES	46	M	AC073947.3	29192 ... 30115
767	OR52A1	0	11		MHQGSMVCLIGVAVAF	72	M	NM_013620. 1	1 ... 945
768	OR2AEn	0	7	98.36	HLGGCMGNIHIVSSLLL	48	M	AC073769.1	143294 ... 142353
769	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	40	M	NM_010983. 1	178 ... 975
770	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	41	M	NM_010983. 1	178 ... 975
771	OR7MnP	7	10	149.44NVYVSL.....	29	M	AC073947.3	43325 ... 42733
772	OR13Cn	0	9	86.77	MFGACGTDVQFMSNVLI	69	M	AJ133428.1	61 ... 1017
773	OR13Cn	0	9	86.85	MLGTCGANVQFMATFTM	71	M	AJ133425.1	61 ... 1014
774	OR2InP	6			LLGSC.....	79	M	AL078630.1	151152 ... 150391

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
775	OR4An	0	11	50.28	LHGGVVGHFQVVNSICV	58	M	AB030895.1	1 ... 924
776	OR2InP	3		RRRRRMARILL	77	M	AL078630.1	151152 ... 150391
777	OR4AnP	4	11	50.28	LHGGVVGSGFQVVNGICV	53	M	AB030896.1	1 ... 906
778	OR4AnP	7	11	50.28	PHGGAVAHFQVVNGICV	57	M	AB030896.1	1 ... 906
779	OR8C1P	2	11		LCVHCGMGVHCMIVVVV	72	M	AC068905.1 2	76922 ... 75948
780	OR4AnP	1	11	50.28	LHGDVVGHFQVVNGICV	56	M	AB030896.1	1 ... 906
781	OR7E15 P	5	11		MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
782	OR10A1	0	11		MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
783	OR2An	0			TSAVCTCLVHLI.....	70	M	AF102521.1	22 ... 669
784	OR7EnP	6			MAGGELFHLHIMPAFGL	57	M	AF073989.1	547 ... 1515
785	OR7En	0			MAGGDFLDLHIVPAFVL	54	R	AF091580.1	7 ... 663
786	OR51A1 P	5	11		MHTLSARLPLLAVITFL	43	R	AF079864.1	632 ... 1576
787	OR7E47 P	4			KAGTNLLDLYIMPTFGL	56	M	AF073989.1	547 ... 1515
788	OR5B5P	2	3		MAATNICNIHELVANIS	48	M	AF146372.1	509 ... 1456
789	OR1F10	0	3		MFVDNGVNLHLIEGVM	72	R	M64377.1	1 ... 939
790	OR8G2	0			..IIIGLGIHFVLSNIT	75	M	AF102518.1	52 ... 669
791	OR1Sn	0	11	54.08	MIVVNILITHLLVGIVF	55	M	AC073769.1	133488 ... 132556
792	OR4AnP	3	11	50.73	LHGGAVGHFQVVSGLCV	56	M	AB030896.1	1 ... 906
793	OR4AnP	7	11	50.76	LHGGILGHFQVVNGMCV	58	M	AB030896.1	1 ... 906
794	OR4AnP	5	11	50.66	LHGGVLGHFQVVNGMRV	56	M	AB030896.1	1 ... 906
795	OR4AnP	7	11	50.73	PHGGVVGRFQVVKVICV	54	M	AB030896.1	1 ... 906
796	OR4AnP	1	11	50.81	LHGGIVGHFQVVSGMCV	60	M	AB030896.1	1 ... 906
797	OR4AnP	10	11	50.81	LHGGVVGNFQVVNGICV	55	M	AF102522.1	40 ... 660
798	OR4An	0	11	50.73	LHAGVAGHVQFMNGICV	62	M	AB030895.1	1 ... 924
799	OR4An	0	11	50.73	LHGGVVGHVQFVNGICV	57	M	AB030896.1	1 ... 906
800	OR7E42 P	4			MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
801	OR2M3P	2			ITLGCFLDIDALCCMIF	55	M	AF102537.1	16 ... 669
802	OR4H11P	2	4		MHGCILGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
803	OR7E57P	5			MAXGEFLDLHILPAFGL	51	M	AF102536.1	22 ... 669
804	OR2B1P	0	5		LLGAYATNWLLLVSFHI	78	R	L34074.1	73 ... 1011
805	OR7E34P	2			MAGGDSLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
806	OR7E56P	4			MAGDEFFLHILPAFGL	52	M	AF073989.1	547 ... 1515
807	OR3AnP	1	5		LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
808	OR4H5P	2	5		MHGCILGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
809	OR1En	0	5		MLGDSLLHLHLIMGILI	82	R	Y07557.1	1 ... 942
810	OR51CnP	2	11	3	MKTVSYYYIXQ.....	48	M	AF121975.1	50 ... 1012
811	OR2WnP	2	6	30.51	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
812	OR51B1P	5	11		AHSVSGRSPVRPLITIL	68	M	AF071080.2	15931 ... 16851
813	OR7E81P	3			MAGGEFFSLHIMPAFGL	54	M	AF102536.1	22 ... 669
814	OR7E44P	1			MAGGELFDLHIMLAFGL	53	M	AF073989.1	547 ... 1515
815	OR5B7P	2	6		MAATNICNIHELVANIS	47	M	NM_013728.1	1 ... 948
816	OR7E36P	4			MAGGELFFLHIMPAFGL	58	M	AF073989.1	547 ... 1515
817	OR2A5	0	7		TMAHCTCLVHLIASILG	74	M	AF102521.1	22 ... 669
818	OR5B1P	2	8		MAATNICNIHELVANIS	47	M	AF146372.1	509 ... 1456
819	OR8B8	0	11	137.68	LLVVS GMGAHCVVVDIV	72	M	AC069559.8	120212 ... 119283
820	OR8B4P	0	11	137.71	LCVNCGVGAHSFVVITL	87	M	AC068910.2 1	133103 ... 132162

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
821	ORnP	15	11	137.77	LCVENRRRTATHCKSHII	35	M	AC069563.9	60295 ... 59327
822	OR8B3	0	11	137.77	LLVICAMGAHCVVNVIV	85	M	AC069563.9	129775 ... 130725
823	OR2Bn	0	6	30.51	LLGSCASNQLWLISFLI	89	R	L34074.1	73 ... 1011
824	OR8B6P	6	11	137.77	LAFFCGLSAHCVAAAVI	73	M	AC069559.8	96224 ... 95292
825	OR8B5P	6	11	137.77	LFFFXGLGAHCVVANTV	73	M	AC069559.8	96224 ... 95292
826	OR4E2	0	14	1.7	LHACIAGHGQLINSISS	90	M	AF259072.1	104176 ... 105099
827	OR8B7P	4	11	137.77	FCVICGWGAHCVAAIFV	71	M	AC069559.8	96224 ... 95292
828	OR11JnP	3	15	1.82	FSCAGFGSMPLCVSIII	56	M	AF121972.1	171 ... 1109
829	OR4E1P	3	14	1.7	MHACIAGHALLINSISV	92	M	AB030893.1	37 ... 930
830	OR10DnP	7	11	137.96HHHILLGNVLSI	85	M	AC074177.4	12106 ... 13038
831	ORnP	10	14	1.7	VFRGGFHKFFF.....	23	M	AF102536.1	22 ... 669
832	OR8D2	0	11	137.77	LLVIGVLWVHRLIGNTA	70	M	AC073947.3	29192 ... 30115
833	OR11InP	1	1	126.31	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
834	OR11JnP	1	15	1.82	FSCACFGWTPLCISIIL	56	M	AF121972.1	171 ... 1109
835	OR10AnP	3	11	5.64	MFGVCTPVVQWAGTVVI	74	M	AF247657.1	1 ... 945
836	OR8C3P	5	11	137.77	LCVHCGMGVHCMIVVVV	73	M	AC068905.1 2	76922 ... 75948
837	OR2DnP	6	11	5.64	LLGCCGSVVDFITGILI	62	M	AF073987.1	2 ... 649
838	OR4PnP	0	11	51.03	LHGGIVGHSQL.....	59	M	AB030895.1	1 ... 924
839	OR7E21P	5			MAGGEFIDLHIMPAFGL	50	M	AF073989.1	547 ... 1515
840	OR2M1	0			IVLGCFLDIYAICSMFLF	55	M	AF102537.1	16 ... 669
841	OR7AnP	4	19		NLAGVVMNLQM.....	63	M	AF073970.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Rang
842	OR5D11 P	1	8		LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
843	OR7E50 P	7	8		IVVCDMLDLHVFLDIFL	57	M	AF102536.1	22 ... 669
844	OR7E45 P	3			MAGGELFDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
845	OR7E77 P	6			MAGGEFLDLHIMPAFGL	51	M	AF073989.1	547 ... 1515
846	OR8B2	0	11	137.77	LLVICAMGAHCVVVNIV	84	M	AC069563.9	129775 ... 130725
847	OR8D1	0	11	137.77	LVVVGALSTHALIANTV	87	M	AC073947.3	29192 ... 30115
848	OR8B1P	4	11	137.77	LLVCGMGAHCVVVNIV	84	M	AC069559.8	96224 ... 95292
849	OR7A1P	2	19		MIVVSVVYLQMMTSLGG	72	R	M64376.1	1 ... 999
850	OR7E8P	4	8	13.72	MVACGVLDLHIIDSFGL	53	M	AF102536.1	22 ... 669
851	OR4DnP	7	11	55.86	MHGGVAGHVQLMNNISL	58	M	AC019272.4	183633 ... 182701
852	OR7E80 P	7	8	13.72	MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
853	OR4DnP	5	11	55.86	MHGGGAAGHVQLMNNLTL	62	M	AC019272.4	183633 ... 182701
854	OR7E10 P	8	8	13.72	IVACDLLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
855	OR10B1 P	3	19	17.91	MLGCCLSVIEMILSVVM	85	M	AC012302.5	54283 ... 55224
856	OR2InP	3		LLLLMARILL	75	M	AL078630.1	151152 ... 150391
857	OR4Dn	0	11	55.86	MHGGVGGHAQLMNNVSF	65	M	AC019272.4	183633 ... 182701
858	OR5ACn	0			.VVVVIIHVHLIFGIQP	65	R	AF091575.1	52 ... 663
859	OR2I1	0	6	33.63	LLGSCASNAQLMARILL	79	M	AL078630.1	151152 ... 150391
860	OR10H1	0	19	19.86	MFGFSCGMVVAGLVTAL	88	M	AC023604.2	245345 ... 246298

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
861	OR7E59 P	5			CPEARVFLHIMPAFGL	53	M	AF102536.1	22 ... 669
862	OR7E28 P	4			MAGGELLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
863	OR5B3	0			MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978
864	OR2A6	0			TLAHCAFLVPLIACILG	75	M	AF102521.1	22 ... 669
865	OR6Cn	0			.VVVVCAIPPLVMAALI	47	M	NM_010991.1	1 ... 939
866	OR7E54 P	5			MAGGEFLDLHIMPAFGL	52	M	AF073989.1	547 ... 1515
867	OR7E48 P	3			MAGGEFLDLHIMPAFGL	57	R	AF091580.1	7 ... 663
868	OR67An P	3	11	76.42	MHSCAGTLPAQGIASL	83	R	AF091561.1	52 ... 663
869	OR4DnP	1	11	55.86	MHGGVAGHVQLMNNLTL	63	M	AC019272.4	183633 ... 182701
870	OR4CnP	1	11	50.91	VHGCILGHAQLLSICS	57	M	AB030896.1	1 ... 906
871	OR4DnP	2	11	55.86	IHGGIAGHVQLMNNVTL	65	M	AC019272.4	183633 ... 182701
872	OR10H2	0	19	19.94	MFGFSCGMVVAGLVMAL	85	M	AC023604.2	245345 ... 246298
873	OR10H3	0	19	19.94	MFGFSWGMVMGLVTAI	75	M	AC023604.2	214343 ... 213396
874	OR55Cn P	2	11	2.65	VYLLYLQPGGG.....	45	M	AF121980.1	160 ... 1053
875	OR55Bn P	3	11	2.65	.VVVVLQVPLLMCTVS	53	M	AF121980.1	160 ... 1053
876	OR52Vn P	4	11	4.19	LHNHIMVYXFLGTTSP	48	M	NM_013619.1	118 ... 969
877	OR2B3	0	6	33.64	LLGACFINLQLFSILI	75	R	L34074.1	73 ... 1011
878	OR52Tn P	6	11	4.22	FGHFLIFLDFLDILTIS	45	M	AF121975.1	50 ... 1012
879	OR2J1P	5	6	33.64	LLGTCASTLHFLMSFVI	57	R	L34074.1	73 ... 1011
880	OR52Hn P	3	11	4.19	LHFVSGRPCLGVPTVT	60	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	#	S	Acc	Range
881	OR2J3	0	6	33.64	LLGTCASNLHFLTSFVI	58	R	L34074.1	73 ... 1011
882	OR52An	0			FHSVS.....VURLFS	75	R	AF079864.1	632 ... 1576
883	OR4Qn	0			.VVVVAGHMQLVNSLSV	56	M	AB030893.1	37 ... 930
884	OR52Bn P	2	11	4.22	LHFVSVRTSILGVPSVL	60	M	AF121975.1	50 ... 1012
885	OR2N1P	9	6	33.64	LHGGCPIYSEALVCMLV	81	M	AJ132195.1	79 ... 906
886	OR51En P	1			FHSASVRFPLLGAIAMV	90	R	AF079864.1	632 ... 1576
887	OR2J2	0	6	33.64	LLGICAILHFLMSFVI	57	R	L34074.1	73 ... 1011
888	OR2In	0		RRRRRRMARILR	77	M	AL078630.1	151152 ... 150391
889	OR2J4P	5	6	33.64	LLGTCASNLHFLTSFVL	56	R	L34074.1	73 ... 1011
890	OR7E40 P	4			MAGGDILDLYILPDFGL	55	M	AF073989.1	547 ... 1515
891	OR2H4P	3	6	33.64	LLGAYLTQIQAMASLLM	63	M	AL078630.1	41097 ... 40165
892	OR7E52 P	5			IVVCDVLDLHVCDIFGL	61	M	AF073989.1	547 ... 1515
893	OR2InP	9			LLGSC.....	80	M	AL078630.1	151152 ... 150391
894	OR6C1	0			LIGVFTVIPALGCATLF	52	M	NM_010991. 1	1 ... 939
895	OR7E30 P	3			MAGGEFLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
896	OR5BAn P	0	11	53.69	LVVTSVFNIQNLFVTL	51	R	AF091579.1	7 ... 663
897	OR7H1P	3	19	11.38	MMGGTVLYIQLLVALDV	74	M	AF073989.1	547 ... 1515
898	OR5B2	0	11	54.45	MVATNGCNFHLTSNIF	47	R	U50948.1	34 ... 978
899	OR5AZn P	1	11	53.69	MIGTCTVNLLCILCLIF	48	R	AF091579.1	7 ... 663
900	OR5Bn	0	11	54.45	MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
901	OR52Bn	0	11	4.22	KILFSARIPSLGAASTL	64	M	NM_013619.1	118 ... 969
902	OR5BnP	2	11	54.45	MAATNICNIHELVANIS	49	R	U50948.1	34 ... 978
903	OR52Dn	0	11	4.19	MHYASVRIPFLGVAAML	66	M	AF121976.2	474 ... 1307
904	OR7A11	1	19	17.72	MVEASAI DLHMMAVLGV	67	M	AF283558.1	1 ... 927
905	OR5BnP	9	11	54.45	MAATSALTVDLLQFFL	41	M	NM_013728.1	1 ... 948
906	OR51AnP	5	11	4.19	THSWFSRMP LLGIVAFV	50	R	AF079864.1	632 ... 1576
907	OR7A15P	4	19	17.72	MIVGSVTHLHMMALGG	74	R	M64376.1	1 ... 999
908	OR7C2	0	19	17.72	IIGCNGIGLETMTVLGF	98	R	AF091580.1	7 ... 663
909	OR7E23P	7	21	20.89	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
910	OR2E1	8	6	32.05	AHACCTINLQI.RRRRR	43	M	AL078630.1	106872 ... 105934
911	OR1I1	0	19	17.87	MHGTS AIQIHLIFGVGS	57	R	AF091566.1	1 ... 663
912	OR1RnP	3	17	3.12	MVGISAVHLHLIEGVVA	45	R	M64377.1	1 ... 939
913	OR4F3	0	8	0.07	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
914	OR2AEn	0	7	98.7	HLGGCMGNIHIVSSLLL	49	M	AC073769.1	143294 ... 142353
915	OR2InP	7		TTTTMARILL	72	M	AL078630.1	151152 ... 150391
916	OR52AnP	2			IHSASVRFP LLGXPPPP	94	R	AF079864.1	632 ... 1576
917	OR7C1	0	19		ITGCNGIGLETIATLGI	81	R	AF091580.1	7 ... 663
918	OR2A3P	2	7	149.11	MLAACTCLINLVGGVLG	63	M	AF102521.1	22 ... 669
919	OR7A5	0	19		MIAGNAMY LQMITVLGG	74	M	AF283558.1	1 ... 927
920	OR2InP	3		MARILL	67	M	AL078630.1	151152 ... 150391
921	OR7A10	0	19		MLVG NAMNLQMMAVLGG	76	R	M64376.1	1 ... 999
922	OR2An	0			81	M	AF102521.1	22 ... 669
923	OR2M2	0			IISGCFLDIDAICCM LF	57	M	AF102537.1	16 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
924	OR7A8P	2	19		MLAVSSLNLQMIATLGG	71	M	AF283558.1	1 ... 927
925	OR2An	0			TSAVCTTLIHL.....	78	M	L14566.1	62 ... 667
926	OR7E20 P	4			MAGGELLFLHIMPAFGL	56	M	AF073989.1	547 ... 1515
927	OR2AnP	3			TLAHCTCLVHL.....	65	M	AF102521.1	22 ... 669
928	OR5BHn P	7			MVASC GGKTVS.....	34	M	Y15525.1	1 ... 705
929	OR1En	0			LMGDSLLHLHLIMGISI	92	M	AC068902.1 1	196434 ... 195499
930	OR1EnP	1			MLGDSLLHLHLIIGVVL	98	M	AF073976.1	32 ... 649
931	OR5Bn	0	11	54.45	FVITSGCNIHNIVVND	51	R	U50948.1	34 ... 978
932	OR8RnP	12	11	73.74	LFLSYGGGAHH.....	52	M	AC069561.1 0	7848 ... 8783
933	OR5ANn	0	11	55.69	YSGLSGTAFQATLTFGA	55	R	AF091564.1	7 ... 663
934	OR5ANn P	1	11	55.69	YSGLCGTGIQATLTFGT	59	M	Y15525.1	1 ... 705
935	OR5BRn P	8	11	55.69	MSNVCGTVIQATLTFGT	33	M	Y15525.1	1 ... 705
936	OR2A1	0	7	149.18	TLGHCTCLAHLIACFLG	77	M	AF102521.1	22 ... 669
937	OR10An	0	11	6.81	MLGGCFLLVQWAGTIIV	54	M	AF247657.1	1 ... 945
938	OR2A9	3	7	149.18	TLAHCTCLVHLIACILG	78	M	AF102521.1	22 ... 669
939	OR2A7	0	7	149.18	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
940	OR10A3	0	11	6.81	MLGGCFSVVQWAGTIVV	58	M	AF247657.1	1 ... 945
941	OR10Cn	0	6	33.36	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
942	OR7A2P	0	19		MVIVSVMNLQVMAALDG	73	M	AF283558.1	1 ... 927
943	OR10Wn P	2	11	54.3	MIGSCASLQLFVAAAIV	47	M	AC012302.5	54283 ... 55224
944	OR7A17	0	19		MVGGSAINSQMMAALAG	76	M	AF283558.1	1 ... 927
945	OR5Bn	0	11	54.3	MAATNGINIQLDISNVF	47	M	AF102528.1	52 ... 669
946	OR5BnP	5	11	54.3	MVATNGCNLRDLMSNVL	47	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
947	OR1Q1	0	9	106.13	TIAVNMLHLHLIEGVIG	54	M	AF073967.1	2 ... 649
948	OR2Hn	0	6	33.33	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
949	OR7EnP	5	3	90.04	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
950	OR7A14	0	19	17.72	MVIVSAMNI.....	71	M	AC073772.1	227187 ... 226252
951	OR1B1	0	9	106.13	FYGVTLVHLRLIEGLMG	49	M	AC068902.1 1	83719 ... 84647
952	OR12D2	0	6	33.23	LHGSSTIHLHMLVTIAG	81	M	AL359381.1	105330 ... 104407
953	OR7EnP	4	3	11.92	MVACDVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
954	OR8BnP	5	15	74.31	LXVVEGMAHCVVVNIV	82	M	AC069559.8	96224 ... 95292
955	OR1L1	0	9	106.13	MLGNSLIHLHLVEGVIT	57	M	AC023167.7	60743 ... 61663
956	OR11An	0	6	33.36	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
957	OR7AnP	4	12	44.29HLLDCYIRTTLSG	55	M	AF102534.1	52 ... 669
958	OR1C1	0	1	254.35	LVVNSGVHLHLIVGLAT	56	M	AC073769.1	133488 ... 132556
959	OR1D2	0	17	2.99	LVVANLLYIHLLTGIFI	50	M	AF073967.1	2 ... 649
960	OR1L3	0	9	106.13	MLGNSFFHLHLAEGSVA	53	M	AC023167.7	14677 ... 15636
961	OR12Dn P	1	6	33.36	LHGSATIHLMSTGIAG	76	M	AL359381.1	105330 ... 104407
962	OR4G1P	4	16	83.04	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
963	OR2B4P	1	6	33.53	LLGSCGSNVQLLGLLM	90	M	AL359352.1	95024 ... 95965
964	OR11H1	0	22		FFGTCLCWIPLCLSVIG	61	M	AC027184.3	54955 ... 54017
965	OR4Fn	0	16	83.04	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
966	OR56An P	5	11	4.73	MNLPSFQLPVLQAGFLS	38	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
967	OR8NnP	7	4	164.13	REIIRVDAFLKKTANMI	34	M	AF102528.1	52 ... 669
968	OR7EnP	5			MVACDVLDLHIFDFGL	54	R	AF091580.1	7 ... 663
969	OR4Pn	0	11	50.95	LHGGIVGHSQLVNSIAV	56	M	AB030895.1	1 ... 924
970	OR6Cn	0			LIGVFCSTPPLGFATLF	51	M	NM_010991.1	1 ... 939
971	OR5BCnP	2	11	54.3GCQIHFLLANIF	41	M	AC069561.10	51687 ... 50743
972	OR10QnP	4	11	54.3	MLGGCGLLQLLVSVLV	48	M	AC012302.5	54283 ... 55224
973	OR5BnP	6	11	54.3	TDASNGGNIHELVTNIF	45	R	U50948.1	34 ... 978
974	OR10PnP	2	12	115.61	MIGICTTTTHLVATFII	46	M	AF247657.1	1 ... 945
975	OR1L4	0	9	106.22	MMGNSGIHFRLVETVIT	62	M	AF073967.1	2 ... 649
976	OR2APnP	3	12	115.61	YMGAFLLLLLL.....	49	M	AF073987.1	2 ... 649
977	OR1L6	0	9	106.22	MMGNSGIHFRLVETVIT	63	M	AF073967.1	2 ... 649
978	OR6UnP	6	12	115.61	DIGAFTLFMPDLAALG	52	M	NM_010991.1	1 ... 939
979	OR5C1	0	9	106.06	MAADCAGSVHLLICIQA	50	R	X80671.1	203 ... 1129
980	OR11InP	1	15	70.72	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
981	OR4AnP	6	11	50.78	LYGGVVGHFQVNVGVCV	57	M	AB030896.1	1 ... 906
982	OR4GnP	14	2	114.45	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
983	OR10Vn	0	11	56.15	MVGGCGLLPLLLISVLI	48	M	AL136158.14	29455 ... 30402
984	OR4G2P	2	2	114.45	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906
985	OR10VnP	3	11	56.15	MIGRCGLLQLLMVSFLV	45	M	X92969.1	8035 ... 8961
986	OR4F4	0	2	114.45	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
987	OR4G3P	14	19	63.51	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
988	OR5AKnP	4	11	52.82	LGATCSMNINFLFVNLC	65	R	U50948.1	34 ... 978
989	OR10YnP	14	11	56.15	MIRGCGLLFLLLCGHHL	43	M	AF247657.1	1 ... 945
990	OR4GnP	2	19	63.51	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
991	ORnP	9	5	111.92	IMCSRTTYVXQLHGFFT	23	M	AF073989.1	547 ... 1515
992	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
993	OR8A1	0	11	137.56	LLVICVIGIELVSANIV	61	M	AC069559.8	96224 ... 95292
994	OR8Bn	0	11	137.56	LCVVSGMGAHSVVDVM	66	M	AC069559.8	120212 ... 119283
995	OR6DnP	3	10	47.91	AYVSSLLLRTH.....	55	R	AF034901.1	2110 ... 3078
996	OR7E14 P	7	11	16.31	MAGGELDLHIMPAFGL	58	R	AF091580.1	7 ... 663
997	OR2M4	0			IVLGCALDIVALCCMLF	57	M	AF102537.1	16 ... 669
998	OR4WnP	3	X		LLLLL.....LLFFII	36	M	AC069559.8	73704 ... 74636
999	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
1000	OR7EnP	3			MAGGESLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
1001	OR4GnP	4	19	63.51	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
1002	OR10JnP	1			LLGVCGITIQSTISVLL	60	M	X92969.1	8035 ... 8961
1003	OR52En	0	11	4.58	MHTASIRMPLLGNILL	71	M	AF121979.1	53 ... 1106
1004	OR4RnP	24	11		VHGAIMGHVXSFANNCL	54	M	AF102522.1	40 ... 660
1005	OR4Cn	0	11		AHGAIVGHIQFVNSICL	75	M	AF102522.1	40 ... 660
1006	OR4AnP	10	11		GLGGIVGHIQL.....	44	M	AF102522.1	40 ... 660
1007	OR4AnP	4	11		LHGGVAGHFQVVNGGCI	55	M	AB030895.1	1 ... 924
1008	OR4AnP	8	11		LHGGVAGHSHSVNGICV	54	M	AF102522.1	40 ... 660
1009	OR9Gn	0	11	52.54	FAAYCVGNIIKMLLNVC	46	M	AC074177.4	106297 ... 105361
1010	OR10An	0	12	59.65	MFGSCGSVLQWASTFIF	64	M	AF247657.1	1 ... 945
1011	OR4Cn	0	11		VHRGVVGHIQFINSICL	73	M	AF102522.1	40 ... 660

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1012	OR10Vn P	8	11	56.15	.FFFFIIXNEXSVVVLV	37	M	AC073945.4	110931 ... 111893
1013	OR10Un P	3	12	59.65	MAGLCATVAQLMLSFIS	56	R	AF034898.1	1 ... 981
1014	OR7E2P	3	11	90.37	MVACDVLDLHICDIFGL	59	M	AF073989.1	547 ... 1515
1015	OR7E35 P	6	4	11.87	MAGGEFLDLHIVPAFVL	53	M	AF102536.1	22 ... 669
1016	OR9KnP	0	12	59.71	LAIVGGCSLQVSLSIIP	49	R	AF091579.1	7 ... 663
1017	OR7E13 P	5	11	90.37	MAGGEFLDLHIMLAFGL	54	R	AF091580.1	7 ... 663
1018	OR7EnP	4	8	6.5	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
1019	OR9Kn	0	12	59.71	LAIVGGCSIQMSLSIIP	49	M	NM_013728. 1	1 ... 948
1020	ORnP	13	11	137.56	PCVIYGIDVHSLXEPAY	34	M	AC069559.8	36251 ... 35322
1021	OR7EnP	8	11	72.11	MAGGNLFFSLLMPAFGL	54	M	AF073989.1	547 ... 1515
1022	OR7EnP	5	3	140.64	MAGGKFLDLHIMPAFGL	53	M	AF073989.1	547 ... 1515
1023	OR3A4P	0	17	3.12	LHAGCMFNTQALAAMGA	44	M	AC073769.1	133488 ... 132556
1024	OR8QnP	9	11	137.56	LSIIIVETEFVFTXIVT	33	M	AC069559.8	137090 ... 138039
1025	OR7EnP	2	11	72.11	ILACGVLDLHIMHNFGGL	55	M	AF073989.1	547 ... 1515
1026	OR7EnP	3	3	140.64	MVACGVLDLHIIHSFGL	56	M	AF073989.1	547 ... 1515
1027	OR3A1	0	17	3.07	LHVGCACNTHALVGMAT	50	M	AF073967.1	2 ... 649
1028	OR5Gn	0	11	52.52	MGEACGMSTHFLLAIGL	69	M	AF146372.1	509 ... 1456
1029	OR5MnP	7	4	42.45	LIIIVYVNAQRRIIMLE	39	M	AF073987.1	2 ... 649
1030	OR7EnP	1	3	136.02	MVACDVLDLHIIDNFGGL	54	M	AF073989.1	547 ... 1515
1031	OR5G1P	2	11	52.51	QGVACGINTHNVVAVGF	68	M	AF146372.1	509 ... 1456
1032	OR5PnP	3	11	6.93	LVGTCAGNSFCPSSVLS	70	M	AF121977.1	262 ... 1197

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1033	OR10AEnP	8	1	157.36	IIIIIGIMVIVQIHCVV	40	M	X92969.1	8035 ... 8961
1034	OR3A2	0	17	3.07	LHAGCACNTHALVGMAT	50	M	AC073769.1	133488 ... 132556
1035	OR10Jn	0	1	157.4	MVATCGIMLHANVSVIV	88	M	X92969.1	8035 ... 8961
1036	OR1D3P	2	17	2.94	LVVANLFYIHLTGIFI	50	R	Y07557.1	1 ... 942
1037	OR10Jn	0	1	157.36	TVAICGIMVQSNVRVIV	72	M	X92969.1	8035 ... 8961
1038	OR1D4	0	17	2.99	LVVTNLLYLLLLTGIFT	49	R	Y07557.1	1 ... 942
1039	OR5GnP	8	11	52.51	QGVVYVANTHAVVAVLV	55	M	NM_013728.1	1 ... 948
1040	OR4SnP	1	11	50.99	LHGCIGGHIQLVNSIAG	61	M	AB030895.1	1 ... 924
1041	OR5GnP	4	11	52.51	LGVVCGVSTHFLVLGL	75	M	AF146372.1	509 ... 1456
1042	OR9HnP	2	1	254.35	FSGIAGWNAQMLLCIIS	59	R	AF091579.1	7 ... 663
1043	OR1A1	0	17	2.99	MIGNSGINPHLMGVIFV	86	M	AF073966.1	41 ... 643
1044	OR1A2	0	17	2.99	MIKSGISPHMLGVFL	80	M	AF073966.1	41 ... 643
1045	OR8AnP	6	11	137.68	FLVICVMVIELVFANLI	50	M	AC069561.1 0	51687 ... 50743
1046	OR1P1P	1	17	2.99	LLGDIALLTRLLLGVII	82	M	AF102538.1	139 ... 675
1047	OR7E12P	7	11	1.92	MAGGEFFSLHIMPAFGL	55	M	AF073989.1	547 ... 1515
1048	OR4A1P	4	11		LHGGVVGHFQVVGICV	57	M	AB030896.1	1 ... 906
1049	OR10G3	0	14	1.7	LHGSCGAHLQLTDIVVS	91	M	AF259072.1	19582 ... 18644
1050	OR10G1P	3	14	1.7	LHGSCGAHIQLTDIVAS	93	M	AF259072.1	55611 ... 54658
1051	OR10G2	0	14	1.7	LHGSCGAHIQLTDVVAS	91	M	AF259072.1	55611 ... 54658
1052	OR5Tn	0	11	51.94	MVGTCAAHIALFVIEV	52	M	AF121977.1	262 ... 1197
1053	OR7EnP	8	3	136.02	MVACGVLDLHIIGSFGL	53	R	AF091580.1	7 ... 663
1054	OR7EnP	5	3	136.02	MAGGKFLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
1055	OR4AnP	2	11	50.93	LHAGVVGHVQFMNGICV	61	M	AB030895.1	1 ... 924
1056	OR4C1	1	11	50.93	LHGGIIGHVQFVNSMCL	66	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1057	OR1EnP	7	17	2.9MMMYTLIMGILI	80	M	AF073961.1	32 649
1058	OR7KnP	11	14	5.99	MIGCNFIELYMMIGIFG	49	R	AF071580.1	7 ... 663
1059	OR4CnP	3	11	50.93	LHDGIEGHIQFVNSMCA	61	M	AF102522.1	40 ... 660
1060	OR1RnP	11	17	2.9	MVGISAVHLHLIEGVVA	44	R	M64377.1	1 ... 939
1061	OR5AU _n	0	14	1.22	MAATCGANIHCFLANLS	51	M	AC069559.8	85584 ... 84655
1062	OR4C _n	0	11	50.96	LHAGVVGHIQFVNSICI	69	M	AF102522.1	40 ... 660
1063	OR4C _n	0	11	50.96	VHGCIVGHVQLLSICV	57	M	AB030895.1	1 ... 924
1064	OR13D _n P	2	9	86.89	MLGSCWITLRLFTVIVL	58	M	AJ251154.1	2703 ... 1747
1065	OR5 _n				ASASLTSYVHNEEEVFV	44	M	AL359352.1	111313 ... 112242
1066	OR2H _n				LLGTCVMQVQSLSSLVV	83	M	AL078630.1	48786 ... 47851
1067	OR _n				25	M	AC074177.4	88434 ... 88916
1068	OR _n			EINLLLARGKAL	29	M	AF283814.1	1 ... 930
1069	OR _n				NNNNNFXSLHLCCCILI	29	M	AC074177.4	128803 ... 129726
1070	OR _n				TLLLLTFQHHL.....	27	M	L14569.1	62 ... 667
1071	OR6F _n				..CCCWPIPTSAIAVIS	46	R	M64386.1	130 ... 975
1072	OR _n			ILLLLL	33	R	U50947.1	418 ... 1350
1073	OR _n				..CCCLIPFFFTSGYSW	24	R	M64392.1	1 ... 942
1074	OR10A _n				PLGECDPPEEQMYVGLVM	51	M	AF247657.1	1 ... 945
1075	OR _n				IPNASRRRRRR....PP	25	R	M64388.1	1 ... 942
1076	OR2L _n				FLAGAGINAHYVSTFLF	51	M	AF102527.1	22 ... 669
1077	OR10J _n				LTGICGIMVQSNVSVLL	57	M	X92969.1	8035 ... 8961
1078	OR1K _n				LLLLLMVNLYLIKGVVT	50	R	M64377.1	1 ... 939
1079	OR10D _n				LHGSCGLHILLSNVISG	69	M	AC074177.4	12106 ... 13038
1080	OR _n			CCCIH	41	R	M64376.1	1 ... 999

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1081	OR2Ln				SLACGGLNAHFVRTLSF	52	M	AF102537.1	16 ... 669
1082	ORn				HHHHHRLESSLLLLLL	38	M	AC073945.4	152209 ... 153150
1083	ORn			LLLLLS	27	M	AL365336.1	41087 ... 41711
1084	OR2n			GGGGGG	57	M	AF102521.1	22 ... 669

5 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that various changes and modifications can be practiced without departing from the spirit of the invention. Therefore the foregoing descriptions and examples should not be construed as limiting the scope of the invention.

10

All patents, patent applications, and publications cited herein are hereby incorporated by reference in their entirety. In particular, the following documents are hereby incorporated by reference in their entirety: United States Provisional Patent Applications Serial Nos. 60/145,412, filed July 23, 1999; 60/155,126, filed September 22, 1999; 60/158,495, filed October 8, 1999; 60/158,615, filed October 8, 1999; 60/181,113, filed February 8, 2000; 60/181,115, filed February 8, 2000; 60/184,809, filed February 24, 2000; 60/188,332, filed March 9, 2000; and United States Patent Applications Serial Nos. 09/620,753, filed July 21, 2000; and 09/621,122, filed July 21, 2000.

CLAIMS

What is claimed is:

- 5 1. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence that is at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through
10 SEQ ID NO:152 and encoding a polypeptide having olfactory receptor function.
2. An expression vector comprising a polynucleotide sequence of claim 1.
3. A host cell comprising the expression vector of claim 2.
- 15 4. An isolated and purified olfactory receptor polypeptide comprising the translated sequence of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of the translated sequence of SEQ ID
20 NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152 and having olfactory receptor function.
5. A host cell expressing a polypeptide of claim 4 or a functional fragment thereof.
- 25 6. A phage expressing a polypeptide of claim 4 or a functional fragment thereof.
7. A preparation containing a polypeptide of claim 4, further comprising
30 biological or synthetic molecules which maintain the functional structure of the polypeptide.

8. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 or a nucleotide sequence having a sequence at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 and encoding a polypeptide having olfactory receptor function.

9. An expression vector comprising a polynucleotide sequence of claim 8.

10. A host cell comprising the expression vector of claim 9.

11. An isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function.

12. A host cell expressing a polypeptide of claim 11 or a functional fragment thereof.

13. A phage expressing a polypeptide of claim 11 or a functional fragment thereof.

14. A preparation containing a polypeptide of claim 11, further comprising biological or synthetic molecules which maintain the functional structure of the polypeptide.

15. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

16. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 50 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through
5 SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

17. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 100 polynucleotides of SEQ ID NO:1 through
10 SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

18. A library of olfactory receptors according to claim 15, wherein the library
15 comprises the expression products of at least 200 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

19. A library of olfactory receptors according to claim 15, wherein the library
20 comprises the expression products of at least 500 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

20. A library of olfactory receptors suitable for determining the interaction
25 pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

21. A library of olfactory receptors according to claim 20, wherein the library
30 comprises at least 50 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,

wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

22. A library of olfactory receptors according to claim 20, wherein the library
5 comprises at least 100 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

23. A library of olfactory receptors according to claim 20, wherein the library
10 comprises at least 200 polypeptides of SEQ ID NOS of SEQ ID NO: 1085 through SEQ
ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional
fragments of said polypeptides.

24. A library of olfactory receptors according to claim 20, wherein the library
15 comprises at least 500 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

25. A method for determining the binding pattern of a composition with
20 olfactory receptors, comprising the steps of:
exposing the composition to a library according to claim 21; and
determining whether the composition binds to each olfactory receptor, thereby
determining the overall binding pattern of the composition.

26. The method of claim 25, wherein the composition consists essentially of one
25 compound or chemical.

27. The method of claim 25, wherein the composition comprises at least two
30 compounds or chemicals.

28. The method of claim 25, wherein the step of determining whether the
composition binds to each olfactory receptor further comprises a determination of the

approximate binding constant with which the composition binds to each receptor or functional fragment thereof.

29. The method of claim 25, further comprising the step of determining whether
5 a receptor or functional fragment thereof to which the composition binds is activated.

30. The method of claim 29, further comprising the step of determining the
absolute or relative amount by which the receptor or functional fragment thereof is
activated.

10

31. A DNA array or a DNA chip comprising DNA segments derived from SEQ ID
NO: 153 through SEQ ID NO: 1084.

32. A method of determining differences among individuals with respect to their
15 olfactory faculties, comprising the steps of comparing the olfactory DNA of the individual
against the array or chip of claim 31.

33. A method to determine single nucleotide polymorphisms in olfactory receptors,
comprising the steps of uniquely amplifying olfactory receptor sequences from DNA
20 obtained from one or more individuals, based on primers designed according to the first 25
bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through
SEQ ID NO: 1084, and determining the similarities and differences between said amplified
DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

FIGURE 1

SEQ. ID NO:1

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1 GGNTTATNCC NCGTTGNACT GCAGGGGNNC AACNCACAGN ACGCCCGNTG CTGAGGCTAT AAATGANCGG
71 NTTAAGGAGA GGAGTGAAGA CAGTAAAAAA ACACAGAGAT AAATTTATCA ATTGGGAAGC TTTCAAAGGG
141 CCAAATATAG ATGAATATTA ATGGGCCAAA GAAGAGAAGC ACAACAGTAA TGTGGGCAGA CAGAGTGGAA
211 AGGGCCTTGG ACATCCCATC AGAGGCTTGG CGATGCACAG TAGCAAGCAT GATAGTGTCA GAAATGAGCA
281 AAAGGAGGAA ACACATAAGT GAGAGCAGAC CACTGTTAGT GAGCACCAGT ATCTCAAAAC CATAGGTGTC
351 TAAGCAGGCA AGCTTGATCA CTAGGAGGAG GTCACAGAAA AAATTGTCTA CCCTGTTGGG TCCACAGAAA
421 GGCAGATTGA CTTTGAATGC CAGGTGGGTG GCTGAGTGTG AGATGCCAAT GGCCAGGAA ACCCCACCA
491 GAACAGTTCA CACCTCCGG TTCATGATGG TTATGTAGTG CAGAGGTTTG CATATAGCAA TGTATCTATC
561 ATAGGCCATG GCAACAAGAA GCACCATCTC ACTACCCCA AAAACATGCA AGN

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SEQ. ID NO:2

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1 GGNNTNTNAC ACGGACTCCA AGCAGTGGTA ACAACGCAGA GTACGCCCGT TCCTGAGTGA GTAGATGAAG
71 GGGTTCAGCA TGGGATTGAT GACAGTGTG AAAATTCCAA CAGCTTTATC CTTGTCTGAA AGCTTGGTTG
141 AACCCAGTCG CATATAGTTA AAGATACCTG AACCATAGAA TATGGCAACC ACAGTGAGGT GGGAGCCACA
211 TGTGGAGAAG GCTTCTTCC TGCCCTCTAC AGAGCGAATT CGCAGGACTG CAGCTGCCAC GTGGATATAG
281 GAGATGACAA TGAGAGCCAT GGGGGTACCT GCCATTATAA AACCACAGC AAAAAGCAGC AGCTCATTGA
351 GTTGGGTGCT GGAGCAGGAG AGCTGGAAGA GCTGTGGGAG GTCACAGTAG AAGTGATTGA TCACATTGGG
421 GCCACAGAAG TTGAGCGTGG ACATGGCCAC AGTGTGGGTC AGTGC GTTGG TGAAAGCACA AGCCAGGAC
491 GCAGCCACCA ACATCCTCTG GACTGTCTGA CTCATGCGGG TGCTTGTAGG TGAGGGGCC GGCAGATGGG
561 CAGGAATCGG TCATAGGG

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SEQ. ID NO:3

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1 TGGNNTTTTA TCNCCNTTGG AGCTCCNAAG CAGTGGTAAC AACGCAGAGT ACGCCCGTTG CGAAGCGTGT
71 AGATTAGGGG GTTCAGTAGG GGAGTGATGA CAGTGTAGGT CACCGAGATC AGCTGGTCAT GTTCTCTGGT
141 GTTCTCTGAC TTGGGCTTGA GGTAGGCAAT GGAGGCACAG CTGTAGTGGA CAATGACCAC AGTGAGGTGG
211 GATGCACAGG TGGCAAAAGC CTTCTCCGG CCTCAACTG AAGTAATCTT GAGGATTGTA GAGATAATGA
281 GAACATAAGA AATGAAAACC AGACCCATAG GTACAACAAG CACCAGCACA CTGATAATCA AAGTCAGGAT
351 TTCATTGACA GTGGTGTCAA TGCAGGAGAG CTTTCATCACA GGGCGGATGT CACAGAAGAA GTGGGGCACC
421 TTTTCTAGCA CAGAAGGGTA ACCTGAATAC AGATGTCACT TGC GTTATTG CTACAATCAG CCCAATGCTG
491 CAAGGCCCCC AGGACAAGTT GGATACGAG CCTCTTGTTT ATAATAACCA TGTATCTCAA GGGGGTTGCA
561 AGATGGCCAC ATAGCNGNTC ATATTCCN

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SEQ. ID NO:4

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1 GTNGTTNTTA ACNCCATTGG AGCTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCCCAA TGTATTTTTT
71 TTTGAGAAAC TTGTCTTTCT TAGATTTTGG TTACATCTCT GTCACAATTC CAAAATCTAT TGTTAGTTCC
141 TTGACTCATG ATACTTCCAT TTCTTTCTTT GGGTGTGCTC TGCAAGCCTT CTTTTTCATG GACTTGGCAA
211 CTACGGAGGT AGCCATCCTT ACAGTGATGT CCTGTGACCG CTATATGGCC ATCTGCCGGC CTTTACATTA
281 TGAGGTCATC ATAAACCAAG GTGTCTGTCT GAGGATGATG GCCATGTCGT GGCTCAGTGG GGTGATCTGT
351 GGATTCATGC ATGTGATAGC AACATTCTCA TTACCATTCT GTGGGCGCAA TAGAATACGT CAATTTTTCT
421 GTAATATTCC ACAACTNCTA AGCCTCTTAG ACCCCAAAGT AATTACCATT GAGATTGGAG TCATNGGNTT
491 TTGGTACAAG TCTTNGATA ATCCTCTTGG NTGNAATTAC TCTCTCCTAC ATGTNCATTT TTTTTTGNCA
561 TCATGAGGGA TTCCTTCTAA AGG

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SEQ. ID NO:5

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1 GNGGNTTNTT NCCNCCNTTG GACTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCGTGT GTAAATGAAT
71 GGGTTCAACA TGGGAGTCAT AACAGTGATG GACAATGATA GCAGCTTCGT GCCCTCAGGT GAATTATTTG
141 ATTTAGGCCG GAAGTAGGTG AGGCTTAATG ATATATAGAA AAGAGAGACA ACAAGGAGGT GTGAGGAACA
211 TGTAGAAAAG GCTTTATTCT TCCCTTTAGC TGATGGGATC TTGAGGATGG CAGCAGCAAT GCGAGTATAG
281 GAACACAAGA TCAGCAAGCA GGGGATCATG ACCACCAGAA TGGTTCCGAC GATGGCGTAG ATCTCAAACA
351 GTGCTGTGTC TGCACAGACC AGCCTCAGCA CAGGTGGGCT GTCACAGAAG AAGTGGTTCA CCTTGTGGT
421 GCCACAGAAT GGAAACTGA AGAGCCATGT GGTCTGCACA GTAGCTACAG GAAAGCCTGG GAACCAGGAG
491 GCAGCAGCCA GTTTGGCAGC AGTCCTTTGG TTCATGATGA CTGGGTAGTG CAAGGGACTN GCAGATNNNC

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561 NCATTCGGTC ATATGNCATG GNAG

SEQ. ID NO: 6

1 CNTTGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCGCTCCGCA GAGAATAGAT GAAAGGGTTC
 71 AGGGTCGGGG GCACGACTGT GTAGAACGCA GACAGGAAAA CATCCAGAAC GGGGGGAGAA TTTGAAATTG
 141 GCTTCACATA GGCAATGCTG CCAGATATCA TAAAGAGTGT TACAACCACA AGATGTGGAA TGCAGGTAGA
 211 AAATGTTTTT GATCTACCCT CCTTAGAAGG AATCTTCATG ATGACAGAAA AAATGTACAT GTAGGAGAGA
 281 GTAATTACAA CAAAGGAGAT TATCACAAGA CTTGTACCAA AAACCATGAC TCCAATCTCA ATGGTAATTA
 351 CTTTGGGGTC TAAGAGGCTT AGGAGTTTGT GGAATATTAC AGAAAAATTG ACGTATTCTA TTGCGCCAC
 421 AGAATGGTAA TGAGAATGTT GCTATCACAT GCATGAATCC ACAGATCACC CCACTGAGCC ACGACATGGC
 491 CATCATCCTC AGACAGACAC CTTGGTTTAT GATGACCTCA TAATGTAAAG GCCGGCAGGA TGGCCATATA
 561 GCGGTCATAG GA

SEQ. ID NO: 7

1 GCAGTGGTAA CAACGCAGAG TACCGCCCCC TATGTACTTT TTCTTGGGAA ACTTGTCTGT GTTTGACATG
 71 GGTTCCTCCT CAGTGACTTG TCCCAAAATG CTGCTCTACC TTATGGGGCT GGGCCGACTC ATCTCCTACA
 141 AAGACTGTGT CTGCCAGCTT TTCTTCTTCC ATTTCTCTCG GAGCATTGAG TGCTTCTTGT TTACGGTGAT
 211 GGCCTATGAC CGCTTCACTG CCATCTGTTA TCCTCTGCGA TACACAGTCA TCATGAACCC AAGGATCTGT
 281 GTGGCCCTGG CTGTGGGCAC ATGGCTGTTA GGGTGCATTG ATTCCAGTAT CTTGACCTCC CTCACCTTCA
 351 CTTTGGCACA CTGTGGTCCC AATGAAGTGG ATCACTTCTT CTGTGACATT CCAGCACTGT TGCCCTTGGC
 421 CTGTGCTGAC ACATCCTTAG CCCAGAGGGT GAGCTTCACC AACGTTGGCC TCATATCTCT GGCTGCTTTC
 491 TGCTAAATCT TTTATCCTAC ACTAGAATCA CAAATATCTA TCTTAAGCAT TCGTACAAC

SEQ. ID NO: 8

1 GGAACAACGC AGAGTCGCCC CCGATGTACT TGTTCTTCTC CAACCTGTCC TTTGCTGACA TTTGTGTTAC
 71 TTCCACCACC ATTCCAAAAA TGCTGATGAA CATCCAGACA CAGAACAAG TCATCACCTA CATAGCCTGC
 141 CTCATGCAGA TGTATTTTTT CATACTCTTT GCTGGATTG AAAACTTCCT CCTGTCCGTG ATGGCCTATG
 211 ACCGGTTTGT GGCCATCTGT CACCCCTGCT ACTACATGGT CATTATGAAC CCTCACCTCT GTGGACTGCT
 281 GGTTCTGGCA TCCTGGACCA TGAGTGCTCT GTATTCTTGT CTACAAATCT TAATGGTAGT ACGACTGTCC
 351 TTCTGCACAG CCTTAGAAAT CCCCCACTTT TTCTGTGAAC TTAATCAGGT CATCCAACCT GCTTGTCTCTG
 421 ATAGCTTTCT TAATCACATG GTGATATATT TTACAGTTTG CGCTGCTGGG TGGAGGTCCC TGACTGGGAT
 491 CCTTTACTTC TTACTCTAAG ATAATTCTT CATACATGCA ATCTCANCAA GNTCAGGG

SEQ. ID NO: 9

1 GGGTTTTNAC CCNNTNGGAG CTCCNAGCAG TGGTAACAAC GCAGAGTACG CCCGTTTCGT AGGCTATAAA
 71 TGAAGGGGTT GAGTGAGGGA GTCACCACTC CATAGAAGAG GGCCATGAAC TTGGGTTGAT CCCTTGAGAT
 141 GGAGGAGGGG GGCTGAAGGT ACATGCTGAT GGCTGGGCCA TAAAATAAGA AAACCTACAAT AAGATGGGAG
 211 GAGCATGTCC CAAAGGCCTT TNTCCTTCCC TTGGAAGATT TGATCTTAAA TACAGCACTT NCAATACTAG
 281 CATAGGAAGC AAGAATTAAG CATANTGGGA CAGCTAACAT AAAAATGCAT ACCACAGAGA GTGTGAGCTC
 351 GTTAGAACCC TTTTCACCAC AGGCAATCTT TATCAGAACA GGAATCTCAC ACACCAAGTG GTCCAGCTTA
 421 TTGAGACCAC ACAGTGGNAA TTTGTATTGT GGCAGTGGCC CTCTGAGAAC GGCATAGATT ATACCAANTT
 491 AACCACNACN GCGGNAACTA ANGATTCAGA CGCNCCTGGAT TCATGATGAG GGTNTAGTGA AGAGGTTNTC
 561 AGAATGGCCA CATACCGNTC AAA

SEQ. ID NO: 10

1 GCTGCTNCCA GCAGTGGTAA CAACGCANAG TACGCCCCCA ATGTATTTGT TCTTCGGCCA TCTGTCTCTC
 71 CTGGATGTCT GCTTCATCAC CACTACCATC CCACAGATGT TGATCCACCT CGTGGTCAGG GACCACATTG
 141 TCTCCTTTGT ATGTTGCATG ACCCAGATGT ACTNTGTCTT CTGTGTTGGT GTGGCCGAGA GCATCCTCTT
 211 GGCTTTTCATG GCCTATGACC GNTATGNTGC TATCTGCTAC CCACTTAACT ATGTCCCGAT CATAAGCCAT
 281 AAGGTCTGTG TCAGGCTTGT GGGAACTGCC TGGNTCTTTG GGCTGATCAA TGGCATCTTT NTGGGTATA
 351 TTTTCATTCT AGAGCCCTTC CGCAGAGACA ACCACATAGA AAGCTTCTTC TGCGAGGCCC CCATAGTGAT
 421 TTGGCCTCTT TTGTGGGGGA CCCTNANANT AGTCTGTGGG CAAATCTTTN GCCGATGCCA TCGTGGTAAT
 491 TCTNAGNCCC ATNGGTGCTN ACTGNTACTT ACCTATNTGC ACATTCTGT CCACCATCCT AGNNAAAGTC
 561 CTCCTTCTN

SEQ. ID NO: 11


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1 GGNNTTTTAC CNCNATTGGA GCTCCAAAGC AGTGGTAACA ACGCAGAGTA CGCCCCCTAT GTACTTGTTT
71 TTGAGAAACT TGTCTTTCTT AGATTTTGT TACATCTCTG TCACAATTCC AAAATCTATT GTTAGTTCTT
141 TGAATCATGA TACTTCCATT TCTTTCTTTG GGTGTGCTCT GCAAGCCTTC TTTTTCATGG ACTTGGAAC
211 TACGGAGGTA GCCATCCTTA CAGTGATGTC CTATGACCGC TATATGGCCA TCTGCCGGCC TTTACATTAT
281 GAGGTCATCA TAAGCCAAGG TGTCTGTCTG AGGATGATGG CCATGTCGTG GCTCAGTGGG GTGATCTGTG
351 GATTCATGCA TGTGATAGCA ACATTCTCAT TACCATTCTG TGGGCGCAAT AGAATACGTC AAATTTTCTG
421 TAATATTCCA CAGCTCCTAA GCCTCTTAGA CCCCAGAGTA ATTACCATTG AGATTGGAGT CATGGTTTTT
491 GGTACAAGGC TTGNGATAAT CTNCTTTGGT GNAATTACTC TCTCCTACAT GTACATTTTT TCTGCATCAT
561 GAGGATTCTT TCTAAGGAGG GG

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SEQ. ID NO:12

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1 GGNNTTGGACC ACGGAGCTCC AAGCAGTGGT AACAAACGAG AGTACGCCCT CTTGTCCTCG TGCCGATACA
71 TGATGGGGTT CAACATGGGA GTCATAACAG TGTAGGACAA TGATAGCAGC TTCTTGCCCT CAGGTGAATT
141 ATTTGATTTA GGCCGGAAGT AGGTGAGGCT TAATGATATA TAGAAAAGAG AGACAACAAG GAGGTGTGAG
211 GAACATGTAG AAAAGGCTTT ATTCTTCCCT TTAGCTGATG GGATCTTGAG GATGGCAGCA GCAATGTGAG
281 TATAGGAACA CAAGATCAGC AAGCAGGGGA TCATGACCAC CAGAATGGTT CCGACGATGG CGTAGATCTC
351 AAAGAGTGCT GTGTCTGCAC AGACCAGCCT CAGNACAGGT GGGCTGTGAC AGAAGAAGTG GTTCACCTTG
421 TTGGTGGCCAC AGAATGGAAA ACTGAAGAGC CATGTGGTCT GCACAGTAGC TACAGGAAAG CCTGGGAACC
491 AAGAGGTAGC AGCCAGTTTG CACGAGTCCC TTTGGTTNAT GAATGACTGG GGTAGTGCAA GGGACTGCAG
561 ATGGCCACAT ANCGGTCNT

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SEQ. ID NO:13

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1 GNNNTTNNNN CCACTGGAGC TCCAAAGCAG TGGTAACAAC GCAGAGTACG CCCCCAATGT ATTTATTCTT
71 GCTCACCTCT CTTAGATTGA TATCTGTTTT ACCACCAGTA TTGTCCCCCA GCTGCTGTGG AACCTAAAAG
141 GACCTGACAA AACAATCACA TTCCTGGGTT GTGTCATCCA GCTCTACATC TCCCTGGCAT TGGGCTCCAC
211 TGAGTGTGTC CTCCTGGCTG TAATGGCTTT TGATCGCTAT GCTGCAGTTT GCAAACCTCT CCACTATACC
281 GCCGTAATGA ACCCTCAGCT GTGCCAGGCT CTGGCAGGGG TTGCGTGGCT GAGTGGAGTG GGAACACTC
351 TTATCCAGGG CACTGTCACC CTCTGGCTTC CTCGCTGTGG ACACCGATTG CACTAACATT TCTTCGTGAG
421 GTACCCTCCA TGATTAAGCT TGCATGTGTG GACATCCATG ATAATGAGGT TCAGCTCTTT GTTGCTTCAC
491 TGGTCTTGCT CCTCTTGCCC TTAGTGCTAA TACTGCTGCC TATGGACATA TAGCCAAGGT GGCATAAGGA
561 TCAAGTCAGT CCAGCCT

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SEQ. ID NO:14

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1 GGNNTNTNAC TCCATGGACT CCAAGCAGTG GTAACAACGC AGAGTACGCC CATAATGAT GGGGTTTCTT
71 AGGGGAGTGA TGACAGTGTA GGTACCCGAG ATCAGCTGGT CATGTTCTCT GGTGTTCTCT GACTTGGGCT
141 TGAGGTAGGC AATGGAGGCA CAGCTGTAGT GGACAATGAC CACAGTGAGG TGGGATGCAC AGGTGGCAAA
211 AGCCTTCTTC CGGCCCTCAA CTGAAGCAAT CTTGAGGATT GNAGAGATAA TGAGAACATA AGAAATGAAA
281 ACCAGACCCA TAGGTACAAC AAGCACCAGC AACTGATAA TCAAAGTCAG GATTTTCATT ACAGTGGTGT
351 CAATGCAGGA GAGCTTCATC ACAGNGCGGA TGTCACAGAA GAAGTGGGGC ACCTTTCTAG CACAGAAGGG
421 TAACCTGAAT ACAGATGTCA CTTGCGTTAT TGCTACAATC AGCCCAATGC TGCNGGCCCC CAGGACAAGT
491 TGGATACGCA GCCTTNTCGT TCTANTAACC ATGTATCTCA ANGGGCTTGC NGATNNCCAC ATACTNGCAT
561 ANACCATTGC TGNGAGC

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SEQ. ID NO:15

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1 GNCGNTNTTA ACNCCATTGG AGCTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCATTA CGAAAAGTGT
71 AGATGAAGGG GTTCAAGAGG GGTGTGATGA TGCAGCTCAG GACGGAGGCA CCTTTGTTGA GCAGTTTGA
141 CTGAGCCTCT GACATACGAA TGTAGAGAAA GATGGAAGT CCATAGATGA TGACCACCAC TGTAAGATGC
211 GAGGCGCAAG TGGAAAACGC TTTCTTTCGC TCAGCAGCTG TAGGGGCCCT GAGAACAGTG GCAAGAATGC
281 AGGCATAGGA AACTGAGGTC AGAGCCAGTG AGCCAGTAA CACCAACGTA GAGAGCATGA AAGCCACCAG
351 TTTGAGCAGG TGGGTGTCCC CACAAGAAAG CCTGAGCAAG GGCCAAGTGT CACGAAAGAA GTGGTCAATA
421 CCATTGNGGC CACAGAAAGG CATGGCTGGC CATGAGGACA GTGGGGCAAA GGACCCAGAG GAATNCANCT
491 AGCCAGGAGG CCACACTAGT TTGTGAACAG ACATGGCCAT TNATTAGGGT CTCATAGCGG AGTTGTGNC
561 AGATTTGCNT GGTNACGATT CAN

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SEQ. ID NO:16

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1 GGNNTTTTAC CNCNATTGGA CTCCAAAGCA GTGGTAACAA CGCAGAGTAC GCCCCCTATG TATTTATTCT
71 TGCTCACCTC TCCTTAGTTG ATATCTGTTT TACCACCAGT ATTGTCCCCC AGCTGCTGTG GAACCTAAAA
141 GGACCTGACA AAACAATCAC ATTCCCTGGGT TGTGTCATCC AGCTCTACAT CTCCCTGGCA TTGGGCTCCA
211 CTGAGTGTGT CCTCCTGGCT GTAATGGCTT TTGATCGCTG TGCTGCAGTT TGCAAACCTC TCCACTATAC
281 CGCCGTAATG AACCCTCAGC TGTGCCAGGC TCTGGCAGGG GTTGCCTGGC TGAGTGGAGT GGGAAACACT
351 CTTATCCAGG GCACTGTCAC CCTCTGGCTT CCCCCTGTG GACACCGATT GCTCCATCAT TTCTTCGTGA
421 GGTACCCCTC ATGATTAAGC TTGCATGTGT GGACATCCAT GATAATGAGG TTCAGCTCTT TGTGCTTCA
491 CTGGTCTTGC TCCTCTTGCC CTTAGTGCTA ATACTGCTGC CTATGGACAT ATAGCCAANG TGGCATAAAG
561 GATCAAGTCA GTCCAGG

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SEQ. ID NO:17

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1 GNNNNTTNTT CANTCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA
71 GAATTCGCCC TTATTCCGGA GGGTATACAT GAAGGGATTG GTAAGTAGAC GTAACTCGA AGCCAAGAAC
141 AGAATTTCTC TTAGAAAAGA GAATTGAAAC TAAAGAGAAA GAACTAGCAA AGAAGGAAAT ATTGAATATA
211 CAAGAGAGAG GAGACAGATG ATGGAACAAG ACTCTGAAAG AGGTGGAAGG GATTGAATAC AATCAAAAGT
281 ATGGTGACTG CTAGTTCCAA GATGGTGGCG TAGGGGCAAG CTGGCTTTGC TTACCCCCCT GGCAGAAAAC
351 CAAAAACAAA TAGCACCAG ATTATCACTA GCAATATCCC AGAACTCACA TATAAGGATG AGACAGTTCC
421 CAGGGCCCCAG AGAAGATCAG AAGCACAAGT GGGAGAAGTC AGCTTTGGAT GCTACTTTGT TCTAAGGGAG
491 ACAAGTTGGG AGGATGATTG CAGATGTATA TTCAATGTTA TAAACAGCC CATAAAACAA AGATTGGAAA
561 ATGTTGAATT TTGCAACCAG GAGCAAATAC TGGGAAAGGC GAATTCCAGC CACTTGCGNC C

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SEQ. ID NO:18

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1 GNNNNTTNAN TCANTGCCCT NGGGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG
71 CAGAATTCGC CCTTGTGCG CAAGGTGTAA ATGAAAGGGT TTGCGCAGGA GTAAATGAAG GGATTACGCA
141 GGAGTAAATG AAGGGATTAC GCAGGAGTAA ATGAAGGGAT TACGCAGGAG TAAATGAAGG GATTACGCAG
211 GAGTAAATGA AGGGATTACG CAGGAGTAA TGAAGGGATT ACGCAGGAGT AAATGAAGGG ATTACGCAGG
281 AGTAAATGAA GGGATTACGC AGGAGTAAAT GAAGGGATTA CGCAGGAGTA AATGAAGGGA TTACGCAGGA
351 GTAAATGAAG GGATTACGCA GGAGCAAATA CATAGGAAGG GCGAATTCCA GCACACTGGC GGCCGTTACT
421 AGTGGATCCG AGCTCGGTAC CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACCT AAATAGCTTG
491 GCGTAATCAT GGTATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG
561 CCCGGAAGCA TAAAGTGTA AGNCTGGGGT GCCTAATGAG TGACTTACTC CATTA

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SEQ. ID NO:19

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1 GNNANTNATT CCATCCATTG TCCCTTCAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TCTTGGTTTT TGTGCTGATA GATCATGGGA TTCAGCATGG GGGTGACCAC AGTGATACATC
141 ACTGAGGCTG TTGCACTTGA GTGTGAGTTG CGGGTGGCAG CAGAACTAAG GTACACCCCT AGGATTGCAC
211 CATAAAATAA GGAGACAAC T GAGAGGTGAG ATGCACAGGT GGAAGATGCC TTGTACTTCC CCTGAGCTGA
281 TGAGATNGCA TGTATGGAAN GAAATTATNT TANAAGTAAG AGTAAAGNAT NCCAGTCAGG GGNANCNTTC
351 ACCCATCAGN TGCAANTTGT AAAAATTATA TTCAANCNAT NTGNATTTAA NGAAAANCCT TATCANGTAN
421 AACTGCAATA GNTNTGNATT NANCCCTNGN ANTTAANNNT TCNACAAGAA AATAANGTGC GTTNNAATCT
491 TTNTAAGTCC CTNTCNCCAT TAANGTCNAN TCCNTCCNTA TCCCTTTTCN NATTTTGNAN TCNNGANTAC
561 NNTCTNNNGC NNTCNATTTT TNTNNTNNT GACCTACTAA CCNATTNAGT TACNACAAGN CCNTTCNANT
631 CTCTATAATT NCTCGCANGT TNTCCCTCTT NNCANNTNCC CNTTNTTNTC CCTNTTCCCC ATCTNC

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SEQ. ID NO:20

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1 CCATTGGCCCC TCTAGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCT
71 ATGTATTTTC TCTTACTGGG CTTTCCTGGT TCTCAAACCTC TTCAGCTCTC TCTCTTTATG CTTTTTCTGG
141 TGATGTACAT CCTCACAGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC ATCAGTTGCA
211 TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTTGGT ATACCACAGC AGCAGTGCCC
281 AAAGCATGG CCATCCTACT GGAGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG CAGATGTACT
351 TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT GTCTTGCCAT
421 CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCCTG CTCTCAGCGC AACTGGCCTT GGGCTTCTGG
491 GTGGNTGGGT TCGGGGGCAA TGCAGTGCCC ACAGGCCTTC AATCAAGTGG GCTGNTCCTT CTGGTGGCCC
561 CCGGTGCCAA TCAACCACTT TTTTTTGGG ACAATTGCAN CCCTGGAATT GGGCC

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SEQ. ID NO:21

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1 GNNCTTANTT CAATCCCACC NANCCNTGCC GANGCATGCT CGNGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTTCCTATGT ATTTACTCTT ACTGGGCTTT CCTGGNTCTC AAACCTCTTCA GCTCTCTCTC
141 TTTATGCTTT TTCTGGTGAT GTACATCCTC ACAGTTAGTG GTAATGTGGC TATCTTGATG NTGGTGAGCA
211 CNTCCCATCA GNTGCATACC CCCATGTTNT TCTTTCTGAG CNACCTCTCC TTCCTGGAGA TTTGGTATNC
281 CNCAAGCNGC ANNGCCCAAA GCTTTGCNCA TCTTATTGCN CAGANGCNNN CCNNTACANN NACNCTCCTG
351 TTTNTGCTN CCTTNCCTCT TNCTTCNCTC ANNTACTNCN TCTNCTNTAG TNTCTTTCTT CTCTNTCNCT
421 CNTNNCNCCT NTAATNTTCC NCCTNTTCTN NTTTCTNTTT TCCCTNCTCT GTTTCACCCC TACCTCTTAT
491 CCNTNCTNCT NACTTCANNC TCNGNCNNTN NNNCNCNNNT AAATNTANGN NNANNNNTNN ATNTNCTCTT
561 CTCCNTTTAT ATCGCCTCTT CTCNTNCTTC CNNTTCTCTC TCCTCANNCA TATCNANTNT NTTCTACTCT
631 CGTNCNNTAT CTANNCTCCT NTTTCNGTCC TNCTTCTCCT NTCATTTCTA TATTNCTTCT CANACANTNT
701 TCGCATCGTN GCANCATCTC CTCCCATCTC CTGTNCNCTN TTCCN

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SEQ. ID NO:22

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1 GNNNTTAANT CATTCCCCNC TCNATGCATG CTCGAGCGGC CGCCAGNGTG ATGGATATCT GCAGAATTCTG
71 CCCTTGTTTC GGAGGCAGTA GATGAATGGG TTGATGGAAT CTGAGACAGT GCTCTAGAAT CTGTGTTTCA
141 TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTTGCCGAGA GAGGAATCAT
211 CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG GAGATGGGCT
281 TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC AACCTGAAAG
351 ACAAGGACA CGGTGGCATG AGCGCATGTA ACACAATGTA CTCAGGAAAT GGCTGGCATC GTGAGATATG
421 GAGTGAATA CAGTACAGGG CTTTGTA AAC TCAGCTTGGG GTCAGATCAC AGAAAGCCTT GACAAGGAAC
491 TGAAAATGGG TTCTGAAGGC CAGAAGCCCA TTCAAGATTC CCAAAGGGAA AAACACAAAT CAGCTTGGTT
561 TCAGGACGTA ATTCTTGGA GTTGCTAGAA TTACATCAGA AAGGAGGTT ACNT

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SEQ. ID NO:23

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1 GNNNTNANTC ANNCANTGGG CCCTCTAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT CCTATGTATT TCCTCTTACT GGGCTTTCTT GGTTCCTCAA CTCTTCAGCT CTCTCTCTT
141 ATGCTTTTTT TGGTGATGTA CATCCCCACA GTTAGTGGTA ATGTGGCTAT CTTGATGTTG GTGAGCACCT
211 CCCATCAGTT GCATACCCCC ATGTACTTCT TTCTGAGCAA CCTCTCCTTC CTGGAGATTT GGTATACCAC
281 AGCAGCAGTG CCCAAGCAC TGGCCATCCT ACTGGGGAGA AGTCAGACCA TATCATTTAC AAGCTGTCTT
351 TTGAGATGT ACTTTGTTAT CTCATTAGGC TGCACAGAGT ACTTCCTCCT GGCAGCCATG GCTTATGACC
421 GCTGTCTTGC CATCTGCTAT CCTTTACACT ACGGAGCCAT CATGAGTAGC CTGCTCTCAG CGCAGCTGGC
491 CCTGGGCTCC TGGGTGNGGG GGTTCGTGGC CATTGCAAGT GCCCACAAGC CCTAATCAGT GGCCCTGTCC
561 NTCTGGGGGC CCCC GGCCA TTNACCACTT TTTCTGGGA CAATTGCACC CCTGGAATTG G

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SEQ. ID NO:24

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1 TNNTTAANTC ATTCCNTTGN CCCTCNAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT TCCTTGTTAC TGAGGGAGTA GATTAGGGGA TTGATGGAAT CTGAGACAGT GCTCTAGAAT
141 CTGTGTTTCA TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTTGCCGAGA
211 GAGGAATCAT CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG
281 GAGATGGGCT TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC
351 AACCTGAAAG ACAAGGACA CGGTGGCATA AGCGCATGTA ACACAATGTA CTCAGGAAAT GGCTGGCATC
421 CTGAGATATG GAGTGAATA CAGTACAGGG CTTTGTA AAC TCAGCTTGGG GTCAGATCAC AGAAAGCCTT
491 GACAAGGAAC TGAAAATGGG TTCTGAAGGC CAGAAGCCAT TCAAGATTCC CAAAGGGAAA AACACANATC
561 ACTTGTTTTT AGGACGTATT CTTGGGCAGT TGCTAGAATT ACATCAGAAA GG

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SEQ. ID NO:25

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1 GNNNTTANT CCATGCCCCT CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
71 GCCCTGTTT CGCAGCCTAT AAATGAAGGG GTTGATGGAA TCTGAGACAG TGCTCTAGAA TCTGTGTTT
141 ATACAGGATG AGATATAAAT GAAACAAATG CTAAATAATG ACACAAGGTA CTTGCCGAG AGAGGAATCA
211 TCCACCTGGA AGGGTAGGCT GTTTGTGAAT AATGTAGGGT GGGAGAGAGG GCTTTACTAA GGAGATGGGC
281 TTAAAGAATG TGAACGATGT GCTCACAGAG GCCACAGAAG AGAAATTATA GCCAGGAGAA CAACCTGAAA
351 GACAAAGGAC ACCGGTGGCA TAAGCACATG TAACACAATG TACTCAGGAA ATGGCTGGCA TCCTGAGGTA
421 TGGAGTGGAA TACAGTACCG GGGCTTTGTA AACTCAGCTT GGAGTCAGAT CCAGAAAGCC CTTGACAAGG
491 AACTGAAAAT TGGGTTCTTG AAGGCCAGAA GCCATTCAAG GATTCGCCAA AGGGGAAAA CACAAATCAA

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561 GCTTGTTCCT AGGGACCGTT AATTCTGGGG CCAGGTTGCT TGAATTACCT TCANGAAAGG GAGGTTACACA
631 CT

SEQ. ID NO:26

1 GNNCTTATTC ATCCCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTTCGC
71 CCTTCTTTTG TTCCTCAGAG TGATAGATTAG GGGGTTGATG GGGTTGATGG AATCTGAGAC AGTGCTCTAG
141 AATCTGTGTT TCATACAGGA TGAGATATAA ATGAAACAAA TGCTAAATAA TGACACAAGG TACCTTGCCG
211 AGAGAGGAAT CATCCACCTG GAAGGGTAGG CTGTTTGTGA ATAATGTAGG GTGGGAGAGA AGGCTTTACT
281 AAGGAGATGG GCTTAAAGAA TGTGAACGAT GTGCTCACAG AGGCCACAGA AGAGAAATTA TAGCCAGGAG
351 AACAACTGA AAGACAAAGG ACACGGTGGC ATAAGCGCAT GTAACACAAT GTACTCAGGA AATGGCTGNC
421 ATNCTNAGAT ATGGAGNGNG AATACCAGTA CANGGCTTTN TANACTCANC TTGGAGTNCA GAATCACANA
491 ANGCTTGCA AGGAACTGAA AATGGGTTCT GAAAGGCCAG AAGCCNTTNA AGATTCCCCA AGGGAAAAAA
561 CACAAATCAA GCTTTTTTNA AGNACNGTAA TTCNTGGNGC CAGTTGCTTA GAATTNCCAT CANAAANG

SEQ. ID NO:27

1 GGNNTAAGCC TTCCCCCTNC GATGCTGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA GAATTGCCCC
71 TTCCCATGTA TTTCCTCTTA CTGGGCTTTC CTGGTTCTCA AACTCTTCAG CTCTCTCTCT TTATGCTTTT
141 TCTGGTGATG TACATCCTCA CAGTTAGNGG TAATGGGGCT ATCTTGATGN TGGTGAGCAC CNCCCATCAG
211 TTGCATACCC CCATGTACTT CTTTCTGAGC AACCNNTCCN TCCTGGAGAN TTTGGNATAC CACACGCAAN
281 NAGNGNCCNA AGGCACTTGG NCNTNCTACA GNGGAGAAG GCTTGACCAT ANNATTTTAC CATGCCTNGC
351 CTTANGNCAN ACCCNNTTN TNCCTNTNT TCCNCTNNNN GGTNNNTCAN CCGCANNCTT NNATCNNNTG
421 NANCTTCATN GAATATGGNN TNNGTNTNTC TTGAGAGCCT CNNGATCNA TTTTTTCCAN CNNTAAAGN
491 GGNGCTTNTC TCTCTNNNAT CTAGCTTNTT GGNTCTCTTT TNTNTNCTNA CCCGTGNTNT CCTATNTGNT
561 GTCTCTTCCT ACNNNCTGCN NTTATTNTAN ATCANNTCTN NCNTTGCTCT CNTNTACNAC ATNATCATNC
631 TCNCTCCCC CTNTCNCTCT CTATNNCTA CCATCNCTCT CTCTCATTC ANCTCTTNT CATGNTTGT
701 TCANTTANNC ACTCTCCNTC NCATCTTCTA TNCACANTT TTNTNTTTTT NCTCTCTANT TCTNNTTCCA
771 NTGTNCACTC CNNTCTTNNC NNTTNCCTA NCG

SEQ. ID NO:28

1 GTNNTTNANN NCATTGCCCC TCTNGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT
71 CGCCCTTCCT ATGTACTTCC TCTTACCGGG CTTTCTGGT TCTCAAATC TTCAGCTCTC TCTCTTTATG
141 CTTTTTCTGG TGATGTACAT CCTCACGGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC
211 ATCAGTTGCA TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTGGT ATACCACAGC
281 AGCAGTGGCC CAAGCACTGG CCATCCTACT GGGGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG
351 CAGATGTACT TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT
421 GTCTTGCCAT CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCCTG CTCTCAGCGC AGCTGGCCCT
491 GGGCTTCTGG GTGGGTGGGT TTCGGGGCCA TTGCAAGTGC CCACAGCCCT TATCAAGTGG CCTGTCTTC
561 TNGGCCCCC GGGCCCATCA ACCACTTTTT TCTGGGGACA ATTGCACCCT GGAATGGCCC

SEQ. ID NO:29

1 GTNNTTNANN CCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTTTCATGGT TCCGGAAACA GTAAATTATG GGGTTCAGTC ATGGTAACAG GAGGAGGCTG
141 AGTGATGGG CATGGATGGG GGCTGTGAAT GTGGCGGGAG CTCATGGATG TGCTCTCTG AGTGCTTCAC
211 GTTCTGAGT GAAATAAGAA GCAAGGTCAT CACCGAGAGG GAGGAGACAG GCTCGGGTGA GTTTAGTGGA
281 TATGAATCCA AGAGAGACCA TTCAACTTAG TTGTCTATTT TTTTTTCTC CAGTTATAGT CACTTGCATG
351 AATGTAGATG TGGAGTACTT GATCATAAGA TCCATTTTAT GGCAGAAGAC ATTATTTTTC TGAGCCTTCT
421 GCTGTCAGTT TCTAAATAAG CAGGCCAGCC GGGCTGTGCA CCTAAATGTC TGTCTGGGAG GAGCAGGCTG
491 AGAAGTCTTG CAGTCTGCAG GACACCCGAG GAATCGTATT GTGGGAACCG TCCCCGAGAA CCACAGGAGC
561 CGTGCTNCTC AGTNCTGACT GGAANAATGA AATTGNAAGC CAAGTNGTTC NNGGANCNNT

SEQ. ID NO:30

1 GNNNTTNANN CCATTGCGCC CTCTAGATGC ATGCTCGAGC GGCCGCCAGT GTGATGGATA TCTGCAGAAT
71 TCGCCCTTCC TATGTATTTT TCTTCCTAAC GATTGGAATG CCTGGGATTA GGCAGATGAT TTTCTTTTTC
141 CCCCATACCC CTCTATTATT TAGGTGATTG AGTTTAAATC CTTTATCTA CACCCTTCGG AACAAAGGGC
211 AATTCCAGCA CACTGGCGGC CGTTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT

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281 ATTCTAACGC GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC
351 CGCTCACAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG
421 CTAATCACA TTAATTGCGT TGGCTCACT GCCCGCTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT
491 TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTCGCGTA TTGGGCGCTC TTCCGCTTTC TCGCTCACTG
561 ACTCGCTGGG CTTCGGTCGN TCGGCTGCGG CGAGCGGGAT CAGCTCACTC AAAAGG

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SEQ. ID NO:31

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1 GNNNNNNNNNT CANGCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCCG CAGTGTGATG GATATCTGCA
71 GAATTCGCCC TTCTATGTA TTTCTCTTCA CTTTCTCCGA CATCACTCAC AGCCACCCCA CCCTCAGCCT
141 CTCCCTCCTC CCATGTATTT TCTCTTCAAT CTCTCCTTCT TTGATATCCT GAACCTTCTG TAGCTCTTTA
211 TTTTCTCTTC CAATCCCTTC ATATACACGT TTCGTAACAA GGGCGAATTC CAGCACACTG GCGGCCGTTA
281 CTAGTGGATC CGAGCTCGGT ACCAAGCTTG ATGCATAGCT TGAGTATTCT AACGCGTCAC CTAATAGCT
351 TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATCCAC ACAACATACG
421 AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCCTGCGCT
491 CACTGGCCGC TTTCCANGTC GGGAAACCTG TCGGCCAGCT GCATTAAATG AATCGGCCAA CGCNCCGGGA
561 GAGGCGGTTT GCGTATTGGG CGCTNTTTCG TTCTTCGNTN ACTGATCGNT GG

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SEQ. ID NO:32

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1 GNNNNNNNNNT TCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTGTGTGCTT AGAGTGTAAG TAAAGGGTT AACATTGGCT TAGAGGTGAA GAGTAAATAC
141 ATAGGAAGGG CGAATTCCAG CACACTGGCG GCCGTTACTA GTGGATCCGA GCTCGGTACC AAGCTTGATG
211 CATAGCTTGA GTATTCTAAC GCGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG TTTCTGTGT
281 GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAG CCTGGGGTGC
351 CTAATGAGTG AGCTAACTCA CATTAAATTG GTTGCCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCTG
421 TGCCAGCTGC ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTTCG TATTGGGCGC TCTTCCGCTT
491 CCTCGCTCAC TGAATCGCTG CGCTCGGTCG NTGCGCTGCG GCGAGCGGTA TCAAGCTCAC TCAAAGGCGG
561 TAATACGGTT ATCCACAGAA TCAGGGGGAT ACGCANGAAA GAACATGTGA GCAAT

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SEQ. ID NO:33

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1 GNTNTNANTC ATGCCCCCNC CGATGCNTGC NCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTGCG
71 CCTGTGTGCG GAGCGAATAT ATGAAGGGGT TAAGGGAAGA GAAAATACAT AGGAAGGGCG AATTCCAGCA
141 CACTGGCGGC CGTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT ATTCTAACGC
211 GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT
281 TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAACTCACA
351 TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT TAATGAATCG
421 GCCAACGCGC CGGGGAGAGG CGGTTTGCCT ATTGGGCGCT CTNCGCTTC CTCGCTCACT GACTCGCTTG
491 CGCTCGGTCC GTTCGGCTGC GGCGAGCGGT ATCAANTCAC TCAAAGGCG GGAATACGGG TTTNCACAGA
561 AATCAGGGGG ATAACGCNGG AAAGAACATG TGAGCCANAN GGCAGCAAAA GGCNAGGAA T

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SEQ. ID NO:34

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1 GNNNNNNNNNT CANNCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCCG CAGTGTGATG GATATCTGCA
71 GAATTCGCCC TTGTTCGAA GGCTATAGAT GAAGGGGTTT TAGGTTTTTA GGAACACAGG CTAAGGGGGA
141 AGAGAAAATA CATGGGAAGG GCGAATTCCA GCACACTGGC GGCCGTTACT AGTGGATCCG AGCTCGGTAC
211 CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACCT AAATAGCTTG GCGTAATCAT GGTCATAGCT
281 GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT AAAGTGTAAG
351 GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG
421 GAAACCTGTC GTGCCAGCTG CATTAATGAA TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG
491 CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTCGGCTGCG GCGAGCGGTA TCAGCTCACT
561 CAAAGGCGGT AATACGGGTA TCCACAGAAT CANGGGATAA CGCAGGAAAA GACA

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SEQ. ID NO:35

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1 GGNNTTNANT CATTGCCCCG CTNGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
71 GCCCTTCCGA TGTATTTTCT TCTACGTTAA GGTATTTTAA ATTGTTACTA ATGCATAAGG GCAACACATT
141 CTGTAATGCT GACAAGATGA AAGAGCCAAA AGTAATTAAT GATGCTGTTA CCTCACAAT ATGTATGTGT
211 GGATGTATAT ATATCTATTC AATATATGTA ACTATACATA TGTCTGTTT TAATTGAAAA CACCAGGTAA

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281 TTATCATCTG TAGAAACCCT AGTGTCTCAG ATAAGTTGGC TAGTTTTTTG TTTCACATAA AGGAACAAAC
 351 ATTTATAGAT TTATATGTAT ATTAATAATG GTAAAAATTG GCTGGGTGCA GTGGTTCATG CCTATAATAC
 421 CAGCACTTTG GGAAGCCGAG GTGGGCGGAT TACTTGAGGT AAGGAGCCCA GCCTGACCAA CAAGGTGAAA
 491 CCCCATCCCT ACTAAAAATA CAAGAATTAG CCCGGGGATG GTGGTGGCCA CCTGTAATCC CAGCTACTTG
 561 GGAGACTGAA GCCAGGAAAA TCACTTGACC CAGGAAGCNG AGGTTGCAGG NGAG

SEQ. ID NO:36

1 NGNNNTTGAN TCAATTCNNN GNCGANGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
 71 GCCCTTCCTA TGTATTTCTT TCTAGCCAAC CTCCCACTCA TTGATCTGTC TCTGTCTTCA GTCATAGCCC
 141 CCAAGATGAT TACTGACTTT TTCAGCCAGC GCAAAGTCAT CTCTTCAAG GGCTGCCTTG TTCAGATATT
 211 TCTCCTTCAC TTCTTTGGTG GGAGTGAGAT GGTGATCCTC ATAGCCATGG GCTTTGACAG ATATATAGCA
 281 ATATGCAAAAC CCCTACACTA CACTACAATT ATGTGTGGCA ACGCATGTGT CGGCATTATG GCTGTGCGAT
 351 GGGGAATTGG CTTTCTCCAT TCGGTGAGCC AGTTGGCCTT TGCCGTGCAC TTACCCTTCT GTGGTCCCAA
 421 TGAGGTCGAT AGTTTTTATT GTGACCTTCC TAGGGTAACC AAACCTGCCT GTACAGATAC CTACAGGCTA
 491 GATATTATGG TCATTGCTAA CAGTGGTGTG CTCACTGTGT GGTCTTTTGT CTTCTAATCA TCTCATACAC
 561 TATCATCCTA ATGACCATCC AGCATTGCCC TTTAGATAAG TCGTNCAAAG G

SEQ. ID NO:37

1 GNNNTNANTC CNNNCCNCNN CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
 71 GCCCTTCCCA TGTATTTGCT TCTCAGCAAC TTGTCTTCT CTGACCTCTG CTTCTCTTCC GTGACCATTC
 141 CCAAGTTGTT ACAGAACATG CAGAACCAGG ACCCATCCAT CCCCTATGCG GACTGCCTGA CCCAAATGTA
 211 CTTCTTCCTG TTATTTGGAG ACCTGGAGAA CTTCTCTCTT GTGGCCATGG CCTATGACCG CTATGTGGCC
 281 ATCTGCTTCC CCCTGCACTA CACCGCCATC ATGAGCCCCA TGCTCTGTCT CGCCCTGGTG GCGCTGTCTT
 351 GGGTGCTGAC CACCTTCCAT GCCATGTTAC AACTTTTACT CATGGCCAGG TTGTGTTTTT GTGCAGACAA
 421 TGTGATCCCC CACTTTTTCT GNGATATGTC TGCTCTGCTG AAGCAGGCCT TCTCTGACAC TCGAGTTAAT
 491 GAATGGGTGA TATTTATCAT GGGAGGGCTC ATTCTTGTC TCCCATTCCT ACTCATTCCT GGGTCCTATG
 561 CAAGAATTGT CTCCTCATCC TCAAGGTCCC TTTNTAANG GTATCTGCAA GGCCCT

SEQ. ID NO:38

1 NGNNNNTTNA NTCNANGCCN NGNGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG
 71 CAGAATTCGC CCTTCCAATG TATTTACTTC TCAGCCAGCT CTCCCTTATG GACCTGATGT ACATCTCCAC
 141 CACCGTCCCC AAGATGGCGT ACAACTTCCT GTCCGGCCAG AAAGGCATCT CCTTCCCTGG ATGTGGTGTG
 211 CAAAGCTTCT TCTTCTGAC CATGGCGTGT TCTGAAGGCT TACTCCTGAC CTCCATGGCC TACGACCGTT
 281 ATTTGGCCAT CTGCCACTCT CTCTATTATC CTATCCGCAT GAGTAAAATG ATGTGTGTGA AGATGATTGG
 351 AGGCTCTTGG AACTGGGGT CCATCAACTC CTTGGCACAC ACAGTCTTTG CCCTTCATAT TCCCTACTGC
 421 AGGTCTAGGG CTATTGACCA TTTCTTCTGC GATGTCCCAG CCATGTTGCT TCTTGCTGTA CAGATACTTG
 491 GGTCTATGAA TATATGGTTT TTGTAAGGAC AAAGCCTCTT TCTTCTTTN CTTTCTATTG GCATCACTTC
 561 TTCTGNGGGC CGAGTCCTAA TTGCTGGCTA TATAATGCAC TCAAAGGAGG GGAGG

SEQ. ID NO:39

1 TAGNNNNNTT ANNTCANNGC CNNTGNNNGC TCAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC
 71 TGCAGAATTC GCCCTTCCAA TGTATTTTCT TCTCAGCAGG AGAGATATTT ATCCTCACTG CCATGTCCCTA
 141 TGACCGCTAT GTAGCCATCT GCTGTCCCTT GAACTACGAG GCTGCACAGA GTACTTCTCT CTGGCAGCCA
 211 TGGCTTATGA CCGCTGTCTT GCCATCTGCT ATCCTTTTACA CTACGGAGCC ATCATGAGTA GCCTGCTCTC
 281 AGCGCAGCTG GCCCTGGGCT CCTGGGCTGT TGGTTTCGTG GCCATTGCAG TGGCCACAGC CCTCATCAGT
 351 GGCCTGTCTT TCTGTGGCCC CCGTGCCATC AACCATTCT TCTGTGACAT TGCACCCTGG ATTGCCCTGG
 421 CCTGCACCAA CACACAGGCA GTAGAGCTTG TGGCCTTTGT GATTGCTGNT GTGGTTATCC TGAGTTCATG
 491 CCTCATCACC CTTGTCTCCT ATGTGTACAT CATCAGCACC ATCCTTAGGA TCCCCTCTGC AGTGGCCGGA
 561 GCAAAGCCTT CTCCCGTGCT CCTCGCATCT NAACGNNGTG CTCATTGGT ATGGG

SEQ. ID NO:40

1 CATGCTCGAG CGNCGCCAG NGNGATGGAT ATCTGCAGAA TTCGCCCTTC CTATGTATTT GCTTCTCAGC
 71 AGGAGAGATA TTTATCCTCA CTGCCATGTC CTATGACCGC TATGTAGCCA TCTGCTGTCC CCTGAACACT

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141 GAGGTGATTC ATGTGCCCAT TAGAGCTTGA GAAGCACTGC TTGGAAGCCC CTTCTGCCAT CAATGAGGCT
211 GCACAGAGTA CTTCCCTCCTG GCAGCCATGG CTTATGACCG CTGCCTTGCC ATCTGCTATC CTTTACACTA
281 CGGAGCCATC ATGAGTAGCC TGCTCTCAGC GCACCTGGCC CTGGGCTCCT GGGTCTGTGG TTTCTGGGCC
351 ATTGCAGTGC CCACAGCCCT CATCAGTGGC CTGTCTTCT GTGGCCCCCG TGCCATCAAC CACTTCTTCT
421 GTGACATTGC ACCCTGGATT GCCCTGGCCT GCACCAACAC ACAGGCAGTA GAAGCTTGNG GCCTTTGTGA
491 ATTGCTGNTG TGGGTATCCC GAGTTCATGC CTCAIACCC TTGNCTTCTA TGTGTACATC ATCAGGCACC
561 ATTCTCAGGA TCCCTTCTGC AAGNGG

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SEQ. ID NO:41

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1 ATGNNNNNNN NNTTTNNNA ANTTTTNCCC ANTTTGGGCG GNCCCCCCT TCTTTAAGGN AATGGGCCCA
71 TTGGGCCCTT CCCGGAAGGC CCGGGGGCNC CCGGCCCAA AGGTTTGGGT TGGGAAATGG GGGGAATTTA
141 AATTCCTTTG GGCCAAGGNA AAAATTTTCC NGCCCCCCTT TTTTCCCCT TTTGGTTTTT ANCCGGGGGA
211 ANGGGGGGGT TGATTAATTA ATCGGGAAGN TNGGGGGGAA NTTTTTTAAA AAAAACCTTG GGGGAAGGTT
281 CCAACCCAAC AAGTTTGGTT TTCCANGGGA CCGTTGGGAC CAGGCTTTTN GAATCAAGAA TCCCAAAGGG
351 CATTCTTTTG GATTAAGGAA NGGTGCCGGG ACCGGTGAAA GGGAAAAAAC TGGTGGACCC CATACCAAAA
421 TGAGAACCAC GGTGAGATGC CGAGGAGCAC GTGGAGAAAG GCTTTGCTTC CGGCCACTGG CAGAGGGGAT
491 CCTGAGGATG GTGCTTGATG ATGTACACAT AGGGAGACAA GGGTGATGAG GCATGAATC AGGATAACCA
561 CAACAGCNAT CACAAAGGCC ACAAGCTCT ACTGCCTGTG TGTGGGGTGC AGGCCAGGGC AATCCAGGGG
631 TGCAATGTCA CAAGAAAGAA AGTGGTTGAT GGCACGGNG GGCCACAGAA GGACAGGCCA CTTGATGAAG
701 GGCTTGTTGG CACTGCAATG GCCACGAAAC CACCAGACCC AGGAACCCAN GGCCAAGCTT GCGCCTGAAG
771 AGCAAGGCTA CTCATGAATG GCTTCCGTAG TNGTAAAGGA TAGCAAGATG GCAAAGGCAA GCCGGTCATN
841 AAGCCATGGC TTGCCNG

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SEQ. ID NO:42

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1 GNNNTTANN CATTCGCCCC TCTAGATGCA TGCTCGAGCG GCNCGCCAGT GTGATGGATA TCTGCAGAAT
71 TCGCCCTTGT TCGCAAGGA GTAGATGAAC GGATTCAGGG CAAGGGAGTG CTGAGGAGAT AGACGGGTAT
141 AACTGGGCA CAAGTCCATG AGTAATCAAG GCCTGTTATT TAAAAAAGG CTTGAACAAT
211 ATAGAATCCC ATTACCCAGA GATAGACTGG ATGGTGAATT AAACCTTCTG GTGAATTTCT TTCCAGATAT
281 CTCTCTATGC ATATGTATAC ACAAGCAATT TTTGGAAGAA AAGATACTTT ATAAGGATAA GCCTGAAAAC
351 TGCAACGAAT GCAATGTGGA GAATGAAGGC AAGATGTGGC GAAGAAGGGC ACCACAATCT GGTGGCTGAG
421 AGAGTGCAAC TGTCACTACA GCTAAAAGGA GAGCTGGAGA AGCTGGTGAG GACAGTAAGA GATGAATCTG
491 GTTTAAGACA CGCTGAGTCT CAAATGCCAT GGCTCCCCTA GGTTCCTCT TCAGATGTAA ATCTTAAGCT
561 CAAAGCAGGT GGATGAGAAA TCACATTTCA TAGTCCCTGC ACAGACGGCT NTNTTGAGCT

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SEQ. ID NO:43

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1 GNNNNTTAAN TCATTGCCCC GNNNGANGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT
71 CGCCCTTCCC ATGTATTTGC TTCTCAGCAA CTTGTCTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT
141 CCCAAGTTGT TACAGAACAT GCAGAACCAG GACCCATCCA TCCCCTATGC GGACTGCCTG ACCCAAATGT
211 ACTTCTTCCT GTTATTTGGA GACCTGGAGA GCTTCTCTCT TGTGGCCATG GCCTATGACC GCTATGTGGC
281 CATCTGCTTC CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCCTGGT GGCCTGTCTC
351 TGGGTGCTGA CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGTGTTTT TGTGCAGACA
421 ATGTGATCCC CCACTTTTTC TGTGATATGT CTGCTCTGCT GAAGCTGGCC TTCTCTGACA CTCGAGTTAA
491 TGAATGGGTG ATATTTATCA TGGGAGGGCT CATTCCTGCA TCCATTCTTA CTATCCTTG GGTCTATGC
561 AAGAAATGCT CCTCATCCTC AAGGCCCTTC TNTAAGGGTA TCTGCAAG

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SEQ. ID NO:44

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1 GNNNNNTNANT CNTGCCCTGN CCCNCGCNC NNGCGCCGCG GCGGATGGAT ATCTGCAGAA TTCGCCCTTG
71 TTAATAAGAG TATAGATGAA CGGATTCAGG GCAAGGGAGT GCTGAGGAGA TAGACGGGTA TACACTGGGC
141 ACAAGTCCAT GAGTAATCAA GGCTGTTAT TTAAGGAGCT TGAACAATAT AGAATCCCAT
211 TACCCAGAGA TAGACTGGAT GGTGAATTAA ACTTCTGGT GAATTTCTTT CCAGATATCT CTCTATGCAT
281 GTGTATACAC AAGCAATTTT TGGAAAGAAA GATACTTTAT AAGGATAAGC TTGAAAACCTG CAACGAATGC
351 AATGTGGAGA ATGAAGGCAA GATGTGGCGA AGAAGGGCAC CACAATCTGG CAGTAAGAGA TGAATCTGNG TTAAGACACG
421 TCACTACAGC TAAAAGGAGA GCTGGAGAAG CTGGTGAGGA CAGTAAGAGA TGAATCTGNG TTAAGACACG
491 CTGAGTCTCA GATGCCATGG CTTCCCTAGG TTGCCTCTTN CAGATGTAAA TCTTAAGCTC AAAGCANGTG
561 GATGAGAAAT ACACATTTNA TAGTCACCTG CACAGACGGT TTTTGTAT

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SEQ. ID NO:45

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1 CATGCCCCGT CCCNCNAGNT NCNNGCNCCG CGGCCGCNAN GGATATCTGN ANAATTCGCC CTTCCTATGT
71 ATTTACTTCT CCAACTTCTC CTTCCCATCT CTATCATTAG AACCCATTCA TATACACCCT ACGAAACAAG
141 GGCGAATTCC AGCACACTGG CGGCCGTTAC TAGTGGATCC GAGCTCGGTA CCAAGCTTGA TGCATAGCTT
211 GAGTATTCTA ACGCGTCAAC TAAATAGCTT GCGGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT
281 TATCCGCTCA CAATTCCACA CAACATACGA GCCGGAAGCA TAAAGTGTA AGCCTGGGGT GCCTAATGAG
351 TGAGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCCG TTTCCAGTCG GGAAACCTGT CGTGCCAGCT
421 GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCTCGCTCA
491 CTGACTCGCT GCGCTCGGTC GTTCGGCTGN GCGGAGCGGT ATCAGCTCAC TCAAAGGCGG NAATACGGTT
561 ATCCACAAGA ATCAGGGGGA TAACGCAAGA AAAGACATGT GA

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SEQ. ID NO:46

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1 GNNNTNATTN ATTGCATTGG GCCCTCTAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TAGTGAGTAG ATGAAAGGGT TCAGCATGGG GGTCACCACA GTGTACATCA TAGCCATGAC
141 AGTGTCCTTT AGAGTAGAAC TATTAGCTGA TGAGCATAAG TAGAGACCAA TAACGGTTCC ATAGAACAGT
211 GACACCACAG ATAGGTGGGA GCCACAAGTA GAGAAGGCCT TGCAGACACC CTTAGAAGAA GGGACCTTGA
281 GGATGGAGGA GACAATTCTT GCATAGGACC CAAGGATGAG TAGGAATGGG ATGACAAGAA TGAGCCCTCC
351 CATGATAAAC ATCACCATT CATTAACTCG AGTGTCAGAG AAGGCCAGCT TCAGCAGAGC AGACATATCA
421 CAGAAAAGGT GGGGGATCAC ATTGTCTGCA CAAAAACACA ACCTGGCCAT GAGTAAAGTG TGTAAATGAG
491 CATGGAAGGT GGTGAGCACC CAGGACAGCG CCACCAGGGC GAGACAGAGC ATGGGGCTCA TGAGGGCGGT
561 GTAGTGCAGG GGAAGCAGA TGGCCACATA GCGGTCATAG GCCATGGCCA CAAGGAGGAA

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SEQ. ID NO:47

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1 CNATGGGCCC TCTAGATGCA TGCTCGAGCG GCGGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCA
71 ATGTATTTGC TTCTCAGCAA CTTGTCTTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT CCAAGTTGT
141 TACAGAACAT GCAGAACAG GACCCATCCA TCCCCTATGC GGACTGCCTG ACCCAAATGT ACTTCTTCT
211 GTTATTTGGA GACCTGGAGA GCTTCTCTCT TGTGGCCATG GCCTATGACC GCTATGTGGC CATCTGCTTC
281 CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCCTGGT GCGCGTGTCC TGGGTGCTGA
351 CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGTGTTTT TGTGCAGACA ATGTGATCCC
421 CCACTTTTTT TGTGATTTGT CTGCTCTGCT GAAGCTGGCC TTCCCTGACA CTCGAGTTAA TGAATGGGTG
491 ATATTTATCA TGGGAGGGCT CATTCTTGTC ATCCCATTC TACTCAATCC TTGGGTCTAT GCAAGAAATT
561 GTCTTCTTCA TNCTCAANG CCCTTTCTTC TAANGGTATC TTGCAAG

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SEQ. ID NO:48

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1 ANNNCNTNG GAGCTCCAAA GCAGTGGTAA CAACGCAGAG TACGCCCCCT ATGTACTTAC TTTTGTAAAG
71 TCCAACCTCC ATCCTCCTTG GCCTTTTGAT TCAATTGATC ACTCCTTCCT CCTCAAAACA CCTTGTTTAC
141 TCATCCTTTC TCAGTCTCCT TTGTGGATTG TTCTCATTT ATTTGACCTC TTGCTGGTGA ACCCTTTCAT
211 ATACACTCTC CGTAACAAAG AGGGCGTACT TCTGTCGTCT TGAGCGNACT GATGGNACCC AGCTTTTGT
281 CCCTTTAGTG AGGGNTAATT GCGCGCTTGG CGNAATCATG GNCATAGCTG NTTNCTGNNGN GAAANTGNTA
351 TTTCGNTNAC AATTNCACAC AACATACNAG CCGGGAGCAT AAAGGGNNAA GNCCTGGGGN GCCTAATGAG
421 GGAGCTTACT CACAATAATT GGGGTGNGCC CACTGGCCCC TTTTCAGGCG GGAAAACCTN GCGGGGCCAG
491 CTGGAATAAA TGAATCGGGC CACGCGCCGG GGAGGAGGGC GGGTTNNGGA ATTGGGCGCT TTTTCCNTTT
561 CTNGGTAAAT GGACTNGGTN GGCNNNGTCC GTTCGGTTGG GGGGANCGGN NNT

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SEQ. ID NO:49

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1 AACGCAGAGT ACCGCCACT ACGTAATCTG TACATGAAAG GGTTTAAAAG AGACTGGGAA GAGAGGAATT
71 GGCAAGATCA AGCAGAGGCA ACTCCTTCTA GTCCTTCTAG TACCGCAAGG GGCAGATAAA TGGAAATGGT
141 AACACCTAGA GGAAAGTATA CTTGCCAAAA GCAAATNCAT AGGGGGGAGT ACATTATCGG GTTGAAAAAA
211 GTATTCCATG CAGATAAAAA CAAAAGCAA ATACATCGGG GCGGTACTTC TGTCGTCTTT GAGCGTACTG
281 ATGGTACCCA GCTTTTGNTC CTTTAGTGAG GGTAAATTGC GCGCTTGGCG TAATCATGGT CATAGCTGGT
351 TTCTGTGTGA AATTGTTATC CCGCTCACAA TTCACACAAC ATACGAGCCC GGGAGCATAA AGTGTAAGC
421 CTGGGGTGCC TAATGAGTGG AGCTTACTTA CATTAAATTG CGTTGCGCTC ACTGGCCGCT TTTCCAAGTC
491 GGGAAACCTG TCGTGNACAG TTCANTAATG AATCGGCCAA CGCCGCGGGG AGAGGCGGGT TGCGTATTGG
561 GCGCTCTTCC GCTTCTTNGT TNACTGACTT CGG

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SEQ. ID NO:50

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1 GNNNTTTAAC NCCGGNGCTN CNAGCAGTGG AACACGCAG AGTACGCCCC CGATGTACTT TCTTTTTCAG
71 TCTCAAGTCT TCCTCTTCTC CAAAGATTTT GTCTTTTCTA CTACCTGAGC TACCAAATCC CTTGTCATCA
141 ATTTCAATAA CTGTATTCTC TTCATCATTT CAACTTCAAA CGTGTCATCT CAGAACAAGC TTCATGTTAC
211 TTCCAATTTT ATCCTTCTTG TTTGCTGATT CCAAGAATTC CAGTCCCATC TAGGCCCCGCA ATGCATTGTT
281 CCTGCCACCC TTTTCATATC CTCAATTCCC TTGTATCATC ACTTTCCTTT TATATAGCAC AGATTCCATG
351 ATTCATAACA ATAATTATGT TTTTTTTTGC ATGTGCTCTT AATTTCCTTT CTGTCTCCTA TTATCTTCTA
421 TCATACTTTT CTGGAAACAC TAATTCTGGT GAAATATACT CTTTGTGGAC TTTGCACTTA TGCTCAGTCA
491 GCTGAAGATG ATGGCTAGAC AAATACTCAC AATCATGCTG ACTGGCCCCA TTTATAGTCA TGACCACCGA
561 TTACAAACCC CTTCAATTTAT TCTCCGCAAC AGGGGCGTCT TCTGCGCTTG AGCGTCCGGT GGGG
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SEQ. ID NO:51

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1 GCAGTGGTAA CAACGCAGAG TACGCCCCGT ACGGAGGCTG TAAATAAAGG GGTGAGGAA GTAAAGTACT
71 TCACAGTACT GGAGCACACA GCATGTGAAT TTCAGCCAAA GGACAAATGC CTCCAAAAAA AGTTAATTCA
141 CAGTGCAGCA GGGCGAGGCA CTTGTCTTAT TCGCTGGTTC TCACATTGAC CCTGAAAGGA CTTTTTTTGT
211 TTAATCCCAT TTTACAGAT GGGAAAGGGA CTCTGTATGG TTGTCACTTT TATCCAAAGT CTCATAGCCA
281 GTAAGAAGCT GCCCTCAAAG TCCCTACCCT GTCTTCCATT CGACTATTCT GAGGTTTCTA CCCAGAAACC
351 CCATACCTCT GCCTTATATT TTAATGAAAA GTATGTCTCC AGGTTTATGT GGAGAATAAC CAAGACCTCA
421 GAAACATTTA GTGAAATCA GAGCTAGAAG GAATCTGTTT TTTTGCGAGT TCAGAGAAAC TGACTTGGAT
491 AAGACATCAA AGTTGTCTTG TGCAGCAAAT TCTCCTCCGG CACATAGTAG GCACTCTGAT AAATTCAAAA
561 AGGCTTCTAA GAAGAGGCAG AAGN
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SEQ. ID NO:52

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1 GTGAANCCAN NNTAANNCCN ATTGGAGCTC CAAGCAGTGG TAACAACGCA GAGTACGCCC CCGATGTAGT
71 TTCTTCTTTC CTTCCCTTCC TCCTTCCTTC CTTCTTTCTT TTCTCTCTCT CTCCCTCTCC CTCTCCCTCT
141 CCCTCTCTCT CTCCTTTTTT TTCTCCTTCC TCCTCCTCCC CCAATCCGT TCATGACTTC TTCTTCTTCC
211 TCTTCTTCTT CTTTCTTTCT TTCTTCTTTT TCTCTAAGCA GGATCCTGGG CTGTTCAAAC CAGAGAGCTG
281 TAAGTCTTTT CTTTCCCCAT TACTGTTAGA TCCGTTGAAT CGGCTCCAGA AACCAAACAA GTTAACCTT
351 GCATTTACAC GTTTCGTAAC GGGCGTACTT CTGTCGTCTT GAGCGTACTG ATGGTACCCA GCTTTTGTTC
421 CTTTTAGTGA GGGTTAATTG CGCGCTTGGC GTAATCATGG TCATAGCTGT TTCCTGTGGG AAATTGTTAT
491 CCGCTCACAA TTCCACACAA CATACGAGCC GGGAGCATAA AAGTGTAAG CCTGGGGTGC CTNATGAGTG
561 AGCTAACTCA CATTAATTGC GTTGCGCTTA CTGNCCGTTT TCAGTCNGGA AAN
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SEQ. ID NO:53

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1 TNANNCCNNT TAANNCCCAT TGGAGCTCCA AAGCAGTGGT AACACGCAG AGTACGCCCC CGATGTACTT
71 GCTTCTTCTT CTTTGGAGTG GCTGAATGCT TCCTCCTGGC TACCATGGCA TATGACCGCT ATGTGGCCAT
141 CTGCAGTCCC TTGCACTACC CAGTCATCAT GAACCAAAGG ACTCGTGCCA AACTGGCTGC TGCTCCTGG
211 TTCCAGGCT TTCTGTAGC TACTGTGCAG ACCACATGGC TCTTCAGTTT TCCATTCTGT GGCACCAACA
281 AGGTGAACCA CTTCTTCTGT GACAGCCAC CTGTGCTGAG GCTGGTCTGT GCAGACACAG CACTGTTTGA
351 GATCTACGCC ATCGTCGGAA CCATTCTGGT GGTCATGATC CCCTGCTTGC TGATCTTGTG TTCCTATACT
421 CGCATTTGCTG CTGCCATCCT CAAGATCCCA TCAGCTAAAG GGAAGAATAA AGCCTTTTCT ACATGTTTCT
491 CACACCTCCT TGGTGGCTCT CTTTTCTATA TATCATTAAAG CCTCACCTAC TTCCGGCCTA AATCAAATAA
561 TTCACCTGAG GGCACGAAGC TGCTATCATT GCCTACACTG NTATGACTCC A
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SEQ. ID NO:54

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1 GTTNTTCCAT GGACTCCCAA GCAGTGGTAA CAACGCAGAG TACGCCCCCT ATGTACTTAC TTCTTGCTGG
71 CTTATCATTT ATAGATATCA TTTATTCTTC ATCCATTTC CACAGATCGA TTTCAGACTT GTTCTTTGGG
141 AATAATTCCA TATCCTTCCC ATCTTGCTTG GCCAGCTCT TTACAGAGCG CTTTTTTGGT GGGTCAGAGG
211 TCTTCTTCT GTTGGTGATG GCCTATGACC TTGCATTACT TGGTTATCAT GAGACAATGG GTGTGTGTTT
281 TGCTGCTGGT AGTGTCTTGG GTTGGAGGAT TTCTGCACTC AGTATTTCAA CTTAGTGTTA TTTATGGGCT
351 CCCATTCTGT GACCTCAATG TCATTGATCA TTTTTCTGT GATATGCACC CTTTATTGAA ACTGGTCTGT
421 ACCGATACCC ATGTTATTGG CCTCTTAGTG GTGGCAATGG AGGACTAGGT TGCATATTG GGNTTCTGCT
491 CTTACTCATC TCTTATGGNN CATCTGCACT CTCTAAAGAA CCTTAGTCAG AAAGGGAGGT GAAAAGCCCT
561 CTCACCTGAC AGTTCCACAT AACTGGGGGG TGTTTTCTTC TTTGTN
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SEQ. ID NO:55

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1 TTANNCCNNT TNAATNCCNT TGGAGCTCCA AAGCAGTGGT AACACGCAG AGTACGCCCC CAATGTACTT
71 GCTTCTTCTT TTTTGGGGCT GCTGAGTGCT GCCTCCTGGC CACCATGGCA TATGACCGCT ACGTGGCCAT
141 CTGTGACCCC TTGCACTACC CAGTCATCAT GGGCCACATA TCCTGTGCCC AGCTGGCAAG CTGCCCTCTG
211 GTTCTCAGGG TTTTCAGTGG CCACTGTGCA AACACATGG ATTTTCAGTT TCCCTTTTGT TGGCCCCAAC
281 AGGGTGAACC ACTTNTNTG TGACAGCCCT CCTGTTATTG NACTGGTCTG TGCTGACACC TCTGTGTTTT
351 GAACTGGAGG CTCTTGACAG CCACTGCCTA ATTCATTCTC TTTCTTTTCT TGCTGATCCT GGGATCCTAT
421 TTCGCATTCT CTTCATATC TTTAAGGATG CCGTCAGCTG AGGGGAAACA TNAGCATCTC NCACCTGTTT
491 CGCCACCTC TTGGGTGGCT CTCTCTCTA TAGCACTGGC AATCCTTAAC GTATTTTCCG ACCCAATTCT
561 AAGTGCCTTT TTNTGAGAAG CAAAGAACT GGTGTGCTACT TTTTTCCTAC AAGGGGNGAC TTCCAATGTT

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SEQ. ID NO:56

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1 GNGNTTTNNN CCATGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCCCCATGTA CTTTCTTCTT
71 CTTTGGAGTG GCTGAATGCT TCCTCCTGGC TACCATGGCA TATGACCGCT ATGTGGCCAT CTGCAGTCCC
141 TTGCACTACC CAGTCATCAT GAACCAAAGG ACTCGTGCCA AACTGGCTGC TACCTCCTGG TTCCCAGGCT
211 TTCCTGTAGC TACTGTGCAG ACCACATGGC TCTTCAGTTT TCCATTCTGT GGCACCAACA AGGTGAACCA
281 CTTCTTCTGT GACAGCCAC CTGTGCTGAG GCTGGTCTGT GCAGACACAG CACTCTTGA GATCTACGCC
351 ATCGTCGGAA CCATTCTGGT GGTCAATGAT CCGTGCTTGC TGATCTTGTG TTCTTACTAT CACATTGCTG
421 CTGCCATCCT CAAGGTCCCA TCAGCTAAAG GGAAGAATAA AGCCTTTTCT ACATGTTTCT CACACCTCCT
491 TGNTGTCTCT CTTTCTATA TATCATTAAG CCTCACCTAC TTCCGGCCTA AATCAAATAA TTCACCTGAG
561 GGCAAGAAGC TGCTATCATT GNCCTACACT GTTATGACTC CATGTTGAAC CCCATAATTT ATTCATTGAG
631 C

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SEQ. ID NO:57

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1 TTATNNCCAT TGGAGCTCCA AAGCAGTGGT AACAAACGCA GAGTACGCCC CCCATGTATT TTCTTTTCTT
71 TGGGGNAGCT GNATGCTTCC TNCTGGCTAC CATGGNATAT GACCGGCTAT GNGGNCATCT GCAGTCCCTT
141 GNNCTCCCAG TCATTATGAA CCAAAGGACA CCGGCCAAAC TGGCTGGTGN TTCCTGGGCT CCAAGCTTTC
211 CTGNAGCTAC TGNGCAAGAC CACAATGGCT CTTNAGNTTT CCATTCTGNG GCACCAACAA GGTGAACCAC
281 TTNTTCTGN GACAGCCGGC TGTGCTGAAA GCTGGTCTGN TGCAAGACAC AGCACTGTTT GAGATCTACG
351 CCATCGTCGG AACCATCTCTG GTGGTCAATG AACCCCTGCT TGCTGATCTT GNGTTCCTAT ACTCGNATTG
421 GTGCTGCTAT CCCTCAAGAA CCCATCAAGC TAAANGGGAA GCAATAAAGN CCTTCTCTA CGTGCTCCTT
491 AACACCTCCC TTGGTGGCCT CTCTTTTCTA ATATAATCNT CTAAGCCTCA ACCTACTTCT TGGGCCNTAA
561 NTCAAATAAA TTCTTCTGGA GAGGCAAGAA GGTGGTATTC ATTTATNCTA CACTGGTNGN GACTCCATGN
631 TGGAACT

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SEQ. ID NO:58

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1 GTNATNCCNT TTAATNCCNT TGGAGCTCCA AGCAGTGGTA ACAACGCAGA GTACGCCCCG TCCTCAGACA
71 GTATATGAAT GGGTTAAAAA TGGGCCAGAG CAGATGCAGG AAGATCAAAT AGGAGGCTAC TGCAGTAGAG
141 TCAAATCTAG GGCTGATGGT TTCTTGGGAT GCATAGTAAT AGGTAGATAG AGAAAGTCTT TAGGAGGTAG
211 AATGGACAGG ACTTCACAAT GCATTAAATG TAGGGAGAAA AAAAATGATT CCTGGGTTTC TAGCTTGAGC
281 TAGTAGGGAT AGTGGTAGAA TTTACTGATA TGGAAACTG GAGGAAAAAG AGTTTGGGAG AGAAAGATGG
351 CAAGTTAAAT ACCTGTGGGA AATATAATCA CAGACACTAA ATAGGCAGCT GTGTGGGTGG CAAAGGAGAG
421 CCATGGGCTA GGAACATACA GTGGGATTCC CTGGCATGTC ATTGGTTACT GAAGTCAGAG TGTATGAGAC
491 AGCCTAAGGA GAGAATNCAC ACAGGAGAAG AAAGAATAA ACATTAGTG GCTGGCCAGA GGATGAGAAA
561 CCAAGAGAT TGGACTGTTT AGGAGCAACA GTGTTGNGAA AAGGGAGAAA NGGTTGAAAT T

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SEQ. ID NO:59

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1 GGNTTTANNC NCTGGAGCTC CAAAGCAGNG GTAACAACGC AGAGTACGCC CATTGCGTAG CGTGACATA
71 AAGGGGTGAG AGCTGAAGGA GGAGATAAAG AAGAAGACAG CCAGAACCTT GTCCTCTGTC GGAGATCGCA
141 GGGATCTTGG GCCGTAGATA GGTATAAGCA AAGGGTGCAT AGTAGAAAGT CACTACAGTG AGGTGGGTGC
211 TGCAGGTCGA ATAGGCCTTC TTCCTCCCTT CTGCAGAGTG CATGTGGTAG ACAGCAAGGA GAATCCGGCC
281 ATAGGAACAT GCAATACAAA TGAAGGGAAA CACAAGAAAA ATGGTGGTGC TCAAAAACAC CGTGCACTCA
351 TAGACCCAGG TATCCGTGCA GGCTAGGGTC AACATAGCTG GAACATCACA GAAAAATGA TTGATGGCTC
421 TGGACTTGCA ATATGGGATA CGGAGTGCAT ATACCGTGTG AGCACAAGAG TTGATGGAGC CTATCATCCA

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491 AGATCCTGTT ATCATCAGTG CACACACTCT TTTTCTCATA CGGATGAGAT AGTGGAGAGG AAAGCAAATA
561 GCCACATAAC GATCATAGGC CATTGATGTC AGGAGCAGCG CTTCTGCACC TGCTAAAGTC AGGAAGAAGA
631 T

SEQ. ID NO:60

1 TGTTANTCCN NTTTNCNTCC ATTGGAGCTC CCAAGCAGTG GTAACAACGC AGAGTACGCC CTCCTTGT TT
71 CTGAGAGTGT AGATGAAGGG GTTATAGGAG ATAAAGATCA GGGCAATATG TAGGACAAGG ACACAGACAC
141 TGACAACAAA GTTGATTATC TCATTGACAG TGGTGTCTGT GCAGGCCAGC TTCAGCAGGG GTCTCACATC
211 ACAGAAGAAG TGGGAGATGA CAAAGTCATC ACAAAGGGG AGGCCAAACA TAGATGTTAC TTGGACAATA
281 GCCATGCCCA GGCCAATCCT CAGTGACCCA GATCCCAGTC AGACACAAGC CCTCTTACCT ATGAATACCG
351 TAAGGGGTTG CAGAAGACCA CATAGCAATC ATATCCCATG GCTATGAGAA GAAAGCAGTT GTTGATGCCA
421 AAAGTCACAT AGAAGAGCTG AGTGACACAG CCTTGCAATG CAATAAGCTA GTGAGGATTG AAGAGGCGAG
491 AAAGCATATG GGGAGTAATG GCCACCATGT AGCAGGTCTC AGAGATAGAC AGCAATGCTT AGGAAAAGT
561 ACATGGGCCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTTCCCTTT

SEQ. ID NO:61

1 GTNANNCCNN TGTAGCTCCN AAGCNGAGCT AACAAACNNAG AGAACAACGC AGAGTACGCC CCCGATGTAC
71 TTGTTCCCTAC TCTTTGCTGG ATTTGAAAAC TTCCTCCTGT CCGTGATGGC CTATGACCGG TTTGTGGCCA
141 TCTGTCACCC CCTGCACTAC ATGGTCATTA TGAACCTCA CCTCTGTGGA CTGCTGGTTC TAGCATCCTG
211 GACCATGAGT GCTCTGTATT CCTTGCTACA AATCTTAATG GTAGTACGGC TGTCCTTCTG CACAGCCTTA
281 GAAATCCCCC ACTTTTCTG TGAACCTAAT CAGGTCATCC AACTTGCTTG TTCTGATAGC TTTCTTAATC
351 ACATGGTGAT ATATTTTACA GTTGCGCTGC TGGGTGGAGG TCCCCTCACT GGGATCCTTT ACTCTTACTC
421 TAAGATAATT TCTTCCATAC ATGCAATCTC ATCAGCTCAG GGGAAGTACA AGGCATTTTC ACCTGTGCAT
491 CTCACCTCTC AGTTGTCTCC TTATTTTATG GTGCAATCCT AGGGGTGTAC CTTAGTCTGC TGCCACCCCG
561 AACTCACACT CAAGTGCAAC AGCCTCAGTG ATGTACACTG GGGCACCCCT AT

SEQ. ID NO:62

1 GNNNNNNNAT TTNATGCCNT TNTTGATTCC CNTTNNNNNN NCAAGCAGNG GTAACAACGC AGAGTACGCC
71 CCCTATGTAT TTCTTCTTAA GATCCAAATA TTAATAATAA AGACAGTCAT CCCACCTA ACTAAAGTAC
141 TGTTTCCAC ACTTCTCTAT TAAGAAGCAT GTGAGATACT TGTACAAAC ATAACATCCT GGTCCCACCC
211 CAAAGCCACT CAATCAAATA CTCCAGGGAA GGGATCTAGG AATTCGTAGG TTTAACGAGT GCCCCAAAT
281 GATTATTACC TGTTGGAGAA TCTAGGCAAC AATGAATTAA GGAAAGCTCT CTACCATTG GTACTGGTAC
351 CAGGTTTGGAG GATCAGAGG AAGAGGGTAA GCATATCAGA CTAGCAGAGC TGCCAGAACT CGGGCTTTCA
421 AAAGAGAGGT GCCACCCTCT CCCATGTCCA TGTAAGTAGC AAACAACCCCT CTCATGTACA CTCTGAGGAA
491 CAAGGGGGCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTCCTTTTA GTGAGGGTTA
561 ATTGCGCGCT TGGCGTAATC ATGGTCATAG CTGTTTCTCTG TGTGAAATTG TTATCCGCTC ACAATTCT

SEQ. ID NO:63

1 TGTAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCT CTTGGTTACG TAAGGGAATA GATGATGGGG
71 TTCAGCATGG GGGTGACTAC AGTGATACAT ACAGTGGCCA CACGGTCCCA CTCTGCTCGC GTCGGGACGT
141 GGCCTGGAAG TAGACTGCAA TGACTGTCCT ATAGAAAGAG GCTCACCACA NCCAGGTGGG AGCCACAGGT
211 GGGNCACAAG TCCCGGAGCC TCCAGAGGC TTGAGGGCAG CTGGAGCAGG GGNAAGCTTG NTATGGNCCC
281 ACAAGGAGGC GAGGATGAGC AGNAAGGGAG TGACCACCAC TTGCNCGGCC CTNNGTGAAG ATGAGCAGCT
351 TGGATGTGGT GGNTGTCAGA GCACGAGAGC CTTTAAGAGA GGCTTGGTGG GTCACAGAAG AAGTGGGNGC
421 ACTTTGTGGG AAAGCACAGA AAGGACAAGC GAGCCATGAG CAGGATATAC AGGAGGGAGT TGCCGTGGG
491 ACACCAAGCA TGCCATTCCA ACCAGGGCTG CGCACATNGC CGGGGACATT CTCGTGGGAT AAGGGAAGGG
561 GTGCCGGATN GGCACGTATC AGTCATAGGC CTTGGNCGCC AGAAGACAGC TTTNAATTTA CCCCAGG

SEQ. ID NO:64

1 GTTANNCCNT NTANCTNCAA NNGAGGTAAC AACGCAGAGT ACGCCCCCA TGTATTTGCT TCTTGTCCAA
71 CCTGTCCTTT GTAGAGATCT GCTACACCAC CGTTGTGGTG CCCTTGATGC TTTCCAACAT TTTTGGGGCC
141 CAGAAGCCCA TTCCATTGGC TGGATGTGGG GCCCAAATGT TCCTCTTTCT CACTTGGT GGTGCTGACT
211 GTTTCCTCTT GGCGATCGTG GCCTATGACC GCTATGTGGC CATCTGCCAC CCTTTGCACT ACCCCTCATC
281 ATGACCTGCA GTCTGTGCGT GCAGATGCTG GGCGGCGCTG TGGGCCTGGC CCTCTTCTC TCCCTGCAGC
351 TCACCGCCTT AATCTTCACC TTGCCCTTCT GCGGCTACCG CCAGGAAATT AACCATTCC TCTGCGATGT

421 ACCTCCGTCC TGCGCCTGGC CTGCGCTGCA TCCGTGTTCA CCAGGCTGCC TCTATGTCGT GAGCATCCTC
 491 GTGCTGACCG TCCCCTTCTT GCTCATCTGC GTCTCCTACG TGTTTCATCAC CTGTGCCATC CTGAGCATCC
 561 GTTCTGCTGA GGGCCGGCAC CAGGCCTTTT CAACTGCTCT TCCGG

SEQ. ID NO: 65

1 TGTAGCTCCN AAGNNGAGNT ANCAACGCAG AGTACGCCCG CGGAATCTAT AGATGAAAGG GTTTGGNGAG
 71 TCAGAAGAAG GAAGTACATG GGAGTCATAA CAGTGTAGGA CAATGATGGC AGCTTCTTGC CCTCAGGTGA
 141 ATTATTTGAT TTAGGCCGGA AGTAGGTGAG GCTTAATGAT ATATAGAAAA GAGAGACAAC AAGGAGGTGT
 211 GAGGAACATG TAGAAAAGGC TTTATTCTTC CCTTTAGCTG ATGGGATCTT GAGGATGGCA GCAGCAATGT
 281 GAGTATAGGA ACACAAGATC AGCAAGCGGG GGATCATGAC CACCAGAATG GTTCCGACGA TGGCGTAGAT
 351 CTCAAAGAGT GCTGTGTCTG CACAGACCAG CCTCAGCACA GGTGGGCTGT CACAGAAGAA GTGGTTCCACC
 421 TTGTTGGTGC CACAGAATGG AAAACTGAAG AGCCATGTGG TCTGCACAGT AGCTACAGGA AAGCCTGGGA
 491 ACCAGGAGGT AGCAGCCAGT TTGGCACGAG TCCTTTGGTT CATGATGACT GGGTAAGTGC AAGGGACTGC
 561 AGATGGCCAC ATAGCCGGTC ATATGCCATT GGTAGCCACG GANGAAGCT

SEQ. ID NO: 66

1 GTTATNCCTT GTTGCTCCCN AGCAGAGGTA ACAACGCAGA GTACGCCCCCT ATTTCTCAGA TATANGATGA
 71 AGGGGTTTCA AAAAAGAATG AGCAAAGAAA ATCTGGGCCA GGCGGGCATC AAAAGAAATA GTCTTGTGCT
 141 CAACCAGAAA GTCTGCAATC ATTTTAGGGG TAGCAGAAGA GGCAACACAT ACGTCTATAA ATGACAGGTT
 211 GGCAAGAAGC AAATACATTG GGGGCGTACT TCTGTCTGCT TGAGCGTACT GATGGTACCC AGCTTTTGTT
 281 CCCTTTAGTG AGGGTTAATT GCGCGCTTGG CGTAATCATG GTCATAGCTG TTTCTGTGT GAAATTGTGA
 351 TCCGCTCACA ATTCCACACA ACATACGAGC CGGGAGCATA AAGTGTAAG CCTGGGGTGC CTAATGAGTG
 421 AGCTAACTCA CATTAAATTGC GTTGCGCTCA CTGCCCGCTT TCAGTCGGGA AACCTGTCGT GCCAGCTGCA
 491 TTAATGAATC GGCCAACGCG CCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CTCGCTCACT
 561 GACTCGCTTG CGCTCGGTG TTCGGCTTGC GCGAGCGGT ATCAAGCTCA CTCAAA

SEQ. ID NO: 67

1 GGGTTTTACN CTGTGCNCCC CCAGCAGNGG TAACAACGCA GAGTACGCCC TTGTTGCGAA GAAATAAATG
 71 AATGGGTTTA AAATAGACGT GAAGATGGTG TAGAATACAG CAAGGACTTT GTCAACTGAG TAACTGCTGA
 141 AGGGCCACAC ATAGATGAAA ATACACGATC CAAAGAATAA AGTGACCACA GTGATGTGAG CAGTCAATGT
 211 GGAGTGGGCC TTCACCATGC TTACAGAGGA GCGATTCTTA ACTGTAATAA GTATTACAGT GTAGGANACA
 281 ACCAANAGGA GAAAGGAACT CAGAGAAAGA AAGCCACCAT CTGCAACTAT TAGTAGGCTG ACAACATAAG
 351 TGTCTATGCA GGCTAACTTN GTNGCTAGAG GAAGGTCACA GAAAAAACT ATCTACCTTA TTAGGACCAC
 421 ANAATGGCAG ATTAACCGTG AATGCCAACT GGCTGGTGGT ATGGATGAAG CCCACAAACC AGGAAATGAG
 491 GACGAGCACA ACACATACAC AGNAGCTCAT GATTGANATG TAGTGNGGAG GTTNTCTNTN GCTCATANCC
 561 GTNTTNGCCA TNGNAACTNG GANCAACATT TTACTTGCAG TGNNGGAGNG AACATGAAAT N

SEQ. ID NO: 68

1 GTTANNCCNN TTAAATNCNA TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CGATGTACTT
 71 GTTCCTACTC TTTGCTGGAT TTGAAAACCT CCTCCTGTCC GTGATGGCCT ATGACCGGTT TGTGGCCATC
 141 TGTACCCCC TGCATACAT GGTCAATTATG AACCCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA
 211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCTTCTGCAC AGCCTTAGAA
 281 ATCCCCCACT TTTTCTGNGA ACTTAATCAG GTCATCCAAC TTGCTTGTTT TGATAGCTTT CTTAATCACA
 351 TGGTGATATA TTTTACAGTT GCGCTGCTGG GTGGAGGTCC CCTCACTGGG ATCCTTTACT CTTACTCTAA
 421 GATAATTTCT TCCATACATG CAATCTCATC AGCTTAGGGG AAGNACAAGG CATTTCACAC CTGTGCATCT
 491 CACCTTTCAG TTGCTCCTTA TTTTATGGNG CAATCTAGGG GTGACCTTAG TTTTGCTGNC ACCCGCAACT
 561 CACACTTAAG TGCAACAACC TCAGTGATGT AACTGGGGT CACCCCATGC C

SEQ. ID NO: 69

1 GNGNNNCAG NTTANNCTT GGAATCCCAG TAGAGCTACN ANGANTNCGC CNAGCGCGCA NTTNNNCCAG
 71 GGTNNTNTTN GTATACCAA TGAATAGAAA ACAGACACCA CCTTGTCCTT GCCTAGCAAG TAGCTGGAGC
 141 TGGGTCGCAA GTACACGAAA AGGGCTGTCC CAAACAGCAG AGTCACCACC ATCAGATGCG AGGCACACGT
 211 GTTGCAGGCT TTCCATCGGC CCTCTGCTGA AGGGATCTTC AGGACCGCAG AACTATGTA ACCATAGGAG
 281 ATAAGGAGTT GGAGGAACGA TGTTCCCTCCG ACGGTGACCA CCACGAGGAA ATTCACCACT TGAAGGAGGA
 351 AGGTGTCAGA GCAAGACAGA GCCAGGACTG GTGGGAGGTT GCAGAAGAAG TGGTTGATGA TGGTGGGTCC

421 GCAAAAGTGA AGCCTAAATA TGGAGCTGGC CTGGATCAGG GAGCTCAGGA AGCCACCAAC ATATGCCCCA
491 ACCACCATGC GTGTACAGAG GCCCTGGGTC ATGATAGTGG GGTANAGAAG GGGGCTGGAG ATGGCTTGCA
561 TATCGGTCGT ATGCCATAGC AGTCANGAGG AGGCACTCAA GACAGACCCA TGCCGACNAA GAAAT

SEQ. ID NO:70

1 GNNNNTTTTA CCCCTGNNGC ACANAGCAGT GGTNACAACG CNCGAGTACG CCCCCTATGT ATTTTTTCCT
71 ATTCTGGACA CGCTACTCCT GACCGTGATG GCCTATGACC GGTTTGTGGC TGTCTGCCAC CCTCTGCACT
141 ATATGATCAT CATGAACCCC CACCTCTGTG GCCTCCTGGT TTTTGTCAAC TGGCTCATTG GTGTCATGAC
211 ATCCCTCCTC CATATTTCTC TGATGATGCA TCTAATCTTC TGTAAGATT TTGAAATTCC ACATTTTTTC
281 TGCGAACTGA CGTACATCCT CCAGCTGGCC TGCTCTGATA CCTTCCTGAA CAGCACGTTG ATATACTTTA
351 TGACGGGTGT GCTGGGCGTT TTTCCCCTCC TTGGGATCAT TTTCTCTTAT TCACGAATTG CTTTCATCCAT
421 AAGGAAGATG TCCTCATCTG GGGGAAAACA AATAGCACTT TCCACCTGTG GGTCTCACCT CTCCGTCGTT
491 TCTTTATTTT ATGGGACAGG CATTGGGGTC CACTTCACTT CTGCGGTGAC TCACCCTTCC CAGAAAATCT
561 CCGTGGCCTC GGTGATGTCA CTGNNGTCAC CCCCATGTTG ACCCTTTCAT TTACACCCTT AGCAAG

SEQ. ID NO:71

1 GNNNNNNNNN GTTNATNCCN NTTTTAATGC CANTNGAGNT AACAACGCAN GAGTACNCCN NNGNGTACGC
71 CCAGGGTTCA ACCNNTGAAT AGAAAACAGA CACCACCTTG TCCCTGCCTA GCAAGTAGCT GGAGCTGGGT
141 CGCAAGTACA CGAAAAGGGC TGTCCCAAAC AGCAGAGTCA CCACCATCAG ATGCGAGGCA CACGTGTTGC
211 AGGCTTTCCA TCGCCCTCTG CTGAAGGGAT CTTCAGGACC GCAGACACTA TGTAACCATA GGAGATAAGG
281 AGTTGGAGGA ACGATGTTCC TCCGACGGTG ACCACCACGA GGAAATTAC CACTTGACTG AGGAAGGTGT
351 CAGAGCAAGA CAGAGCCAGG ACTGGTGGGG AGGTTGCAAG AAGAAGTGGT TGATGATTGT TGGGTCCCGC
421 AAAAGTGAAG GCCTAAATAT NGAGCTGGCC TGGATCAGGG GAGCTCAGGA AGCCACAACA TATGCCCCAA
491 CCACCATGCG TGTACAGAGG CCCTGGGTCA TGATAGTGGG GGTNGAGAAG GGGGCTGGA GATGGCTGCA
561 TATCGGTCGT TGCCATAGCA AGTCAGGAGG AGGCACTTCA GACAGACCCA TGCCNCNAAG AAAAAAACT
631 GNC

SEQ. ID NO:72

1 GNNNNNNNNN NTTNNNNCN TNACTCCNGC AGTGGTAACA ANNANTACGC NCAGCGCGCA GTTAACCCCTC
71 ACTAANGGTA ANNTNAGCTG GAACACATCA NTACGNTCAN GNNNGCNCNA TGACCGGTTT GTGGNCATNT
141 GTCACCCCTT GCACATCATG GGTCAATTATG AACCCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA
211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCCTTCTGCA CAGCCTTAGA
281 AATCCCCCAC TTTTCTGTG AACTTAATCA GGCATCCAAC TTGCTTGTTT TGATAGCTTT CTTAATCACA
351 TGGTGATATA TTTTACAGGT TGCGCTGCTG GGTGGAGGTC CCCTGACTGG GATCCTTTAC TCTTACTCTA
421 AAGATAATTT CTTNCATACA TGCAATCTCA TCAGCTCAAG GGGAAAGTCAA GGCATTTTTT ACCTGTGCAT
491 CTACCCCTCA GTTGCTNCTT ATTTTATGGN GCAATCCTAG GGGTGACCTT AGTTCTGGTG GCACCCGCAA
561 CTACACTCAA TGCACAAGCT CAGTGATGTA CACTGTGGCA CCCATGCTGA ACCN

SEQ. ID NO:73

1 GTNNNNNNNN TTGATTNCCA TTGGAGCTCC AAAGCAGTGG TAACAACGCA GAGTACGCCC CCTATGTATT
71 TTTTCCTATT CTGGACACGC TACTCCTGAC CGGGATGGCC TATGACCGGG TTGNGGCTGG CTGCCACCCT
141 CTGNANTATA TGATCATCAT GAACCCCCAC CTNTGTGGCC TCCNGGTTTT TGNCACCTGG CTCATTGGTG
211 TNATGACATN CCTCCTCCAT ATTTCTCTGA TGATGCATCT AATCTTCTGT AAAGANTTTG AAANTNCACA
281 TTTTTTTNTG CGAACTGACG TACATNCTCC AGCTGGCCTG CTCTGATACC TTCCTGAACA GCACGTTGAT
351 ATACTTTTATG ACGGGTGTGC TGGGCGTTTT TCCCTCCTTG GGATCATTTT CTTCTTATTC ACGAATTGNT
421 TTNATCCATA AGGAAGAATG TCCTCATNTG GGGGAAAACA AATAAGCACT TTNACACCTG TGGGNTCAA
491 CCTCTCCCGN CGTTTCTTTA TTTTATGGGG ACAGGCATTT GGGGTCCCAC TTTACTTTTT GNGGNGACTC
561 ACCCCTTCCA GAAAANTTTC CGTGGGCNTC NGGGATGTAC ACTGGNGGCA CCCCATGTT GAACCCTTTT

FIGURE 2

SEQ. ID NO: 111

ggtcccntcg	ngtatncntt	naccctctga	tgctgctcga	gcggccggca	gggtgatgga	60
tatctgcaga	attcgccctt	ctgttacgca	ggaatatata	aaggggttac	tgaggaataa	120
ataaatgggt	tactgaggaa	taaataaatg	ggttactgag	gaacaaatac	ataggggttg	180
aagaactgta	aaatagaaaa	aggacctnt	gctgctcctc	aggatggcgg	nacttagggg	240
ccatgtacat	gacgatgnng	ctgccnntna	agagtccac	tntcancng	cctcagcccg	300
nccttttnt	cacnnncnt	ntttntctnc	cctctnnnc	tctttntctc	ctattcccc	360
ccctccnct	cctccctttt	gcntnaccat	tgncctnat	ccctttaatt	cnntcnntcn	420
tctccctct	attccttcnn	tnttcgnctt	cantctctnc	ctctttctcc	cccctttct	480
ctctctnct	cttctctng	tcatcctngt	tcntctctt	ncctantcc	ctctancctt	540
ntcttatnc	tcctctatnc	cctctcatct	cactctctnt	cctctctnt	tactttnctc	600
nnctctccn	ctccgtctnc	cnccttctct	tcntnagcc	acccctcnnn	cntnctctct	660
ntctctctt	cactctctcc	tctccctncn	cntcactntt	ctcncctct	acntcctatn	720
ctcncnttct	nncttnactt	tgtcacgctc	tcctctctct	ctctacgcac	nttttatctc	780
ttatctcncn	catcncctc	nnctctncac	ncattnact	ctttctctnc	atactntatn	840
ctcctntcnn	cttanatcnc	ctccctctcn	tnancnntc	actgcn		886

SEQ ID NO: 112

gctgctcgag	cgncgcagcg	tcggcagtgt	nagggnnatn	tgccnnntn	gcnnntagat	60
nanaggnntn	agtatggggg	tgaccacagt	ggtacataac	tgaggctgtt	gcacttgagt	120
gtgagttgag	gggtggcagca	gaactaaggt	acacccttag	gattgcacca	taaaataagg	180
agacaactga	gaggtgagat	gcacaggtgg	aaaatgcctt	gtacttcccc	tgagctgatg	240
agattgcatg	tatggaagaa	attatcttag	agtaagagta	aaggatccca	gtcaggggac	300
ctccacccag	cagcgcaact	gtaaaatata	tcaccatgtg	attaagaaaag	ctatcagaac	360
aagcaagttg	gatgacctga	ttaagttcac	agaaaaagtg	ggggatttct	aaggctgtgc	420
agaaggacag	ccgtactacc	attaagattt	gtagcaagga	atacagagca	ctnatgggtcc	480
aggatgccag	aaccagcagt	cacagagggg	gnnggtttca	tantgncct	gtagngtcag	540
cnnngacna	gatggccnca	aaccgntctt	nggccctcac	gnccctggna	ggnggttttc	600
tantccacca	cnnntnttct	nannc				625

SEQ ID NO: 113

catgcnnag	caggctcgag	cgccggcagn	gtgagggata	tctgcagaat	tcgcccttcc	60
tatgtacttt	ttcctgagcg	tatacacaat	cccatcatgt	actggggaga	agncagacca	120
tatcattnac	aagctgnctt	tngcagatgn	actttgnttt	ctcattaggc	tgcnacagagt	180
acttctctct	ggcagccatg	gcttatgacc	gctgtcttgc	catctgctat	cctttacact	240
acggagccat	catgagtagc	ctgctctcag	cgcagctggc	cctgggctcc	tggtgngtg	300
gtttcgcgcn	cantgcagcg	cccacagccc	tcagnagcgg	tcttgctctt	ctgngncccc	360
cgtgccatta	accactnctt	tngcngcant	gcncctgca	ttgtcttgtc	ctgcccacca	420
nacagcagna	nancntgnn	cnnttngatc	gctgntncgc	tctcngntct	cactccnttc	480
cacctttnc	ntcgcattcc	nnntccnnc	tcgncctct	gnccnntcnn	tctcctcttc	540
tnaacgcgtc	ctccgannng	nctnnatgnt	cgtctctntn	ntgngcnng	ncagcnnnnn	600
nnccannnn	tnngtgcgcc	gctcc				625

SEQ ID NO: 114

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agaattcgcc	cttggtccgc	aaacaataga	tgaaaggatt	aagtgaagga	gtgccaccg	120
catagaagag	accaaagaac	ttgcccctcc	cttgggcata	cggatttttg	ggctggaggt	180
agacagcnat	gactgagctg	tagaagaggg	tgaccacagt	gagatgggag	gagcaggtcc	240
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cataagaggc	aaggatgagg	ctgagaggca	caaccacgaa	gatgacactg	gacacagcca	360
actggatttc	attgnaggag	gcatctccac	aggagagtn	gnatcagaga	tgggancctc	420
acataaaaaa	gtcatctatc	tgntggtggg	gacagaatgn	ccatgtggag	gntnnatgtn	480

cgntntennac	ctcttattttt	tnttnccctt	ttctttcgt	cnntccctt	tntccennct	540
cgccanttc	atncnctct	ntcnntttt	ttntntnacc	ntntntcat	ntctctctt	600
tattctctt	ctcttgntc	tcccttctct	ctctnttcc	canctctccc	g	651

SEQ ID NO: 115

ggntctcgg	acaanacttg	gccctctaga	tgcattgctg	agcgcccgcc	agtgtgatgg	60
atatctgcag	aattcgccct	tccaatgtat	ttattcctgt	tatttgagaga	cctggagagc	120
ttctctcctg	tggccatggc	ctatgaccgc	tatgtggcca	tctgttccc	cctgcactac	180
accgccatca	tgagcccat	gctctgtctc	gccctgggtg	cgctgacctg	gggtgctgacc	240
accttccatg	ccatgttaca	cactttactc	atggccagnt	tgtgcttntg	tncennacna	300
ttgttgntnc	cccactnnnc	tntgtntnta	gtctnctctn	ccntnnactg	ctctctctct	360
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atcctttctt	tantntcca	tntnttca	nattntctct	tatecncnt	ntcncctcc	480
anctctnctn	tagcttactn	ttctntgctc	tcnngngctc	ancctttctn	ccatatnttc	540
ttctctcncn	tntctctcnc	tnnncccn	nnntctctgc	ntctctgctc	ctctctnacc	600
tctntnncnt	tatttantnt	ctcncnctn	tctcngctc	cancgngta	ccngccctat	660
nnctctctcc	gannntgntc	atggcatctn	cacattnngc	cctactatnn	ncgatctatn	720
ttcncgncat	ntattncaca	tccacntgca	ctcctactcn	ctctctancc	ncgtagacac	780
gennctacng	ntgncnntcn	nccgctctn	cgcccnctat	nnctccactt	tntctnggtc	840
cccctctccg						850

SEQ ID NO: 116

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ctttttcctg	aagaacctct	ctgttttgga	tctgtgctac	atctcagtc	ctgtgcctaa	120
atccatccgt	aactccctga	ctcgcagaag	ctccatctct	tatcttggt	gtgtggctca	180
agcctatttt	ttctctgctt	ttgcatctgc	tgagctggcc	ttccttactg	tcattgttta	240
tgaccgctat	gttgccattt	gccacccctt	ccaatacaga	gccgtgatga	catcaggagg	300
gtgcatccag	atggcagtc	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tcttccgtga	420
catccctcag	gtgttgcccc	tggtttcctg	ngaggttttc	ttttagagag	tttgaccng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anatcttctn	aanggggctc	nagaatccct	tnaggaccag	antcnagcta	aaagcctttn	600
cccnctgct	ccccccacg					620

SEQ ID NO: 117

tggcncctng	atgcatgctc	gagcgcccg	cagtgtgatg	gatatctgca	gaattcgccc	60
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cctatgaccg	ctatgtggcc	atctgcttcc	ccctgcaacta	caccgccatc	atgagcccca	180
tgtctgtct	cgccctgggtg	gcgtgtcct	gggtgctgac	cacctccac	gccatgttac	240
acactttact	catggccagg	ttgtgtttt	gtgcagacaa	tgtgatcccc	cactttttct	300
gtgatatgct	tgtctgctg	aagctggcct	tctctgacac	tcgagttaat	gaatgggtga	360
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aagaattgtc	tcctccatcc	tcaaggctcc	ttcttctaag	ggtatctgca	aggccttctc	480
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tacttatgct	ctncagctaa	tagttctact	ctaaaggaca	ctgcatggct	atgatgtaca	600
ctgtggtgac	ccccatgctg	aacctctt				628

SEQ ID NO: 118

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gactggcca	tctactggg	gagaagacag	accatatcat	ttacaagctg	ccttttgag	180
atgnacnntg	ttttctcant	angcentaca	gnngnncatgt	ttncgcnngc	cntgacttat	240
gacgcgcntn	cnnnntatc	nnntntnct	ntnacnncac	ttctcatna	tntgnnctn	300

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nnttcnccn tggennctn nntcneggnc ttncctntgn ncgtcntnc ccttnggcct 360
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tccctccct ctctgnntgc nntcnennn catctnnntg ntctgatcnc tntctnnnt 480
ccatcnngtn ctnttctct gntctctctn cncgcncct gcatcactgn gcattatatn 540
cncngtctca tnnctatctt ccgtncctgt cnccttctct ctatgcncga cgtcntntnn 600
tactatctgc ntctcnntat tnnngcctgt tccnnngcnc ccgnncntcc anntactctc 660
cangntctnc ctntccctnt ncnctgtcta attcnctnt accgcntctn gntctntcct 720
cgtcnntccc nnttctctcc nctcnegnnn centtcagct ntcnanttct antnngnnn 780
cnc 783

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SEQ ID NO: 119

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gcccaagtta ctgtttagtt tttgggtctgc gaacaacagc atctctttca cactctgtat 180
gatacaactg tacttcttca ttgctcncat gngcacagaa tgcgtgcttc tggccgccat 240
ggcctatgac cgntatgtgg ncatctggcg cccactccac taccacaacca taantgagcc 300
atgggctcct gctcnnccct cgtntnnna tanngaaccn acagngtagc gncantccc 360
tgtncgagaa tctacttcat cntnctgcct tanntntgt gggcccaatg tgcntaanca 420
cttngntctg nggacatttn ctccagnant tnaantctct tntctcnaca aganactgtt 480
cnttancttg annatnttn ggnacattnt tcttanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngtgc tantcngtgc cattcntgtg nctnccntt 600
tcatngcntn ncctccncg aaagcnaant aagtngngt cttnactttc gccccccacn 660
ncatcnant ggcc 674

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SEQ ID NO: 120

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cctatgaccg ctatgtggcc atctgcttcc ccctgacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggtg gcgctgtcct ggggtgctgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagacaa tgtgatcccc cacttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tngagggtc cattctgtc atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcct cctcaaaggc cccttcttct aanggtatc tgcaaggcct 480
tctctacttg gtggtcccc ccctgntgt ggtgtcactg ttctatttg aaaccgntat 540
tgggactcta ctatgtctc tcangctaag agttttactc ttangggaca ctgncaatgg 600
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SEQ ID NO: 121

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cctatgaccg ctatgtggcc atctgcttcc ccctgacta caccgccatc atgagcccca 180
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aagaattgnc tcttccatc tcaaggncct ttnttctaaa gggatatctgc aaggccttct 480
ctanttggtg ctcccacct gtcttggtgn tggcactgnt tctaattgga accggaatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
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SEQ ID NO: 122


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SEQ ID NO: 123

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aacccttnt 610

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SEQ ID NO: 124

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SEQ ID NO: 125

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caagaattgt ctctccatc ctcaaggctc cttcttctaa gggatatctg aaggccttct 480
ctacttngg ctcccactg tcttngngg cactgttcta tgggaaccgg tattggctct 540
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acactgtggt gaccccnat gctgacccat tc 632

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SEQ ID NO: 126

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SEQ ID NO: 127

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cntctnacc	gnnagtcgnt	tncttatctn	tgantnccc	tngggcgncn	ncctgncct	420
cagcnttngt	cancnttctc	cncacnnntt	cgctcgtgtt	ncctcagtnct	gtncctcnc	480
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gccagcncn	nangntccnc	ccctctccct	cntgtctnct	cncctcctnt	cttctntctc	600
tnnctcatnn	nnncgncnc	ncgtctctcn	ccctntctn	tacgactcnc	gncgtctctn	660
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SEQ ID NO: 128

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agtttttttt	ctttgtcggc	atgggtctgt	ctgagtgcct	cctcctgact	gctatggcat	240
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SEQ ID NO: 129

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catctccagc	ccccttctcn	acccactat	catgacccag	ggcctctgta	cacgcatgga	300
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SEQ ID NO: 130

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SEQ ID NO: 131

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SEQ ID NO: 132

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 ggactcccca cttntgcctc ccnn 624

SEQ ID NO: 133

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 tngntgntnt ncnnnattnn ccnntctttn tccntcann tatcattntc attccttncn 540
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SEQ ID NO: 134

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tgatctctct tgcctttccc cacacactgc aacctctgcc tccacattca agtgattctc 180
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tgntatccgc tcacaaatc cacacaacat acgagccnga agcaataagn nntaaagcct 600
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SEQ ID NO: 135

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cagcagtgcc caaagcaccg gccatcctac tggggagaag tcagaccata tcatattaca 180
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cacttcttct gtgacattgc accctggant gccctggcct gcaccaacac cacaggcagn 480
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SEQ ID NO: 136

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SEQ ID NO: 137

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SEQ ID NO: 138

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670

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SEQ ID NO: 139

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635

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SEQ ID NO: 140

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709

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SEQ ID NO: 141

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nntcnntnc	g					671

SEQ ID NO: 142

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SEQ ID NO: 143

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SEQ ID NO: 144

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SEQ ID NO: 145

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SEQ ID NO: 146

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SEQ ID NO: 147

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tacctggcaa tctgccgacc actccgctat gagacctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttctctggg tctttgccc cactgtctc 240
atggccagcc tgcttttctg tggccccaat ggtattgacc acttcttctg tgacagttgg 300
cccttgctca ggctttcttg tggggacacc cacctgtga aactggnggc ttcatgctc 360
tctagttgg tgttactggg ctactggct ctgacctcag nttctange ctgcattctt 420
gtcactgtct caggncctt nnagntgctg ngcgaaggaa agcgcnttct acttgcgcct 480
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ccttcttctg aacctncc 618

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SEQ ID NO: 148

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cntagatgca ngctcgagcg ggcgccagcg tgnngnanat ctgcagaatt cgcccttcca 60
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ttntngat gccngntcn tataaaaanc annctggcg ggtcacagt cttngnata 480
gcattngtc nccttnatnn catennattt gcctngngt ccctcgttcc cantntncan 540
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SEQ ID NO: 149

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ttctgctgct cctcaggatg gcgggactta ggggccatgt acatgacgat ggcgctgcca 180
aagaagagtc ccactacgca gaggtgggag gagcaggtgg agaaggcctt tctgcggccc 240
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cagagtgggc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360
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acgaggccca canaaagggc agtccttagga tgaggntcac atggaccata gccaggaggg 480
agccacattg tcccaggaag ngntgnccag agtgatgcag acttttcagg tcntgatgat 540
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SEQ ID NO: 150

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gccactgcc aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggtcttt 600
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SEQ ID NO: 151

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gcacactggc ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180
agtattctaa cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttctctgtg 240
tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300
gcctgggggtg cctaatagagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
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SEQ ID NO: 152

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ctcgagcggc gcagtgtgat ggatatctgc agaattcgcc ctctctatgt attatttctc 60
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gaccttctgt ctgaaagana gaccatctcc ttcaatcatt gctccactca gatgtttcta 180
ttccacctta ttggaggggc ggntgtatnt nnnccntgtt ncccnatgag cctncttttc 240
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gnaatacgtc ntctccgnc nctgtctgct catccttgc gttncgntn canctcatcg 360
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SEQUENCE LISTING

<110> DigiScents; Yeda Research
 Bellenson, Joel; Smith, Dexter; Lancet, Doron; Glusman, Gustavo;
 Fuchs, Tania; Yanai, Itai

<120> OLFACTOR/ RECEPTOR SEQUENCES

<130> 422852000200

<140> 06/158,615

<141> 1999-10-08

<160> 2747

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 613

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 8, 11, 17, 28-29, 34, 40, 48, 67, 71, 613

<223> N can be any nucleotide

<400> 1

ggnttatncc	ncgttgnact	gcaggggnnc	aacncacagn	acgcccngtg	ctgaggctat	60
aaatgancgg	nttaaggaga	ggagtgaaga	cagtaaaaaa	acacagagat	aaatttatca	120
attgggaagc	tttcaaaggg	ccaaataagg	atgaatatta	atggggccaaa	gaagagaagc	180
acaacagtaa	tgtgggcaga	cagagtggga	agggccttgg	acatcccatc	agaggcttgg	240
cgatgcacag	tagcaaggat	gatagtgtca	gaaatgagca	aaaggaggaa	acacataagt	300
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ggcagattga	ctttgaatgc	caggtgggtg	gctgagtgtg	agatgccaat	ggcccaggaa	480
acccccacca	gaacagttca	caccctccgg	ttcatgatgg	ttatgtagtg	cagaggtttg	540
catatagcaa	tgtatctatc	ataggccatg	gcaacaagaa	gcaccatctc	actacccccca	600
aaaacatgca	agn					613

<210> 2

<211> 578

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 4, 6, 8

<223> N can be any nucleotide

<400> 2

ggntntnnc	acggactcca	agcagtggta	acaacgcaga	gtacgcccgt	tcctgagtga	60
gtagatgaag	gggttcagca	tgggattgat	gacagtgttg	aaaattccaa	cagctttatc	120
cttgtctgaa	agcttggttg	aaccagtcg	catatagtta	aagatacctg	aaccatagaa	180
tatggcaacc	acagtgaggt	gggagccaca	tgtggagaag	gctttcttcc	tgccctctac	240
agagcgaatt	cgcaggactg	cagctgccac	gtggatatag	gagatgacaa	tgagagccat	300
gggggtacct	gccattataa	aaccacagc	aaaaagcagc	agctcattga	gttgggtgct	360
ggagcaggag	agctggaaga	gctgtgggag	gtcacagtag	aagtgattga	tcacattggg	420
ggcacagaag	ttgagcgtgg	acatggccac	agtgtgggtc	agtgcgttgg	tgaaagcaca	480
agcccaggag	gcagccacca	acatcctctg	gactgtctga	ctcatgcggg	tgctttaggg	540
tgagggggccc	ggcagatggg	caggaatcgg	tcataggg			578

<210> 3
 <211> 588
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 4, 5, 13, 16, 27, 576, 578, 588
 <223> N can be any nucleotide

<400> 3
 tgggnntttta tcncnnttgg agctccnaag cagtggtaac aacgcagagt acgcccgttg 60
 cgaagcgtgt agattagggg gttcagtagg ggagtgatga cagtgtaggt caccgagatc 120
 agctgggtcat gttctctggg gttctctgac ttgggcttga ggtaggcaat ggaggcacag 180
 ctgtagtgga caatgaccac agtgagggtg gatgcacagg tggcaaaagc cttcttccgg 240
 ccctcaactg aagtaatctt gaggattgta gagataatga gaacataaga aatgaaaacc 300
 agacccatag gtacaacaag caccagcaca ctgataatca aagtcaggat ttcattgaca 360
 gtgggtgtcaa tgcaggagag cttcatcaca gggcggtatg cacagaagaa gtggggcacc 420
 ttttctagca cagaagggtg acctgaatac agatgtcact tgcgttattg ctacaatcag 480
 cccaatgctg caaggccccc aggacaagtt ggatacgag cctcttggtc ataataacca 540
 tgtatctcaa gggggttgca agatggccac atagcngntc atattccn 588

<210> 4
 <211> 583
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3, 7, 13, 437, 485, 488, 506, 521, 524, 545, 558
 <223> N can be any nucleotide

<400> 4
 gtngttntta acnccattgg agctccaaag cagtggtaac aacgcagagt acgcccccaa 60
 tgtatntttt tttgagaaac ttgtctttct tagatntttg ttacatctct gtcacaattc 120
 caaaatctat tgtagtttcc ttgactcatg atacttccat ttctttcttt ggggtgtgctc 180
 tgcaagcctt ctttttcatg gacttggcaa ctacggaggt agccatcctt acagtgtatg 240
 cctgtgaccg ctatatggcc atctgccggc ctttacatta tgagggtcatc ataaaccaag 300
 gtgtctgtct gaggatgatg gccatgtcgt ggctcagtg ggtgatctgt ggattcatgc 360
 atgtgatagc aacattctca ttaccattct gtgggcgcaa tagaatacgt caatttttct 420
 gtaatatctc acaactncta agcctcttag accccaaagt aattaccatt gagattggag 480
 tcatngntt ttggtacaag tcttngnata atcctcttgg ntgnaattac tctctcctac 540
 atgtncattt ttttttgnca tcatgaggga ttcttcttaa agg 583

<210> 5
 <211> 584
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2, 5, 8-9, 11, 14, 17, 550, 557-559, 561, 576, 582
 <223> N can be any nucleotide

<400> 5
 gnggnttntt nccnccnttg gactccaaag cagtggtaac aacgcagagt acgcccgtgt 60
 gtaaatgaat gggttcaaca tgggagtcac aacagtgtag gacaatgata gcagcttcgt 120
 gccctcaggt gaattatttg atttaggccg gaagtaggtg aggcttaatg atatataaga 180
 aagagagaca acaaggaggt gtgaggaaca tgtagaaaag gctttattct tcccttttagc 240
 tgatgggatc ttgaggatgg cagcagcaat gcgagtatag gaacacaaga tcagcaagca 300

ggggatcatg	accaccagaa	tggttccgac	gatggcgtag	atctcaaaca	gtgctgtgtc	360
tgcacagacc	agcctcagca	caggtgggct	gtcacagaag	aagtgggtca	ccttggttgg	420
gccacagaat	ggaaaactga	agagccatgt	ggtctgcaca	gtagctacag	gaaagcctgg	480
gaaccaggag	gcagcagcca	gtttggcacg	agtcttttgg	ttcatgatga	ctgggtagtg	540
caagggactn	gcagatnnnc	ncattcggtc	atatgncatg	gnag		584

<210> 6
 <211> 572
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2
 <223> N can be any nucleotide

<400> 6						
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gaaaggggtc	agggtcgggg	gcacgactgt	gtagaacgca	gacaggaaaa	catccagaac	120
ggggggagaa	tttgaaattg	gcttcacata	ggcaatgctg	ccagatatca	taaagagtgt	180
tacaaccaca	agatgtggaa	tgcaggtaga	aaatgttttt	gatctaccct	ccttagaagg	240
aatcctcatg	atgacagaaa	aaatgtacat	gtaggagaga	gtaattacaa	caaaggagat	300
tatcacaaga	cttgtaccaa	aaaccatgac	tccaatctca	atggtaatta	ctttggggtc	360
taagaggctt	aggagtttgt	ggaatattac	agaaaaattg	acgtattcta	ttgcgcccac	420
agaatggtaa	tgagaatgtt	gctatcacat	gcatgaatcc	acagatcacc	ccactgagcc	480
acgacatggc	catcatcctc	agacagacac	cttggtttat	gatgacctca	taatgtaaag	540
gccggcagga	tggccatata	gcggtcatag	ga			572

<210> 7
 <211> 549
 <212> DNA
 <213> Homo Sapien

<400> 7						
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gtttgacatg	ggttttctct	cagtgaactg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggcccagctc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttctctgg	180
gagcattgag	tgcttcttgt	ttacggtgat	ggcctatgac	cgcttcactg	ccatctgtta	240
tcctctgcca	tacacagtca	tcatgaaccc	aaggatctgt	gtggccctgg	ctgtggggac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtgggtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggg	gagcttcacc	aacgttggcc	tcatatctct	480
ggctgctttc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

<210> 8
 <211> 548
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 537, 542
 <223> N can be any nucleotide

<400> 8						
ggaacaacgc	agagtgcgcc	ccgatgtact	tgttcttctc	caacctgtcc	tttgctgaca	60
tttgtgttac	ttccaccacc	attccaaaaa	tgtgatgaa	catccagaca	cagaacaaag	120
tcatcaccta	catagcctgc	ctcatgcaga	tgtatttttt	catactcttt	gctggatttg	180
aaaacttcct	cctgtccgtg	atggcctatg	accggtttgt	ggccatctgt	caccccttgc	240
actacatggt	cattatgaac	cctcacctct	gtggactgct	ggttctggca	tcctggacca	300

tgagtgtctt	gtattccttg	ctacaaatct	taatggtagt	acgactgtcc	ttctgcacag	360
ccttagaaat	cccccacttt	ttctgtgaac	ttaatcaggt	catccaactt	gcttgttctg	420
atagctttct	taatcacatg	gtgatataatt	ttacagtttg	cgctgctggg	tggagggtccc	480
tgactgggat	cctttacttc	ttactctaag	ataatttctt	catacatgca	atctcancaa	540
gntcaggg						548

<210> 9
 <211> 583
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 8, 13, 14, 16, 25, 232, 271, 305, 438, 488, 497, 500, 505, 512, 524, 544, 558, 578
 <223> N can be any nucleotide

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aggctataaaa	tgaaggggtt	gagtgagggg	gtcaccactc	catagaagag	ggccatgaac	120
ttgggttgat	cccttgagat	ggaggagggg	ggctgaaggt	acatgctgat	ggctgggcca	180
taaaataaga	aaactacaat	aagatgggag	gagcatgtcc	caaaggcctt	tntccttccc	240
ttggaagatt	tgatcttaaa	tacagcactt	ncaatactag	cataggaagc	aagaattaag	300
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ttgagaccac	acagtggnaa	tttgtattgt	ggcagtggcc	ctctgagaac	ggcatagatt	480
ataccaantt	aaccacnacn	gcggnaacta	angattcaga	cgcnctggat	tcatgatgag	540
ggtntagtga	agaggttntc	agaatggcca	cataccgntc	aaa		583

<210> 10
 <211> 569
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 7, 28, 174, 232, 237, 314, 341, 445, 447, 449, 470, 494, 497, 503, 510, 515, 527, 553, 554, 569
 <223> N can be any nucleotide

gctgctncca	gcagtggtaa	caacgcanag	tacgccccca	atgtatttgt	tcttcggcca	60
tctgtctctc	ctggatgtct	gcttcatcac	cactaccatc	ccacagatgt	tgatccacct	120
cgtgggtcagg	gaccacattg	tctcctttgt	atgttgcatt	accagatgt	actntgtctt	180
ctgtgtttgt	gtggccgaga	gcacccctct	ggctttcatg	gcctatgacc	gntatgntgc	240
tatctgctac	ccacttaact	atgtcccgat	cataagccat	aaggtctgtg	tcaggcttgt	300
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tcgtggtaat	tctnagnccc	atnggtgctn	actgntactt	acctatntgc	acattcctgt	540
ccaccatcct	agnnaaagtc	ctccttctn				569

<210> 11
 <211> 582
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-4, 12, 14, 504, 513, 522
 <223> N can be any nucleotide

<400> 11

ggnntttttac	cncnattgga	gtcccaaage	agtggtaaca	acgcagagta	cgccccctat	60
gtacttggtc	ttgagaaact	tgtcttttctt	agatttttgt	tacatctccg	tcacaattcc	120
aaaatctatt	gttagttcct	tgactcatga	tacttcatt	tctttctttg	ggtgtgctct	180
gcaagccttc	tttttcatgg	acttggcaac	tacggaggta	gccatcctta	cagtgatgtc	240
ctatgaccgc	tatatggcca	tctgccggcc	tttacattat	gaggtcatca	taagccaagg	300
tgtctgtctg	aggatgatgg	ccatgtcgtg	gctcagtggtg	gtgatctgtg	gattcatgca	360
tgtgatagca	acattctcat	taccattctg	tgggcgcaat	agaatacgtc	aatttttctg	420
taatattcca	cagctcctaa	gcctcttaga	ccccaaagta	attaccattg	agattggagt	480
catgggtttt	ggtacaaggc	ttngnataat	ctnctttggt	gnaattactc	tctcctacat	540
gtacattttt	tctgcatcat	gaggattcct	tctaaggagg	gg		582

<210> 12

<211> 579

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 384, 528, 572, 578

<223> N can be any nucleotide

<400> 12

ggnntttgacc	acggagctcc	aagcagtggt	aacaacgcag	agtacgccct	cttgtcctcg	60
tgccgataca	tgatgggggt	caacatggga	gtcataacag	ttaggacaa	tgatagcagc	120
ttcttgccct	caggtgaatt	atttgattta	ggccggaagt	aggtgaggct	taatgatata	180
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ttagctgatg	ggatccttgag	gatggcagca	gcaatgtgag	tataggaaca	caagatcagc	300
aagcagggga	tcatgaccac	cagaatgggt	ccgacgatgg	cgtagatctc	aaagagtgtc	360
gtgtctgcac	agaccagcct	cagnacaggt	gggctgtcac	agaagaagtg	gttcaccttg	420
ttggtgccac	agaatggaaa	actgaagagc	catgtgggtc	gcacagtagc	tacaggaaag	480
cctgggaacc	aggaggtagc	agccagtttg	cacgagtcct	tttgggttnat	gaatgactgg	540
ggtagtgcaa	gggactgcag	atggccacat	ancggtcnt			579

<210> 13

<211> 577

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 7-10

<223> N can be any nucleotide

<400> 13

ggnntttnnn	ccactggagc	tccaaagcag	tggttaacaac	gcagagtacg	cccccaatgt	60
atttattctt	gtcacacctt	ccttagttga	tatctgtttt	accaccagta	ttgtccccca	120
gctgctgtgg	aacctaaaag	gacctgacaa	aacaatcaca	ttcctgggtt	gtgtcatcca	180
gctctacatc	tccctggcat	tgggctccac	tgagtgtgtc	ctcctggctg	taatggcttt	240
tgatcgctat	gctgcagttt	gcaaacctct	ccactatacc	gccgtaatga	acctcagct	300
gtgccaggct	ctggcagggg	ttgcgtgggt	gagtggagtg	ggaaacactc	ttatccaggg	360
cactgtcacc	ctctggcttc	ctcgtctgtg	acaccgattg	cactaacatt	tcttcgtgag	420
gtaccctcca	tgattaagct	tgcattgtgt	gacatccatg	ataatgaggt	tcagctcttt	480
gttgcttcac	tggtcttggc	cctcttgccc	ttagtgctaa	tactgctgcc	tatggacata	540
tagccaaggt	ggcataagga	tcaagtcagt	ccagcct			577

<210> 14

<211> 577

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3-4, 6, 8, 252, 375, 474, 506, 515, 532, 541, 545-546, 556, 562, 573

<223> N can be any nucleotide

<400> 14

ggmntntnac	tccatggact	ccaagcagtg	gtaacaacgc	agagtacgcc	catacatgat	60
gggggttcagt	aggggagtg	tgacagtgt	ggtcaccgag	atcagctggg	catgttctct	120
ggtgttctct	gacttgggct	tgaggtaggc	aatggaggca	cagctgtagt	ggacaatgac	180
cacagtgagg	tgggatgcac	aggtggcaaa	agccttcttc	cggccctcaa	ctgaagcaat	240
cttgaggatt	gnagagataa	tgagaacata	agaaatgaaa	accagaccca	taggtacaac	300
aagcaccagc	acactgataa	tcaaagtcag	gatttcattg	acagtgggtg	caatgcagga	360
gagcttcatc	acagngcgga	tgtcacagaa	gaagtggggc	acctttctag	cacagaaggg	420
taacctgaat	acagatgtca	cttgcggttat	tgctacaatc	agcccaatgc	tgcnnggccc	480
caggacaagt	tggatacgca	gccttntcgt	tctantaacc	atgtatctca	angggcttgc	540
ngatnnccac	atactngcat	anaccattgc	tgngagc			577

<210> 15

<211> 583

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 5, 7, 13, 427, 485, 488, 532, 559, 569, 574, 583

<223> N can be any nucleotide

<400> 15

gncgntntta	acnccattgg	agctccaaag	cagtggtaac	aacgcagagt	acgcccatta	60
cgaaaagtgt	agatgaaggg	gttcaagagg	ggtgtgatga	tgcagctcag	gacggaggca	120
cctttgttga	gcagtttgga	ctgagcctct	gacatacgaa	tgtagagaaa	gatggaactg	180
ccatagatga	tgaccaccac	tgtaagatgc	gaggcgcaag	tggaaaacgc	tttccttcgc	240
tcagcagctg	taggggccc	gagaacagtg	gcaagaatgc	aggcatagga	aactgagggtc	300
agagccagtg	agcccagtaa	caccaacgta	gagagcatga	aagccaccag	tttcagcagg	360
tgggtgtccc	cacaagaaa	cctgagcaag	ggccaactgt	cacgaaagaa	gtggtcaata	420
ccattgnggc	cacagaaagg	catggctggc	catgaggaca	gtggggcaaa	ggaccagag	480
gaatncanct	agccaggagg	ccacactagt	ttgtgaacag	acatggccat	tnattaggg	540
ctcatagcgg	agttgtcgnc	agatttgcnt	ggtnacgatt	can		583

<210> 16

<211> 577

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3-4, 12, 14, 549

<223> N can be any nucleotide

<400> 16

ggmnttttac	cncnattgga	ctccaaagca	gtggtaacaa	cgcagagtac	gccccctatg	60
tatttattct	tgctcacctc	tccttagttg	atatctgttt	taccaccagt	attgtcccc	120
agctgctgtg	gaacctaaaa	ggacctgaca	aaacaatcac	attcctgggt	tgtgtcatcc	180
agctctacat	ctccctggca	ttgggctcca	ctgagtgtgt	cctcctgggt	gtaatggctt	240
ttgatecgtg	tgctgcagtt	tgcaaacctc	tccactatac	cgccgtaatg	aaccctcagc	300
tgtgccaggc	tctggcaggg	gttgctgggc	tgagtggagt	gggaaacact	cttatccagg	360
gcaactgtcac	cctctggctt	ccccgctgtg	gacaccgatt	gctccaacat	ttcttcgtga	420
ggtaccctcc	atgattaagc	ttgcatgtgt	ggacatccat	gataatgagg	ttcagctctt	480

tggttgettcac-ctgggtcttgc tctctcttgcc cttagtgeta atactgctgc ctatggacat 540
 atagccaang tggcataaag gatcaagtca gtccagg 577

<210> 17
 <211> 621
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 8, 13, 618
 <223> N can be any nucleotide

<400> 17
 gnnnnttntt cantccattg ggccctctag atgcatgctc gagcggccgc cagtgtgatg 60
 gatatctgca gaattcgccc ttattccgga ggggtatacat gaagggtattg gtaactagac 120
 gtaaaactga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa 180
 gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag 240
 actctgaaaag aggtggaagg gattgaatac aatcaaaagt atggtgactg ctagtccaa 300
 gatggtggcg taggggcaag ctggccttgc ttacccccct ggcagaaaac caaaaacaaa 360
 tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc 420
 cagggcccg agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt 480
 tctaaggagg acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc 540
 cataaaacaa agattggaaa atggtgaatt ttgcaaccag gagcaaatac tgggaaaggc 600
 gaattccagc cacttgcnegc c 621

<210> 18
 <211> 615
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 8, 10, 14, 21, 583
 <223> N can be any nucleotide

<400> 18
 gnnnnttnan tcantgccct ngggccctct agatgcatgc tcgagcggcc gccagtgtga 60
 tggatatctg cagaattcgc ccttggttgcg caagggtgtaa atgaaagggt ttgcgcagga 120
 gtaaatgaag ggattacgca ggagtaaatg aagggtattac gcaggagtaa atgaagggtat 180
 tacgcaggag taaatgaagg gattacgcag gagtaaatga agggattacg caggagtaaa 240
 tgaagggtatt acgcaggagt aatgaagggt attacgcagg agtaaatgaa gggattacgc 300
 aggagtaaat gaagggtatta cgcaggagta aatgaagggt ttacgcagga gtaaatgaag 360
 ggattacgca ggagcaaata cataggaagg gcgaattcca gcacactggc ggccgttact 420
 agtggatccg agctcggtac caagcttgat gcatagcttg agtattctaa cgcgtcacct 480
 aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattggt atccgctcac 540
 aattccacac aacatacgag cccggaagca taaagtgtaa agnctgggggt gcctaattgag 600
 tgacttactc catta 615

<210> 19
 <211> 696
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-3, 5, 7, 287, 300, 309, 313, 328, 331, 343, 345, 347, 360, 366,
 386, 388, 391, 394, 401, 407, 416, 420, 428, 432, 434, 437, 441,
 443, 448, 450, 452, 457-458, 463, 476, 484-485, 493, 503, 506, 514,
 518, 520, 524, 528, 540, 541, 548, 550, 553-554, 557, 561-562,

566-568, 571-572, 575, 582, 584-585, 587-588, 603, 607, 614, 620, 623, 627, 629, 641, 648, 652, 661-662, 665-666, 668, 672, 675, 678, 684, 695

<223> N can be any nucleotide

<400> 19

gmnantnatt	ccatccattg	tcccttcaga	tgcatgctcg	agcggccgccc	agtgtgatgg	60
atatctgcag	aattcgccct	tcttggtttt	tgtgctgata	gatcatggga	ttcagcatgg	120
gggtgaccac	agtgtacatc	actgaggctg	ttgcacttga	gtgtgagttg	cgggtggcag	180
cagaactaag	gtacaccctt	aggattgcac	cataaaataa	ggagacaact	gagaggtgag	240
atgcacagggt	ggaagatgcc	ttgtacttcc	cctgagctga	tgagatngca	tgtatgggaan	300
gaaattatnt	tanaagtaag	agtaaagnat	nccagtcagg	ggnancnttc	acccatcagn	360
tgcaanttgt	aaaaattata	ttcaancnat	ntgnatttaa	ngaaaancct	tatcangtan	420
acactgcnaa	gntntgnatt	nancctnngn	anttaanntt	tcnacaagaa	aataangtgc	480
gttnnaatct	ttntaagtcc	ctntcnccat	taangtcnan	tcntccnta	tcccttttcn	540
nattttgnan	tcnngantac	nntctnnngc	nntcnatttc	tntnntnnct	gacctactaa	600
ccnattnagt	tacnacaagn	ccnttcnant	ctctataatt	nctcgcangt	tntccctctt	660
nncanntncc	cnttntnttc	cctnttcccc	atctncc			696

<210> 20

<211> 615

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 495, 545, 582, 600

<223> N can be any nucleotide

<400> 20

ccattggccc	tctagatgca	tgctcgagcg	gccgccagtg	tgatggatat	ctgcagaatt	60
cgccttccct	atgtattttc	tcttactggg	ctttcctggg	tctcaaactc	ttcagctctc	120
tctctttatg	ctttttctgg	tgatgtacat	cctcacagtt	agtggtaatg	tggtatcttt	180
gatgttggtg	agcacctccc	atcagttgca	tacccccatg	tacttctttc	tgagcaacct	240
ctccttcctg	gagatttggt	ataccacagc	agcagtgccc	aaagcactgg	ccatcctact	300
ggagagaagt	cagaccatat	catttacaag	ctgtcttttg	cagatgtact	ttgttttctc	360
attaggctgc	acagagtact	tcctcctggc	agccatggct	tatgaccgct	gtcttgccat	420
ctgctatcct	ttacactacg	gagccatcat	gagtagcctg	ctctcagcgc	aactggcctt	480
gggcttctgg	gtggntgggt	tcgggggcaa	tgagtgccc	acaggccttc	aatcaagtgg	540
gctgntcctt	ctggtggccc	ccggtgccaa	tcaaccactt	tntttttggg	acaattgcan	600
ccctggaatt	ggccc					615

<210> 21

<211> 745

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-3, 8, 21, 23, 26, 33, 43, 116, 201, 212, 222, 239, 252, 279, 282, 288, 292-293, 308, 320, 325, 328-330, 333-334, 339-341, 344, 354, 360, 365, 372, 377, 382-383, 388, 390, 394, 397, 402, 415, 418, 422, 424-425, 427, 431, 436, 441, 445, 450, 451, 457, 466, 493, 495, 498, 501, 508-509, 513, 515, 517-518, 520-523, 525, 528-529, 535, 538, 540-542, 544-546, 548-550, 553, 555, 565, 584, 586, 592-593, 607-608, 615, 617, 619, 621, 634, 636-637, 644-645, 651, 656, 662, 671, 685, 693, 697, 699, 710, 714, 735, 737, 740, 745

<223> N can be any nucleotide

<400> 21


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gnncttantt caatcccacc nancntgcc gangcatgct cgngeggcgg ccagtgtgat      60
ggatatctgc agaattcgcc ctctctatgt atttactctt actgggcttt cctggntctc      120
aaactcttca gctctctctc tttatgcttt ttctgggtgat gtacatcctc acagttagtg      180
gtaatgtggc tatcttgatg ntgggtgagca cntcccatca gntgcatacc cccatgttnt      240
tctttctgag cnacctctcc ttcttgagga tttggatatnc cncaagcngc anngcccaaa      300
gctttgcncn tcttattgcn cagangcnnn ccntacann nacnctctg tttntcgctn      360
ccttnctctt tntctnctc anntactnctn tctnctntag tntctttctt ctctntcnct      420
cntnnncctt ntaatnttcc nectnttctn nttctntttt tccctnctct gtttcacccc      480
tacctcttat cctnctnctt nacttcannc tcngnctntn nnnncnctt aaatntangn      540
nnannntnnn atntnctctt ctccntttat atcgctctt ctctncttct cmttctctc      600
tcttcannca tatcnantnt nttctactct cgtncnntat ctannctctt ntttcngtcc      660
tntctctctt ntcatttcta tattncttct canacantnt tcgcatcgtn gcancatctc      720
ctcccctctc ctgtnctnctn ttcen                                     745

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<210> 22

<211> 614

<212> DNA

<213> Homo Sapien

<220>

<221> 2-4, 9, 19, 23, 47, 613

<222> (3)...(3)

<223> N can be any nucleotide

<400> 22

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gnnnttaant cattcccnc tcnatgcatg ctcgagcggc cgccagngtg atggatatct      60
gcagaattcg cccttgtttc ggaggcagta gatgaatggg ttgatggaat ctgagacagt      120
gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc taaataatga      180
cacaagggtac cttgccgaga gaggaatcat ccacctggaa gggtaggctg tttgtgaata      240
atgtaggggtg ggagagaagg ctttactaag gagatgggct taaagaatgt gaacgatgtg      300
ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag acaaaggaca      360
cggtggcatg agcgcatgta acacaatgta ctcaggaaat ggctggcatc ctgagatatg      420
gagtgggaata cagtacaggg ctttgtaaac tcagcttgga gtcagatcac agaaagcctt      480
gacaaggaac tgaaaatggg ttctgaaggc cagaagccca ttcaagattc ccaaagggaa      540
aaacacaaat cagcttggtt tcaggacgta attcttgga gttgctagaa ttacatcaga      600
aaggagggttc acnt                                     614

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<210> 23

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 6, 8, 12-13, 16, 507, 561, 583, 592

<223> N can be any nucleotide

<400> 23

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gnnntnante anncantggg cctctagat gcatgctcga ggggccgcca gtgtgatgga      60
tatctgcaga attcgccctt cctatgtatt tctcttact gggctttctt ggttctcaaa      120
ctcttcagct ctctctcttt atgctttttt tggatgatgta catccccaca gttagtggta      180
atgtggctat cttgatgttg gtgagcacct cccatcagtt gcatacccc atgtacttct      240
ttctgagcaa cctctccttc ctggagattt ggtataccac agcagcagtg cccaaagcac      300
tggccatcct actggggaga agtcagacca tatcatttac aagctgtctt ttgcagatgt      360
actttgttat ctcattaggc tgcacagagt acttctctct ggcagccatg gcttatgacc      420
gctgtcttgc catctgctat cctttacact acggagccat catgagtagc ctgctctcag      480
cgcagctggc cctgggctcc tgggtgnggg ggttcgtggc cattgcaagt gcccaagc      540
cctaatacgt ggccctgtcc ntctgggggc ccccgggcca ttnaccactt tnttctggga      600
caattgcacc cctggaattg g                                     621

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<210> 24

<211> 612
 <212> DNA
 <213> Hom Sapien

<220>
 <221> variation
 <222> 2-3, 8, 16, 20, 26, 557
 <223> N can be any nucleotide

<400> 24
 tnnttaantc attccnttgn ccctcnagat gcatgctcga gcggccgcca gtgtgatgga 60
 tatctgcaga attcgccctt tccttggttac tgaggaggta gattagggga ttgatggaat 120
 ctgagacagt gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc 180
 taaataatga cacaaggtag cttgccgaga gaggaatcat ccacctggaa gggtaggctg 240
 tttgtgaata atgtagggtg ggagagaagg ctttactaag gagatgggct taaagaatgt 300
 gaacgatgtg ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag 360
 acaaaggaca cggtaggata agcgcatgta acacaatgta ctcaggaaat ggctggcatc 420
 ctgagatatg gaggtagaata cagtacaggg ctttgtaaac tcagcttgga gtcagatcac 480
 agaaagcctt gacaaggaaac tgaaaatggg ttctgaaggc cagaagccat tcaagattcc 540
 caaagggaaa aacacanatc acttgttttc aggacgtatt cttgggcagt tgctagaatt 600
 acatcagaaa gg 612

<210> 25
 <211> 632
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 9, 614
 <223> N can be any nucleotide

<400> 25
 gnnnnttant ccatgccctt ctagatgcat gctcgagcgg ccgccagtgt gatggatattc 60
 tgcagaattc gcccttggtt cgcagcctat aaatgaaggg gttgatggaa tctgagacag 120
 tgctctagaa tctgtgtttc atacaggatg agatataaat gaaacaaatg ctaaataatg 180
 acacaaggta ccttgccgag agaggaatca tccacctgga agggtaggct gtttgtgaat 240
 aatgtagggt gggagagagg gctttactaa ggagatgggc ttaaagaatg tgaacgatgt 300
 gctcacagag gccacagaag agaaattata gccaggagaa caacctgaaa gacaaaggac 360
 accggtggca taagcacatg taacacaatg tactcaggaa atggctggca tcctgaggta 420
 tggagtggaa tacagtaccg gggctttgta aactcagctt ggagtcagat ccagaaagcc 480
 cttgacaagg aactgaaaat tgggttcttg aaggccagaa gccattcaag gattccccaa 540
 aggggaaaaa cacaaatcaa gcttgttttc agggaccgtt aattctgggg ccaggttgct 600
 tgaattacct tcangaaagg gaggttcaca ct 632

<210> 26
 <211> 628
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-3, 419, 423, 426, 437, 439, 453, 460, 463, 469, 478, 489, 492,
 536, 539, 579, 583, 586, 594, 598, 616, 623, 627
 <223> N can be any nucleotide

<400> 26
 gnncttattc atccccctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg 60
 cagaattcgc cctttctttg ttccctcagag tgtagattag ggggttgatg gggttgatgg 120
 aatctgagac agtgctctag aatctgtgtt tcatacagga tgagatataa atgaaacaaa 180
 tgctaaataa tgacacaagg taccttgccg agagaggaat catccacctg gaagggtagg 240

ctgtttgtga ataatgtagg gtgggagaga aggcctttact aaggagatgg gcttaaagaa	300
tgtgaacgat gtgctcacag aggccacaga agagaaatta tagccaggag aacaacctga	360
aagacaaagg acacgggtggc ataagcgcat gtaacacaat gtactcagga aatggctgnc	420
atnctnagat atgyagngng aataccagta canggccttn tanactcanc ttggagtnc	480
gaatcacana angccttgca aggaactgaa aatgggttct gaaaggccag aagccttna	540
agattcccaa agggaaaaaa cacaaatcaa gcttttttna agnacngtaa ttctngngc	600
cagttgctta gaattnccat canaaang	628

<210> 27

<211> 803

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3-4, 19, 168, 190, 202, 245-246, 250, 260, 266, 280, 281, 284, 286, 289, 301, 303, 305, 313, 332-333, 348, 355, 357, 360, 365-366, 370, 372, 376, 379, 384, 387-390, 394-396, 400, 406-407, 411-412, 416-418, 421, 423, 430, 439-440, 442-443, 446, 448, 462-463, 468-469, 480, 482-483, 490, 493, 498, 506-508, 518-519, 523, 532, 534, 536, 539 547, 549, 556, 559, 573-575, 580-581, 587, 590, 595-596, 600-601, 603, 612, 614, 618, 623, 629, 633, 640, 643, 646, 655-656, 658, 666, 682, 689, 696, 704, 708-709, 718, 721, 732, 738-739, 743, 746, 751, 759, 764-765, 771, 775, 782-783, 788-789, 791-792, 795, 801

<223> N can be any nucleotide

<400> 27

ggnttaagcc ttccccctnc gatgctgctc gagcgccgc cagtgtgatg gatattctgca	60
gaattcgccc ttcccatgta ttctctctta ctgggctttc ctggttctca aactcttcag	120
ctctctctct ttatgctttt tctggtgatg tacatctca cagttagnng taatggggct	180
atcttgatgn tggtagcac cccccatcag ttgcataccc ccatgtactt cttctgagc	240
aaccnntccn tcctggagan tttgggnatac cacacgcaan nagnngccna aggcacttgg	300
ncntnctaca ggnggagaag gcttgaccat annattttac catgcctngc cttangmcan	360
accnntctn tncctntnt tcnctnnnn ggtnntcan ccgcannctt nnatcnntg	420
nancttcattn gaatatggnn tnngtntntc ttgagagcct cnngatcnaa tttttccan	480
cnctaaaagn ggngcttntc tctctnnnat ctagcttntt ggntctcttt tntntnctna	540
cccgtgntnt cctatntgnt gtctcttctt acnnctgcn nttattntan atcanntctn	600
ncnttgctct cntntacnac atnatcatnc tcnctcccn ctntcnctct ctatnncta	660
ccatcnctct cttctcattc anctcttnt cattgnttgt tcanttann actctccntc	720
ncatcttcta tncactannt ttntntttt nctctctant tctnnttcca ntgtncactc	780
cnntcttnc nnttnccta ncg	803

<210> 28

<211> 620

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 4, 7, 9, 10, 11, 24, 563

<223> N can be any nucleotide

<400> 28

gtnnttnann ncattgcccc tctngatgca tgctcgagcg gccgccagtg tgatggatat	60
ctgcagaatt cgcccttctt atgtacttcc tcttaccggg ctttctctgg tctcaaaactc	120
ttcagctctc tctctttatg ctttttctgg tgatgtacat cctcacgggt agtggtaatg	180
tggtatctt ttgttggtg agcacctccc atcagttgca taccctcatg tacttcttctc	240
tgagcaacct ctcttctctg gagatttggg ataccacagc agcagtgcc aaagcactgg	300
ccatctact ggggagaagt cagaccatat catttacaag ctgtcttttg cagatgtact	360
ttgttttctc attaggtgac acagagtact tctctctggc agccatggct tatgaccgct	420
gtcttgccat ctgctatcct ttacactacg gagccatcat gagtagcctg ctctcagcgc	480
agctggccct gggcttctgg gtgggtgggt ttcggggcca ttgcaagtgc ccacagccct	540

tatcaagtgg cctgtccttc tgnngccccc gggcccatca accacttttt tctggggaca 600
attgcaccct ggaatggccc 620

<210> 29
<211> 620
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 3-5, 7-9, 15, 567, 574, 585, 596, 606, 611-612, 616, 618-619
<223> N can be any nucleotide

<400> 29
gtnnntnnnt ccatnccatt gggccctcta gatgcatgct cgagcggccg ccagtgtgat 60
ggatatctgc agaattcgcc ctttcatggt tccggaaaca gtaaattatg gggttcagtc 120
atggtaacag gaggaggctg agtgtatggg catggatggg ggctgtgaat gtggcgggag 180
ctcatggatg tgctcttctg agtgcttcac gtttctgagt gaaataagaa gcaaggatcat 240
caccgagagg gaggagacag gctcgggtga gtttagtgga tatgaatcca agagagacca 300
ttcaacttag ttgtctatct tttttttctc cagttatagt cacttgcagc aatgtagatg 360
tgagtagact gatcataaga tccattttat ggcagaagac attatttttc tgagccttct 420
gctgtcagtt tctaaataag caggccagcc gggctgtgca cctaaatgtc tgtctgggag 480
gagcaggctg agaagtcttg cagtctgcag gacacccgag gaatcgtatt gtgggaaccg 540
tccccgagaa ccacacgagc cgtgctnctc agtntctgact ggaanaatga aattgnaagc 600
caagtngttc nnggancnnt 620

<210> 30
<211> 616
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 2-4, 7, 9-10, 580
<223> N can be any nucleotide

<400> 30
gnnnntnann ccattgcgcc ctctagatgc atgctcgagc ggccgcccagt gtgatggata 60
tctgcagaat tcgcccttcc tatgtatttc tcttcctaac gattggaatg cctgggatta 120
ggcagatgat tttctttttc ccccataccc ctctattatt taggtgattg agtttaaatc 180
cctttatcta cacccttcgg aacaagggcg aattccagca cactggcggc cgttactagt 240
ggatccgagc tcggtaccaa gcttgatgca tagcttgagt attctaacgc gtcacctaaa 300
tagcttggcg taatcatggt catagctgtt tctgtgtgga aattgttatc cgctcacaat 360
tccacacaac atacgagccg gaagcataaa gtgtaaagcc tggggtgcct aatgagttag 420
ctaactcaca ttaattgcgt tgcgctcact gcccgccttc cagtcgggaa acctgtcgtg 480
ccagctgcat taatgaatcg gccaacgcgc ggggagaggc gggttgcgta ttgggcgctc 540
ttcgcgttcc tcgctcactg actcgtctggg ctccggctcgn tcggctgcgg cgagcgggat 600
cagctcactc aaaagg 616

<210> 31
<211> 612
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 2-9, 13, 507, 554, 585, 598, 600, 609
<223> N can be any nucleotide

<400> 31
gnnnnnnnnt cangccattg ggcctctag atgcatgctc gagcggccgc cagtgtgatg 60
gatatctgca gaattcgccc ttcctatgta tttctcttca ctttctccga catcactcac 120

agccacccca	ccctcagect	ctccctcctc	ccatgtatatt	tctcttcaat	ctctccttct	180
ttgatatcct	gaacttttctg	tagtctctta	ttttctcttc	caatcccttc	atatacacgt	240
ttcgtaacaa	ggcggaattc	cagcacactg	gcggccgtta	ctagtggatc	cgagctcggt	300
accaagcttg	atgcatagct	tgagtattct	aacgcgtcac	ctaaatagct	tggcgtaatc	360
atgggtcatag	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	acaacatacg	420
agccggaagc	ataaaagtgt	aagcctgggg	tgcctaata	gtgagctaac	tcacattaat	480
tgcgtgcgt	cactggccgc	tttccangtc	gggaaacctg	tcggccagct	gcattaaatg	540
aatcggccaa	cgcncggga	gaggcggttt	gcgtattggg	cgctntttcg	ttcttcgntn	600
actgatcgnt	gg					612

<210> 32

<211> 616

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-9, 15, 521, 596

<223> N can be any nucleotide

<400> 32

gnnnnnnnnnt	tcatnccatt	gggcccctcta	gatgcatgct	cgagcggccg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttggtgctt	agagtgtaaa	taaaagggtt	aacattggct	120
tagagggtgaa	gagtaaatac	ataggaaggg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcgggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaa	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgtt	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcgggtttgcg	tattggggcg	480
tcttcgctt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggctgcg	gcgagcggta	540
tcaagctcac	tcaaaggcgg	taatacggtt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 33

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4, 6, 8, 19, 27, 31, 464, 526, 554, 578, 598, 600, 615

<223> N can be any nucleotide

<400> 33

gntntnante	atgccccnc	cgatgcntgc	ncgagcggcc	gccagtgtga	tggatatctg	60
cagaattcgc	ccttggttgcg	gagcgaatat	atgaaggggt	taagggaaga	gaaaatacat	120
aggaaggcg	aattccagca	cactggcggc	cgttactagt	ggatccgagc	tcggtaccaa	180
gcttgatgca	tagcttgagt	attctaacgc	gtcacctaaa	tagcttggcg	taatcatggt	240
catagctgtt	tcctgtgtga	aattgttatc	cgctcacaat	tccacacaac	atacgagccg	300
gaagcataaa	gtgtaaagcc	tgggggtgcct	aatgagttag	ctaactcaca	ttaattgctg	360
tgcgtcact	gcccgtttc	cagtcgggaa	acctgtcgtg	ccagctgcat	taatgaatcg	420
gccaacgcgc	cggggagagg	cggtttgcgt	attgggcgct	cttncgcttc	ctcgctcact	480
gactcgcttg	cgctcggtcc	gttcggctgc	ggcgagcggg	atcaantcac	tcaaaaggcg	540
ggaatacggg	tttncacaga	aatcaggggg	ataacgcngg	aaagaacatg	tgagccanan	600
ggcagcaaaa	gggcnaggaa	t				621

<210> 34

<211> 614

<212> DNA

<213> Homo Sapien

<220>
 <221> variation
 <222> 2-9, 13-14, 593
 <223> N can be any nucleotide

<400> 34
 gnnnnnnnnnt caaacattg ggccctctag atgcatgctc gagcgccgc cagtgtgatg 60
 gatatctgca gaattcgccc ttgttccgaa ggctatagat gaaggggttt taggttttta 120
 ggaacacagg ctaaggggga agagaaaata catgggaagg gcgaattcca gcacactggc 180
 ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg agtattctaa 240
 cgcgtcacct aaatagcttg gcgtaatcat ggctatagct gtttcctgtg tgaaattgtt 300
 atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa gcctgggggtg 360
 cctaattgagt gagctaactc acattaattg cgttgcgctc actgcccgtt ttccagtcgg 420
 gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcggggaga ggcggtttgc 480
 gtattgggag ctcttcgctt tcctcgtcga ctgactcgtt gcgctcgggt gtcgggtcgc 540
 gcgagcggta tcagctcact caaaggcggg aatacgggta tccacagaat cangggataa 600
 cgcaggaata gaca 614

<210> 35
 <211> 614
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-4, 7, 9, 23, 599, 611
 <223> N can be any nucleotide

<400> 35
 ggnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatata 60
 tgcagaattc gcccttccga tgtattttct tctacgttaa ggtattttaa attgttacta 120
 atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180
 gatgctgtta cctcacaat atgtatgtgt ggatgtatat atatctattc aatataatgta 240
 actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaacctt 300
 agtgtctcag ataagttggc tagttttttg ttccacataa aggaacaaac atttatagat 360
 ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtgggttcag cctataatac 420
 cagcactttg ggaagccgag gtgggcggat tacttgaggt aaggagccca gcctgaccaa 480
 caaggtgaaa ccccatccct actaaaaata caagaattag cccgggggat gtgggtggcca 540
 cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600
 aggttgacag ngag 614

<210> 36
 <211> 611
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 1, 3-5, 10, 18-20, 22, 26, 605
 <223> N can be any nucleotide

<400> 36
 ngnnnttgan tcaattcnnn gncgangcat gctcgagcgg ccgccagtgt gatggatata 60
 tgcagaattc gcccttccga tgtattttct tctagccaac ctcccactca ttgatctgtc 120
 tctgtcttca gtcatagccc ccaagatgat tactgacttt ttcagccagc gcaaagtcac 180
 ctctttcaag ggctgccttg ttcagatatt tctccttcac ttctttggtg ggagtggat 240
 ggtgatcctc atagccatgg gctttgacag atatatagca atatgcaaac ccctacacta 300
 cactacaatt atgtgtggca acgcatgtgt cggcattatg gctgtcgcac ggggaattgg 360
 cttttctccat tcggtgagcc agttggcctt tgccgtgcac ttacccttct gtgggtccaa 420
 tgaggtcgat agtttttatt gtgaccttcc tagggtaacc aaacttgcct gtacagatac 480
 ctacaggcta gatattatgg tcattgctaa cagtgggtgt ctcactgtgt ggtcttttgt 540

cttctaataca tctcatacac tatcatccta atgaccatcc agcattgccc tttagataag 600
tcgtncaaag g 611

<210> 37

<211> 616

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 6, 8, 12-14, 17, 19-20, 442, 595, 599

<223> N can be any nucleotide

<400> 37

gnnntnanc	cnnnccnenn	ctagatgcat	gctcgagcgg	ccgccagtgt	gatggatatac	60
tgcagaattc	gcccttccca	tgtatttgct	tctcagcaac	ttgtccttct	ctgacctctg	120
cttctcttcc	gtgaccattc	ccaagttgtt	acagaacatg	cagaaccagg	acccatccat	180
cccctatgcy	gactgcctga	cccaaagtga	cttcttccctg	ttatttggag	acctggagaa	240
cttctcctt	gtggccatgg	cctatgaccg	ctatgtggcc	atctgcttcc	ccctgcaacta	300
caccgccatc	atgagcccca	tgtctgtct	cgccctgggtg	gcgctgtcct	gggtgctgac	360
caccttccat	gccatgttac	acactttact	catggccagg	ttgtgttttt	gtgcagacaa	420
tgtgatcccc	cactttttct	gngatatgtc	tgtctgtctg	aagcaggcct	tctctgacac	480
tcgagttaat	gaatgggtga	tatttatcat	gggagggtc	attcttgtca	tcccatcct	540
actcattctt	gggtcctatg	caagaattgt	ctcctcatcc	tcaagggtccc	ttttntaang	600
gtatctgcaa	ggccct					616

<210> 38

<211> 615

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 1, 3-6, 9, 11, 14, 16, 20, 21, 23, 540, 566

<223> N can be any nucleotide

<400> 38

ngnnnnnttna	ntcnangeen	ngngccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttccaatg	tatttacttc	tcagccagct	ctcccttatg	120
gacctgatgt	acatctccac	caccgtcccc	aagatggcgt	acaacttcct	gtccggccag	180
aaaggcatct	ccttccctggg	atgtgggtgtg	caaagcttct	tcttccctgac	catggcgtgt	240
tctgaaggct	tactcctgac	ctccatggcc	tacgaccgtt	atttggccat	ctgccactct	300
ctctattatc	ctatccgcat	gagtaaaatg	atgtgtgtga	agatgattgg	aggctcttgg	360
acactggggt	ccatcaactc	cttggcacac	acagtctttg	cccttcatat	tccctactgc	420
aggtctaggg	ctattgacca	tttcttctgc	gatgtcccag	ccatgttgc	tcttgcgtga	480
cagatacttg	ggctcatgaa	tatatggttt	ttgtaaggac	aaagcctctt	tcttcttttn	540
cctttcattg	gcataccttc	ttctgngggc	cgagtcctaa	ttgctggcta	tataatgcac	600
tcaaaggagg	ggagg					615

<210> 39

<211> 615

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 4-8, 12-13, 17-18, 22-23, 26-28, 469, 591, 596

<223> N can be any nucleotide

<400> 39

tagnnnnntt	anntcanngc	cnntgnnngc	tcagatgcat	gctcgagcgg	ccgccagtgt	60
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gatggatata	tgcagaattc	gcccttccaa	tgtattttct	tctcagcagg	agagatat	120
atcctcactg	ccatgtccta	tgaccgctat	gtagccatct	gctgtccctt	gaactacgag	180
gctgcacaga	gtacttcctc	ctggcagcca	tggcttatga	ccgctgtctt	gccatctgct	240
atcctttaca	ctacggagcc	atcatgagta	gcctgtctct	agcgcagctg	gccctgggct	300
cctgggtctg	tggtttcgtg	gccattgcag	tggccacagc	cctcatcagt	ggcctgtcct	360
tctgtggccc	ccgtgccatc	aaccacttct	tctgtgacat	tgcaccctgg	attgccctgg	420
cctgcaccaa	cacacaggca	gtagagcttg	tggcctttgt	gattgctgnt	gtggttatcc	480
tgagttcatg	cctcatcacc	cttgtctcct	atgtgtacat	catcagcacc	atccttagga	540
tccctctgc	agtggccgga	gcaaagcctt	ctcccgtgct	cctcgcactt	naacnggtg	600
ctcatttggg	atggg					615

<210> 40
 <211> 586
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 14, 21, 23, 479, 498, 534, 584
 <223> N can be any nucleotide

<400> 40	
catgctcgag	cgngcggcag
gcttctcagc	aggagagata
tctgtgtccc	cctgaactac
ttggaagccc	cttctgccat
cttatgaccg	ctgccttgcc
tgctctcagc	gcagctggcc
ccacagccct	ctgccttctt
gtgacattgc	accctggatt
gcctttgtga	attgctgntg
tgtgtacatc	atcaggcacc
	attctcagga
	tcccttctgc
	aagngg
	60
	120
	180
	240
	300
	360
	420
	480
	540
	586

<210> 41
 <211> 857
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 5-12, 16-18, 22, 27, 32, 42, 60, 99, 159, 171, 202, 212, 240, 242, 251, 306, 330, 371, 568, 669, 750, 802, 840, 856
 <223> N can be any nucleotide

<400> 41	
atggnnnnnn	nnnttnnnnaa
aatgggcccc	ttgggccctt
tgggaaatgg	ggggaattta
tttttccctt	tttggttttt
tnggggggaa	nttttttaaa
ttccanggga	ccgttgggac
gattaaggaa	nggtgccggg
tgagaaccac	ggtgagatgc
cagaggggat	cctgaggatg
gcatgaactc	aggataacca
tgttgggtgc	aggccagggc
ggcacgggng	ggccacagaa
gccacgaaac	caccagaccc
ctcatgaatg	gcttccgtag
aagccatggc	ttggcng
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	660
	720
	780
	840
	857

<210> 42

<211> 620
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 8-10, 43, 611, 613
 <223> N can be any nucleotide

<400> 42

gnnnttannn cattgcgccc tctagatgca tgctcgagcg gcnccgagct gtgatggata	60
tctgcagaat tcgcccctgt tgcgcaagga gtagatgaac ggattcaggg caagggagtg	120
ctgaggagat agacgggtat acactgggca caagtccatg agtaatcaag gcctgttatt	180
taaaaaaaaa aaaaaaaaaa cttgaacaat atagaatccc attaccaga gatagactgg	240
atgggtgaatt aaacttttctg gtgaatttct ttccagatat ctctctatgc atatgtatac	300
acaagcaatt tttggaagaa aagatacttt ataaggataa gcctgaaaac tgcaacgaat	360
gcaatgtgga gaatgaaggc aagatgtggc gaagaagggc accacaatct ggtggctgag	420
agagtgcac tgctactaca gctaaaagga gagctggaga agctggtgag gacagtaaga	480
gatgaatctg gtttaagaca cgctgagctc caaatgccat ggctccccta ggttgccctc	540
tcagatgtaa atcttaagct caaagcaggt ggatgagaaa tcacatttca tagtccctgc	600
acagacggct ntnttgagct	620

<210> 43
 <211> 608
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 10, 22-24, 27, 592
 <223> N can be any nucleotide

<400> 43

gnnnttaan tcattgcccc gnnngangca tgctcgagcg gccgagctg tgatggatat	60
ctgcagaatt cgcccctccc atgtatttgc ttctcagcaa cttgtccttc tctgacctct	120
gcttctcttc cgtgaccatt cccaagttgt tacagaacat gcagaaccag gacctacca	180
tcccctatgc ggactgcctg acccaaatgt acttcttctt gttatttgga gacctggaga	240
gcttctcttc tgtggccatg gcctatgacc gctatgtggc catctgcttc cccctgcaat	300
acaccgcat catgagcccc atgctctgtc tcgcccctgg ggcgtgttc tgggtgctga	360
ccaccttcca tgccatgtta cacactttac tcatggccag gttgtgtttt tgtgcagaca	420
atgtgatccc ccacttttct tgtgatattg ctgctctgct gaagctggcc ttctctgaca	480
ctcgagttaa tgaatgggtg atatttatca tgggagggct cattcttgca tccattccta	540
ctcatccttg ggtcctatgc aagaaatgct cctcatcttc aaggcccttc tntaagggtg	600
tctgcaag	608

<210> 44
 <211> 608
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 7, 9, 12, 20, 24, 26, 29, 31-32, 480, 530, 557, 579
 <223> N can be any nucleotide

<400> 44

gnnntnant cntgccctgn ccnengcnc nngcgccgcg gcggatggat atctgcagaa	60
ttcgcccttg ttactaagag tatagatgaa cggattcagg gcaaggaggt gctgaggaga	120
tagacgggta tacactgggc acaagtccat gagtaatcaa ggcctgttat ttaaaaaaaaa	180
aaaaaaagct tgaacaatat agaatcccat taccagaga tagactggat ggtgaattaa	240
actttctggt gaatttcttt ccagatatct ctctatgcat gtgtatacac aagcaatttt	300

tggaagaaaa gatactttat aaggataagc ctgaaaactg caacgaatgc aatgtggaga	360
atgaaggcaa gatgtggcga agaagggcac cacaatctgg tggctgagag agtgcaactg	420
tcactacagc taaaaggaga gctggagaag ctggtgagga cagtaagaga tgaatctggn	480
ttaagacacg ctgagtctca gatgccatgg cttccctagg ttgcctcttn cagatgtaaa	540
tcttaagctc aaagcangtg gatgagaaat acacatttna tagtcacctg cacagacggt	600
tttttgat	608

<210> 45
 <211> 602
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 14, 16, 19, 21, 23-24, 27, 38, 40, 50, 52, 520, 551
 <223> N can be any nucleotide

<400> 45	
catgccccgt ccncnagnt ncnnngcncg cggccgcnan ggatatctgn anaattcgcc	60
cttcctatgt atttacttct ccaacttctc cttcccatct ctatcattag aaccattca	120
tatacacctt acgaaacaag ggcaattcc agcacactgg cggccgttac tagtggatcc	180
gagctcggta ccaagcttga tgcatagctt gagtattcta acgcgtcacc taaatagctt	240
ggcgtaatca tggatcatagc tgtttcctgt gtgaaattgt tatccgctca caattccaca	300
caacatacga gccggaagca taaagtgtaa agcctggggt gcctaattgag tgagctaact	360
cacattaatt gcgttgcgct cactgcccg cttccagtcg ggaaacctgt cgtgccagct	420
gcattaatga atcggccaac gcgcggggag aggcggtttg cgtattgggc gctcttcgcg	480
ttctcgctca ctgactcgct gcgctcggtc gtccggctgn ggcgagcggt atcagctcac	540
tcaaaggcgg naatacgggt atccacaaga atcaggggga taacgcaaga aaagacatgt	600
ga	602

<210> 46
 <211> 620
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 6, 10
 <223> N can be any nucleotide

<400> 46	
gnmntnattt attgcattgg gccctctaga tgcattgctg agcgggccgc agtgtgatgg	60
atatctgcag aattcgccct tagtgagtag atgaaagggt tcagcatggg ggtcaccaca	120
gtgtacatca tagccatgac agtgtcctt agagtagaac tattagctga tgagcataag	180
tagagaccaa taacggttcc atagaacagt gacaccacag atagggtggga gccacaagta	240
gagaaggcct tgcagacacc cttagaagaa gggaccttga ggatggagga gacaattctt	300
gcataggacc caaggatgag taggaatggg atgacaagaa tgagccctcc catgataaac	360
atcaccatt cattaactcg agtgtcagag aaggccagct tcagcagagc agacatatca	420
cagaaaaggt gggggatcac attgtctgca caaaaacaca acctggccat gagtaaagtg	480
tgtaacatgg catggaaggt ggtcagcacc caggacagcg ccaccagggc gagacagagc	540
atggggctca tgaggcggt gtagtgcagg gggaagcaga tggccacata gcggtcatag	600
gcatggcca caaggaggaa	620

<210> 47
 <211> 607
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2, 572, 578, 594

<223> N can be any nucleotide

<400> 47

cnatgggccc	tctagatgca	tgctcgagcg	gcccgcagtg	tgatggatat	ctgcagaatt	60
cgcccttcca	atgtatttgc	ttctcagcaa	cttgctcttc	tctgacctct	gcttctcttc	120
cgtgaccatt	cccaagttgt	tacagaacat	gcagaaccag	gacccatcca	tcccctatgc	180
ggactgcctg	acccaaatgt	acttcttcc	gttatttggg	gacctggaga	gcttctctct	240
tgtggccatg	gcctatgacc	gctatgtggc	catctgcttc	cccctgcact	acaccgccat	300
catgagcccc	atgctctgtc	tcgccctggt	ggcgctgtcc	tgggtgctga	ccaccttcca	360
tgccatgtta	cacactttac	tcatggccag	gttggtgttt	tgtgcagaca	atgtgatccc	420
ccactttttc	tgtgatttgt	ctgctctgct	gaagctggcc	ttccctgaca	ctcgagttaa	480
tgaatgggtg	atatttatca	tgggagggct	cattcttgtc	atcccattcc	tactcaatcc	540
ttgggtctat	gcaagaaatt	gtcttcttca	tntcaangg	ccctttcttc	taanggtatc	600
ttgcaag						607

<210> 48

<211> 613

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 7, 9, 257, 266, 295, 313, 322, 331, 334, 338, 340, 345, 348, 356, 358, 365, 378, 397, 398, 402, 410, 447, 480, 536-537, 557, 563, 576, 580, 584-586, 606, 610-612

<223> N can be any nucleotide

<400> 48

annncntng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaag	tccaacctcc	atcctccttg	gccttttggat	tcaattgatc	actccttcct	120
cctcaaaaaca	ccttggtcac	tcatectttc	tcagtctcct	ttgtggattc	ttcctcattt	180
atttgacctc	ttgctggtga	accctttcat	atacactctc	cgtaacaaag	agggcgctact	240
tctgtcgtct	tgagcgnact	gatggnaacc	agcttttgg	cccttttagtg	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	ntnctngn	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaagggnnaa	gncctggggg	gcctaattgag	420
ggagcttact	cacaataatt	ggggtgngcc	cactggcccc	tttccaggcg	ggaaaacctn	480
gcggggccag	ctggaataaa	tgaatcgggc	cacgcgccg	ggaggagggc	gggttrngga	540
attgggcgct	tttccnttt	ctnggttaat	ggactnggtn	ggcnnngtcc	gttcggttgg	600
ggggancggn	nnt					613

<210> 49

<211> 593

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 177, 298, 506, 515, 578, 582

<223> N can be any nucleotide

<400> 49

aacgcagagt	accgcccact	acgtaatctg	tacatgaaag	ggtttaaaag	agactgggaa	60
gagaggaatt	ggcaagatca	agcagaggca	actccttcta	gtccttctag	taccgcaagg	120
ggcagataaa	tggaatgggt	aacacctaga	ggaaagtata	cttgccaaaa	gcaaatncat	180
aggggggagt	acattatcgg	gttgaaaaaa	gtattccatg	cagataaaaa	ccaaaagcaa	240
atacatcggg	ggcgctacttc	tgctgtcttt	gagcgctactg	atggtaccca	gcttttgntc	300
cttttagtgag	ggttaattgc	gcgcttggcg	taatcatggt	catagctggt	ttctgtgtga	360
aattgtttac	ccgctcacia	ttcacacaac	atacagagccc	gggagcataa	agtgtaaagc	420
ctgggggtgcc	taatgagtgg	agcttactta	cattaaattg	cggtgcgctc	actggccgct	480
tttccaagtc	gggaaacctg	tcgtgncagc	ttcantaatg	aatcggccaa	cgccgcgggg	540
agaggcggtg	tgcgtattgg	gcgctcttcc	gcttcttngt	tnactgactt	cgg	593

<210> 50
 <211> 624
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 11, 16, 20, 22
 <223> N can be any nucleotide

<400> 50
 gnnntttaac nccgngctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60
 tctttttcag tctcaagtct tcctcttctc caaagatttt gtcttttcta ctacctgagc 120
 taccaaattcc cttgtcatca atttcaataa ctgtattctc ttcattcattt caacttcaaa 180
 cgtgtcatct cagaacaagc ttcatgttac ttccaatttt atccttcttg tttgctgatt 240
 ccaagaattc cagtcccatc taggcccgca atgcattgtt cctgccaccc ttttcataatc 300
 ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360
 ataattatgt ttttttttgc atgtgctctt aatttccttt cttgctccta ttatcttcta 420
 tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcaacta 480
 tgctcagtc gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540
 tttatagtca tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600
 tctgcgcttg agcgtccggt gggg 624

<210> 51
 <211> 584
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 584
 <223> N can be any nucleotide

<400> 51
 gcagtggtaa caacgcagag tacgcccgtt acggaggctg taaataaagg ggttgaggaa 60
 gtaaagtact tcacagtact ggagcacaca gcatgtgaat ttcagccaaa ggacaaatgc 120
 ctccaaaaaa agttaattca cagtgcagca gggcgaggca cttgtcttat tcgctggttc 180
 tcacattgac cctgaaagga cttttttttg ttaatcccat tttcacagat gggaaaggga 240
 ctctgtatgg ttgtcacttt tatccaaagt ctcatagcca gtaagaagct gccctcaaag 300
 tccctaccct gtcttccatt cgactattct gaggttcaga cccagaaacc ccatacctct 360
 gccttatatt ttaatgaaaa gtatgtctcc aggtttatgt ggagaataac caagacctca 420
 gaaacattta gtgaaaatca gagctagaag gaatctgttt ttttgcgagt tcagagaaac 480
 tgacttggat aagacatcaa agttgtcttg tgcagcaaat tctcctccgg cacatagtag 540
 gcactctgat aaattcaaaa aggcttctaa gaagaggcag aagn 584

<210> 52
 <211> 613
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 6, 10-12, 16-17, 20, 553, 594, 607, 613
 <223> N can be any nucleotide

<400> 52
 gtgaanccan nntaanncn attggagctc caagcagtgg taacaacgca gactacgccc 60
 ccgatgtagt ttctttcttc ctctcttccc tccttcttcc cttcttttcc ttctctctct 120
 ctccctctcc ctctctctct ccctctctct ctcttttttc ttctcttccc tcctctctcc 180
 cccaatccgt tcatgacttc ttcttcttcc tcttcttctt ctttctttct ttcttctttt 240

tctctaagca	ggatcctggg	ctgttcaaac	cagagagctg	taagtctttt	ctttcccat	300
tactgttaga	tccgttgaat	cggctccaga	aaccaaacia	gttaaccctt	gcatttacac	360
gtttcgtaac	ggcgctactt	ctgtcgtctt	gagcgctactg	atgggtacca	gcttttggtc	420
ccttttagtga	gggttaattg	cgcgcttggc	gtaatcatgg	tcatagctgt	ttcctgtggg	480
aaattgttat	ccgctcacaa	ttccacacaa	catacgagcc	gggagcataa	aagtgtaaag	540
cctgggggtgc	ctnatgagtg	agctaactca	cattaattgc	gttgcgctta	ctgnccggtt	600
tcagtcnngg	aan					613

<210> 53

<211> 611

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4-5, 7-9, 14-15, 601

<223> N can be any nucleotide

<400> 53

tnanncnnt	taanncccat	tggagctcca	aagcagtggt	aacaacgcag	agtacgcccc	60
cgatgtactt	gcttcttctt	ctttggagtg	gctgaatgct	tcctcctggc	taccatggca	120
tatgaccgct	atgtggccat	ctgcagtcct	ttgcactacc	cagtcacat	gaaccaaagg	180
actcgtgcc	aactggctgc	tgccctcctg	ttcccaggct	ttcctgtagc	tactgtgcag	240
accacatggc	tcttcagttt	tccattctgt	ggcaccaaca	aggtgaacca	cttcttctgt	300
gacagccac	ctgtgctgag	gctggctctg	gcagacacag	cactgtttga	gatctacgcc	360
atcgctggaa	ccattctggt	ggctcatgat	ccctgcttgc	tgatcttggt	ttcctatact	420
cgcattgctg	ctgccatcct	caagatccca	tcagctaaag	ggaagaataa	agccttttct	480
acatgttctt	cacacctcct	tggtggctct	cttttctata	tatcattaag	cctcacctac	540
ttccggccta	aatcaaataa	ttcacctgag	ggcacgaagc	tgctatcatt	gcctacactg	600
ntatgactcc	a					611

<210> 54

<211> 606

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 4, 483, 509-510, 606

<223> N can be any nucleotide

<400> 54

gttnttccat	ggactcccaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttcttgctgg	cttatcattt	atagatatca	tttattcttc	atccatttcc	cacagatcga	120
tttcagactt	gttcttttgg	aataattcca	tatccttccc	atcttgcttg	gccagctct	180
ttacagagcg	ccttttttgg	gggtcagagg	tctttcttct	gttgggtgat	gcctatgacc	240
ttgcattact	tggttatcat	gagacaatgg	gtgtgtgttt	tgctgctggg	agtgtcctgg	300
gttggaggat	ttctgcactc	agtatttcaa	cttagtggtta	tttatgggct	cccattctgt	360
gacctcaatg	tcattgatca	ttttttctgt	gatatgcacc	ctttattgaa	actggctctgt	420
accgataccc	atgttattgg	cctcttagtg	gtggcaatgg	aggactaggt	tgactatttg	480
ggnttctgct	cttactcatc	tcttatggnn	catctgcact	ctctaaagaa	ccttagtcag	540
aaagggaggt	gaaaagccct	ctcaacctgc	agttccacat	aactgggggg	tggtttcttc	600
tttgn						606

<210> 55

<211> 630

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 4-5, 8-9, 12, 16, 19, 295, 298, 321, 472, 481, 573, 617

<223> N can be any nucleotide

<400> 55

ttannccnnt	tnaatncnt	tggagctcca	aagcagtgg	aacaacgcag	agtacgccc	60
caatgtactt	gcttcttctt	ttttggggct	gctgagtgc	gcctcctggc	caccatggca	120
tatgaccgct	acgtggccat	ctgtgacccc	ttgcaactacc	cagtcacat	gggccacata	180
tcctgtgccc	agctggcaag	ctgcctcttg	gttctcaggg	ttttcagtgg	ccactgtgca	240
aaccacatgg	attttcagtt	tccctttttg	tggccccaac	agggtgaacc	acttntntng	300
tgacagccct	cctgtttattg	nactgggtctg	tgctgacacc	tctgtgtttt	gaactggagg	360
ctcttgacag	ccactgccta	attcattctc	tttcttttct	tgctgatcct	gggatccctat	420
ttcgcatctt	cttcactatc	tttaaggatg	ccgtcagctg	aggggaaaca	tnagcattct	480
ncacctgttc	cgcccacctc	ttgggtggct	ctctcttcta	tagcactggc	aatccttaac	540
gtattttccg	accccaattc	aagtgccttt	ttntgagaag	caaagaaact	ggttgctact	600
tttttttcac	aagggngnac	ttccaatggt				630

<210> 56

<211> 631

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4, 8-10, 493, 582

<223> N can be any nucleotide

<400> 56

gngntttnnn	ccatggagct	ccaaagcagt	ggtaacaacg	cagagtacgc	cccccatgta	60
ctttcttctt	ctttggagtg	gctgaatgct	tcctcctggc	taccatggca	tatgaccgct	120
atgtggccat	ctgcagtcct	ttgcaactacc	cagtcacat	gaaccaaagg	actcgtgcca	180
aactggctgc	tacctcctgg	ttcccaggct	ttcctgtagc	tactgtgcag	accacatggc	240
tcttcagttt	tccattctgt	ggcaccaaca	agggtgaacca	cttcttctgt	gacagcccac	300
ctgtgctgag	gctgggtctgt	gcagacacag	cactccttga	gatctacgcc	atcgtcggaa	360
ccattctggt	ggtcatgatc	ccctgcttgc	tgatcttctg	ttcctatact	cacattgctg	420
ctgccatcct	caaggctcca	tcagctaaag	ggaagaataa	agccttttct	acatgttctt	480
cacacctcct	tgntgtctct	cttttctata	tatcattaag	cctcacctac	ttccggccta	540
aatcaaataa	ttcacctgag	ggcaagaagc	tgctatcatt	gncctacact	gttatgactc	600
catgttgaac	cccataattt	attcattcag	c			631

<210> 57

<211> 637

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 5-6, 76, 82, 92, 106, 122, 125, 142-143, 190, 214, 223, 244, 247, 259, 283, 290, 320, 402, 416, 455, 470, 529, 558, 561, 607, 618, 620, 630

<223> N can be any nucleotide

<400> 57

ttatnnccat	tggagctcca	aagcagtgg	aacaaccgca	gagtacgccc	cccatgtatt	60
ttctttttct	tggggnagct	gnatgcttc	tnctggctac	catggnatat	gaccggctat	120
gnggncatct	gcagtcctct	gnnctcccag	tcattatgaa	ccaaaggaca	cgggccaaac	180
tggctgggtg	ttcctgggtc	ccaagcttct	ctgnagctac	tgngcaagac	cacaatggct	240
cttnagnttt	ccattctgng	gcaccaacaa	ggtgaaccac	ttntttctgn	gacagccggc	300
tgtgctgaaa	ctgggtctgn	tgcaagacac	agcactgttt	gagatctacg	ccatcgctcg	360
aaccattctg	gtgggtcaatg	aacccctgct	tgtgatctct	gngttcctat	actcgnattg	420
gtgctgctat	ccctcaagaa	cccatcaagc	taaangggaa	gcaataaagn	cctttctcta	480
cgtgctcctt	aacacctccc	ttgggtggct	ctcttttcta	atataatcnt	ctaagcctca	540
acctacttct	tgggcctnaa	ntcaaataaa	ttcttctgga	gaggcaagaa	ggtggtattc	600

atttatncta cactggtn gn gactccatgn tggaact

637

<210> 58

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 6, 9, 16, 19, 507, 597, 611

<223> N can be any nucleotide

<400> 58

gtnatncnt	ttaatncnt	tggagctcca	agcagtggta	acaacgcaga	gtacgcccgt	60
tcctcagaca	gtatatgaat	gggttaaaaa	tgggccagag	cagatgcagg	aagatcaa	120
aggaggctac	tgcatagag	tcaaactctag	ggctgatgg	ttcttgggat	gcatagta	180
aggtagatag	agaaagtctt	taggaggtag	aatggacagg	acttcaca	gcattaa	240
tagggagaaa	aaaaatgatt	cctgggtttc	tagcttgagc	tagtagggat	agtggtag	300
tttactgata	tggaaaactg	gaggaaaaag	agtttggaag	agaaagatgg	caagttaa	360
acctgtggga	aatataatca	cagacactaa	ataggcagct	gtgtgggtgg	caaaggag	420
ccatgggcta	ggaacataca	gtgggattcc	ctggcatgtc	attgggtact	gaagtcag	480
tgtatgagac	agcctaagga	gagaatncac	acaggagaag	aaagaactaa	acattcagt	540
gctggccaga	ggatgagaaa	cccaagagat	tggactgttt	aggagcaaca	gtgttgng	600
aaggagagaaa	nggttgaaat	t				621

<210> 59

<211> 631

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 8, 9, 11, 29

<223> N can be any nucleotide

<400> 59

ggntttannc	nctggagctc	caaagcagng	gtaacaacgc	agagtacgcc	cattgcgtag	60
cgtgtacata	aaggggttgg	agctgaagga	ggagataaag	aagaagacag	ccagaacctt	120
gtcctctgtc	ggagatcgca	gggatcttgg	gccgtagata	ggtataagca	aaggggtgcat	180
agtagaaagt	cactacagtg	aggtgggtgc	tgcaggtcga	ataggccttc	ttcctccctt	240
ctgcagagtg	catgtggtag	acagcaagga	gaatccggcc	ataggaacat	gcaatacaaaa	300
tgaagggaaa	cacaagaaaa	atgggtggtgc	tcaaaaacac	cgtgcactca	tagaccagg	360
tatccgtgca	ggctagggtc	aacatagctg	gaacatcaca	gaaaaaatga	ttgatggctc	420
tggacttgca	atatgggata	cggagtgc	ataccgtgtg	agcacaagag	ttgatggagc	480
ctatcatcca	agatcctgtt	atcatcagt	cacacactct	ttttctcata	cggatgagat	540
agtggagagg	aaagcaaata	gccacataac	gatcataggc	cattgatgtc	aggagcagcg	600
cttctgcacc	tgctaaagtc	aggaagaaga	t			631

<210> 60

<211> 620

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 6, 10-11, 15, 18

<223> N can be any nucleotide

<400> 60

tgttantecn	ntttncncc	attggagctc	ccaagcagt	gtaacaacgc	agagtacgcc	60
ctccttggtt	ctgagagtgt	agatgaaggg	gttataggag	ataaagatca	gggcaatatg	120

taggacaagg	acacagacac	tgacaacaaa	gttgattatc	tcattgacag	tggtgtctgt	180
gcaggccagc	ttcagcaggg	gtctcacatc	acagaagaag	tgggagatga	caaagtcac	240
acaaaagggc	aggccacaca	tagatgttac	ttggacaata	gccatgccc	ggccaatcct	300
cagtgaacca	gatcccagtc	agacacaagc	cctcttacct	atgaataccg	taaggggttg	360
cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcca	420
aaagtcacat	agaagagctg	agtgacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcaggtctc	agagatagac	540
agcaatgctt	aggaaaaagt	acatggggccg	tacttctgtc	gtcttgagcg	tactgatggg	600
accagcctt	tgttccctt					620

<210> 61

<211> 612

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 5-6, 9-10, 20, 25, 37-38

<223> N can be any nucleotide

<400> 61

gtnannccnn	tgtagctccn	aagcngagct	aacaacnnag	agaacaacgc	agagtacgcc	60
cccgatgtac	ttgttcctac	tctttgctgg	atttgaaaac	ttcctcctgt	ccgtgatggc	120
ctatgaccgg	tttgtggcca	tctgtcaccc	cctgcactac	atggtcatta	tgaaccctca	180
cctctgtgga	ctgctgggtc	tagcatcctg	gaccatgagt	gctctgtatt	ccttgctaca	240
aatcttaagt	gtagtacggc	tgtccttctg	cacagcctta	gaaatcccc	actttttctg	300
tgaacttaac	caggtcaccc	aacttgcttg	ttctgatagc	tttcttaatc	acatgggtgat	360
atattttaca	gttgcgctgc	tgggtggagg	tcccctcact	gggatccttt	actcttactc	420
taagataatt	tcttccatac	atgcaatctc	atcagctcag	gggaagtaca	aggcattttc	480
acctgtgcat	ctcacctctc	agttgtctcc	ttattttatg	gtgcaatcct	aggggtgtac	540
cttagtctgc	tgccacccgc	aactcacact	caagtgcaac	agcctcagtg	atgtacactg	600
gggcaccccc	at					612

<210> 62

<211> 628

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-8, 13, 19, 22, 32, 35-41, 49

<223> N can be any nucleotide

<400> 62

gnnnnnnnat	ttnatgcct	tnttgattcc	cnttnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttccac	acttctctat	taagaagcat	gtgagatact	180
tgttacaaac	ataacatcct	ggtcccaccc	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tgttggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactggtag	cagggttgag	360
gatcacaggg	aagagggtaa	gcatatcaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccattgtcca	tgtaaagtagc	aaacaaccct	ctcatgtaca	480
ctctgaggaa	caagggggcg	tacttctgtc	gtcttgagcg	tactgatggg	accagcctt	540
tgtcccttta	gtgagggtta	attgcgcgct	tggcgtaatc	atggatcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

<210> 63

<211> 627

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 191, 214, 263, 271, 277, 303, 325, 333, 363, 418, 528, 570, 596, 614

<223> N can be any nucleotide

<400> 63

tgtagctcca	aagcagtgg	aacaacgcag	agtacgccct	cttggttacg	taaggggaata	60
gatgatggg	ttcagcatgg	gggtgactac	agtgtacatg	acagtggcca	cacgggtccca	120
ctctgctcg	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gctcaccaca	nccaggtggg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggc	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggncct	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgcngcgcc	ctnggtgaag	atgagcagct	tggatgtggt	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtggnggc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgtccgtggg	acaccagcca	tgccattcca	accagggctg	cgcacatngc	cggggacatt	540
ctcgtgggat	aaggggaagg	gtgccggatn	ggcacgtatc	agtcataggc	cttgngcgcc	600
agaagacagc	tttnaattta	ccccagg				627

<210> 64

<211> 605

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 5-6, 9, 11, 14, 17, 21-22

<223> N can be any nucleotide

<400> 64

gttannccnt	ntanctncaa	nngaggtaac	aacgcagagt	acgcccccca	tgtatttgct	60
tcttgtecaa	cctgtccttt	gtagagatct	gctacaccac	cgttggtggtg	cccttgatgc	120
tttccaacat	ttttggggcc	cagaagccca	ttccattggc	tggatgtggg	gccccaatgt	180
tctcttttct	cacacttggt	ggtgctgact	gtttctctct	ggcgatcgtg	gcctatgacc	240
gctatgtggc	catctgccac	cctttgcact	acccctcatc	atgacctgca	gtctgtgcgt	300
gcagatgctg	ggcggcgctg	tgggcctggc	cctcttctct	tccctgcagc	tcaccgcctt	360
aatcttcacc	ttgcccttct	gcggctaccg	ccaggaaatt	aaccacttcc	tctgcgatgt	420
acctccgtcc	tgcgcctggc	ctgcgctgca	tccgtgttca	ccaggctgcc	tctatgtcgt	480
gagcatectc	gtgctgaccg	tcccttctct	ctcatctgca	gtctcctacg	tgttcatcac	540
ctgtgccatc	ctgagcatcc	gttctgctga	gggccggcac	caggcctttt	caactgctct	600
tccgg						605

<210> 65

<211> 609

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 10, 14-15, 19, 22, 67, 603

<223> N can be any nucleotide

<400> 65

tgtagctccn	aagnngagnt	ancaacgcag	agtacgcccg	cggaatctat	agatgaaagg	60
gtttggngag	tcagaagaag	gaagtacatg	ggagtcataa	cagtgtagga	caatgatggc	120
agcttcttgc	cctcaggtga	attatttgat	ttaggccgga	agtaggtgag	gcttaatgat	180
atatagaaaa	gagagacaac	aaggaggtgt	gaggaacatg	tagaaaaggc	tttattcttc	240
cctttagctg	atgggatctt	gaggatggca	gcagcaatgt	gagtatagga	acacaagatc	300
agcaagcggg	ggatcatgac	caccagaatg	gttccgacga	tggcgtagat	ctcaaagagt	360
gctgtgtctg	cacagaccag	cctcagcaca	ggtgggctgt	cacagaagaa	gtggttcacc	420
ttgttggtgc	cacagaatgg	aaaactgaag	agccatgtgg	tctgcacagt	agctacagga	480
aagcctggga	accaggagggt	agcagccagt	ttggcacgag	tcctttggtt	catgatgact	540

gggtaagtgc aagggactgc agatggccac atagccggtc atatgccatt ggtagcccag 600
gangaagct 609

<210> 66
<211> 617
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 6, 20
<223> N can be any nucleotide

<400> 66
gttatncctt gttgctcccn agcagaggta acaacgcaga gtacgcccct atttctcaga 60
tatangatga aggggttcag aaaaagaatg agcaaagaaa atctgggcca ggcgggcatc 120
aaaagaaata gtcttggtgct caaccagaaa gtctgcaatc atttttagggg tagcagaaga 180
ggcaacacat acgtctataa atgacagggt ggcaagaagc aaatacattg ggggcgtact 240
tctgtcgtct tgagcgtact gatggtaccc agcttttgtt cccttttagtg agggttaatt 300
gcgcgcttgg cgtaatcatg gtcatactg tttcctgtgt gaaattgtta tccgctcaca 360
attccacaca acatacgagc cgggagcata aagtgtaaag cctgggggtgc ctaatgagtg 420
agctaactca cattaattgc gttgcgctca ctgcccgtt tcagtcggga aacctgtcgt 480
gccagctgca ttaatgaatc ggccaacgcg ccggggagag gcggtttgcg tattgggcgc 540
tcttcgctt ctcgctcact gactcgcttg cgctcggtcg ttcggcttgc ggcgagcgg 600
atcaagctca ctcaaat 617

<210> 67
<211> 621
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 10, 17, 28, 277, 286, 370, 373, 422, 513, 527, 536, 545, 548, 550, 558,
563, 566, 572, 574, 579, 583, 603-604, 609, 621
<223> N can be any nucleotide

<400> 67
gggttttaacn ctgtgcncce ccagcagngg taacaacgca gactacgccc ttgttgcgaa 60
gaaataaatg aatgggttta aaatagacgt gaagatggtg tagaatacag caaggacttt 120
gtcaactgag taactgctga agggccacac atagatgaaa atacacgac caaagaataa 180
agtgaccaca gtgatgtgag cagtcaatgt ggagtgggcc ttcaccatgc ttacagagga 240
gcgattccta actgtaataa gtattacagt gtagganaca accaanagga gaaaggaact 300
cagagaaaga aagccaccat ctgcaactat tagtaggctg acaacataag tgtctatgca 360
ggctaacttn gtnctagag gaaggtcaca gaaaaaaact atctacctta ttaggaccac 420
anaatggcag attaaccgtg aatgccaaact ggctgggtgt atggatgaag cccacaaacc 480
aggaaatgag gacgagcaca acacatacac agnagctcat gattganatg tagtgnggag 540
gtttncntn gtcatancc gtntngcca tngnaactng gancaccatt ttacttgcag 600
tgnnggagng aacatgaaat n 621

<210> 68
<211> 611
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 5-6, 9-10, 17, 19, 298, 464, 519, 549
<223> N can be any nucleotide

<400> 68

gttannccnn	tttaatncna	tggagctcca	aagcagtggg	aacaacgcag	agtagcggcc	60
cgatgtactt	gttcctactc	tttgctggat	ttgaaaactt	cctcctgtcc	gtgatggcct	120
atgaccgggt	tgtggccatc	tgtcaccccc	tgcactacat	ggtcattatg	aaccctcacc	180
tctgtggact	gctggttcta	gcacccctga	ccatgagtgc	tctgtattcc	ttgctacaaa	240
tcttaatggt	agtacggctg	tcttctgcac	agccttagaa	atccccact	ttttctgnga	300
acttaatcag	gtcatccaac	ttgcttggtc	tgatagcttt	cttaatcaca	tggatgata	360
ttttacagtt	gcgctgctgg	gtggagggtc	cctcactggg	atcctttact	cttactctaa	420
gataatttct	tccatacatg	caatctcatc	agcttagggg	aagnacaagg	cattttccac	480
ctgtgcatct	cacctttcag	ttgctcctta	ttttatggng	caatctaggg	gtgaccttag	540
ttttgctgnc	acccgcaact	cacacttaag	tgcaacaacc	tcagtgatgt	acactggggt	600
caccccatgc	c					611

<210> 69

<211> 625

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4-6, 11, 15-16, 40, 42, 45, 47, 52, 61, 64-66, 74-75, 77, 80, 586, 618

<223> N can be any nucleotide

<400> 69

gngrnnncgag	nttannccctt	ggactcccag	tagagctacn	angantnccg	cnagcgcgca	60
nttannccag	ggtntntntn	gtatcaccaa	tgaatagaaa	acagacacca	ccttgtccct	120
gcctagcaag	tagctggagc	tgggtcgcaa	gtacacgaaa	agggctgtcc	caaacagcag	180
agtcaccacc	atcagatgcg	aggcacacgt	gttgacggct	ttccatcggc	cctctgctga	240
agggatcttc	aggaccgcag	acactatgta	accataggag	ataaggagtt	ggaggaacga	300
tgttccctccg	acggtgacca	ccacgaggaa	attcaccact	tgactgagga	aggtgtcaga	360
gcaagacaga	gccaggactg	gtgggagggt	gcagaagaag	tggttgatga	tggtgggtcc	420
gcaaaagtga	agcctaaata	tggagctggc	ctggatcagg	gagctcagga	agccaccaac	480
atatgccccca	accaccatgc	gtgtacagag	gccctgggtc	atgatagtgg	ggtanagaag	540
ggggctggag	atggcttgca	tatcggtcgt	atgccatagc	agtcangagg	aggcactcaa	600
gacagacca	tgccgacnaa	gaaat				625

<210> 70

<211> 626

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-5, 17-18, 24, 34, 42, 584

<223> N can be any nucleotide

<400> 70

gnnnntttta	cccctgmngc	acanagcagt	ggtnacaaag	cncgagtacg	ccccctatgt	60
attttttcct	attctggaca	cgctactcct	gaccgtgatg	gcctatgacc	ggtttgtggc	120
tgtctgccac	cctctgcact	atatgatcat	catgaacccc	cacctctgtg	gcctcctggg	180
ttttgtcacc	tggtcatttg	gtgtcatgac	atccctcctc	catattttct	tgatgatgca	240
tctaattctc	tgtaaagatt	ttgaaattcc	acattttttc	tgcgaaactga	cgtacatcct	300
ccagctggcc	tgctctgata	ccttccctgaa	cagcacgttg	atatacttta	tgacgggtgt	360
gctgggctgt	tttccccctc	ttgggatcat	tttctcttat	tcacgaattg	cttcatccat	420
aaggaagatg	tcctcatctg	ggggaaaaca	aatagcactt	tccacctgtg	gggtctacct	480
ctccgtcgtt	tctttatttt	atgggacagg	cattgggggtc	cacttcactt	ctgcggtgac	540
tcaccccttc	cagaaaatct	ccgtggcctc	ggtgatgtca	ctgnggtcac	ccccatgttg	600
accctttcat	ttacaccctt	agcaag				626

<210> 71

<211> 633

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-10, 4, 7, 10-11, 33, 35, 39, 50, 57, 60, 61-62, 65, 84-85, 441, 615, 617, 632

<223> N can be any nucleotide

<400> 71

gnnnnnnnnn	gttnatnccn	nttttaaatgc	cantngagnt	aacaacgcan	gagtacnccn	60
nngngtacgc	ccaggggttca	accnntgaat	agaaaacaga	caccaccttg	tccctgccta	120
gcaagtagct	ggagctgggt	cgcaagtaca	cgaaaagggc	tgtcccaaac	agcagagtca	180
ccaccatcag	atgcgaggca	cacgtgttgc	aggctttcca	tcgccctctg	ctgaagggat	240
cttcaggacc	gcagacacta	tgttaaccata	ggagataagg	agttggagga	acgatgttcc	300
tccgacggtg	accaccacga	ggaaattcac	cacttgactg	aggaagggtg	cagagcaaga	360
cagagccagg	actggtgggg	agggtgcaag	aagaagtggg	tgatgattgt	tgggtcccgc	420
aaaagtga	gcctaaatat	ngagctggcc	tggatcaggg	gagctcagga	agccacaaca	480
tatgcccaca	ccaccatgcg	tgtacagagg	ccctgggtca	tgatagtggg	ggtngagaag	540
ggggcctgga	gatggctgca	tatcggtcgt	tgccatagca	agtcaggagg	aggcacttca	600
gacagaccca	tgccncnaag	aaaaaaaaact	gnc			633

<210> 72

<211> 614

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-11, 14-17, 19-20, 22, 28, 42-43, 45, 51, 76, 82-83, 85, 101, 106, 110, 112-114, 117, 119, 135, 139, 434, 507, 520, 614

<223> N can be any nucleotide

<400> 72

gnnnnnnnnn	nttnnnncnn	tnactcngc	agtggttaaca	annantacgc	ncagcgcgca	60
gttaaccctc	actaanggta	anntnagctg	gaacacatca	ntacgntcan	gnnngcncna	120
tgaccgggtt	gtggncatnt	gtcaccacct	gcactacatg	ggtcattatg	aaccctcacc	180
tctgtggact	gctggttcta	gcatectgga	ccatgagtgc	tctgtattcc	ttgctacaaa	240
tcttaatggt	agtacggctg	tccttctgca	cagccttaga	aatccccac	tttttctgtg	300
aacttaatca	ggcatccaac	ttgcttggtc	tgatagcttt	cttaatcaca	tggtgatata	360
ttttacaggt	tgcgtgctg	ggtggaggtc	ccctgactgg	gaccccttac	tcttactcta	420
aagataattt	cttncataca	tgcaatctca	tcagctcaag	gggaagtcaa	ggcatttttc	480
acctgtgcat	ctaccctca	gttgctnctt	attttatggg	gcaatcctag	gggtgacctt	540
agttctgggt	gcaccgcga	ctacactcaa	tgcacaagct	cagtgatgta	cactgtggca	600
cccatgctga	accn					614

<210> 73

<211> 630

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3-6, 8-10, 17, 124, 144, 146, 173, 184, 193, 212, 220, 266, 274, 276, 288, 306, 419, 423, 448, 474, 485, 500, 552, 555, 576, 588, 591, 606

<223> N can be any nucleotide

<400> 73

gtnnnnnnnn	ttgattncca	ttggagctcc	aaagcagtg	taacaacgca	gagtacgccc	60
cctatgtatt	ttttcctatt	ctggacacgc	tactcctgac	cgggatggcc	tatgaccggg	120

ttgnggctgg	ctgccaccct	ctgnantata	tgatcatcat	gaacccccac	ctntgtggcc	180
tcnnggtttt	tgncacctgg	ctcattgggtg	tnatgacatn	cctcctccat	atttctctga	240
tgatgcatct	aatcttctgt	aaagantttg	aaantncaca	ttttttntg	cgaactgacg	300
tacatnctcc	agctggcctg	ctctgatacc	ttcctgaaca	gcacgttgat	atactttatg	360
acgggtgtgc	tgggcgtttt	tcctctcctg	ggatcatttt	cttcttattc	acgaattgnt	420
ttnatccata	aggaagaatg	tcctcatntg	ggggaaaaca	aataagcact	tttncacctg	480
tgggnetcaa	cctcttccgn	cgtttcttta	ttttatgggg	acaggcattt	gggggtcccac	540
tttacttttt	gngnggactc	accctttcca	gaaaantttc	cgtgggcntc	ngggatgtac	600
actgngggca	cccccatgtt	gaaccctttt				630

<210> 74

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3,12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 74

ccnatgtayt tntctcta

18

<210> 75

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 75

ccnatgtayt tntctctc

18

<210> 76

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 76

ccnatgtayt tntctctg

18

<210> 77
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 77
ccnatgtayt tntctcctt

18

<210> 78
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 78
ccnatgtayt tntctctta

18

<210> 79
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 79
ccnatgtayt tntctcttc

18

<210> 80
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 80

ccnatgtayt tncctcttg

18

<210> 81

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 81

ccnatgtayt tncctctt

18

<210> 82

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 82

ccnatgtayt tnccttcta

18

<210> 83

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 83

ccnatgtayt tnccttctc

18

<210> 84
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 84
ccnatgtayt tncttctg

18

<210> 85
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 85
ccnatgtayt tnctttctt

18

<210> 86
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 86
ccnatgtayt tncttttta

18

<210> 87
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variati n
<222> 9
<223> y = t/u or c

<400> 87
ccnatgtayt tnccttttc

18

<210> 88
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 88
ccnatgtayt tnccttttg

18

<210> 89
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 89
ccnatgtayt tnccttttt

18

<210> 90
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 90
ccnatgtayt tnttccta

18

<210> 91
<211> 18
<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 91

ccnatgtayt tnttcctc

18

<210> 92

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 92

ccnatgtayt tnttcctg

18

<210> 93

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 93

ccnatgtayt tnttcctt

18

<210> 94

<211> 18

<212> DNA

<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3, 12

<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 94
ccnatgtayt tnttcetta

18

<210> 95
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 95
ccnatgtayt tnttccttc

18

<210> 96
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 96
ccnatgtayt tnttccttg

18

<210> 97
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 97
ccnatgtayt tnttccttt

18

<210> 98
<211> 18

<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 98
ccnatgtayt tntttcta

18

<210> 99
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 99
ccnatgtayt tntttctc

18

<210> 100
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 100
ccnatgtayt tntttctg

18

<210> 101
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variati n
<222> 9
<223> y = t/u or c

<400> 101
ccnatgtayt tntttctt

18

<210> 102
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 102
ccnatgtayt tnttttta

18

<210> 103
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 103
ccnatgtayt tntttttc

18

<210> 104
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 104
ccnatgtayt tntttttg

18

<210> 105
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<210> 106
<211> 31
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 4, 7, 10, 13, 20, 23, 26
<223> N can be any nucleotide

<220>
<221> variation
<222> 1, 2, 8, 12, 15
<223> y = t or c

<220>
<221> variation
<222> 11, 29
<223> r = a or g

<400> 106
yytngtnytn ryncygatan atnatnggrt t

31

<210> 107
<211> 28
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 6, 9, 12, 17, 23
<223> N can be any nucleotide

<220>
<221> variation
<222> 1
<223> y = t or c

<220>
<221> variation
<222> 3, 14, 20, 26
<223> r = a or g

<220>
<221> variation
<222> 8
<223> k = t or g

<220>
<221> variation
<222> 13
<223> w = t or a

<400> 107
ytrttncckna gnwrtanatr aanggrtt

28

<210> 108
<211> 32
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 9, 12, 15, 21, 24, 27
<223> N can be any nucleotide

<220>
<221> variation
<222> 3, 23
<223> y = t or c

<220>
<221> variation
<222> 6, 18, 30
<223> r = a or g

<220>
<221> variation
<222> 11
<223> k = t or g

<220>
<221> variation
<222> 17
<223> w = t or a

<220>
<221> variation
<222> 26
<223> s = g or c

<400> 108
tcytttrttnc knagngwrtat naynasnggr tt

32

<210> 109
<211> 32
<212> DNA
<213> Unknown: Synthetic construct

<220>
<221> variation
<222> 3, 9, 12, 15, 21, 24, 27
<223> N can be any nucleotide

<220>
<221> variation
<222> 6, 14, 18, 30
<223> r = a or g

<220>
 <221> variation
 <222> 11
 <223> k = t or g

<220>
 <221> variation
 <222> 5, 16
 <223> s = g or c

<400> 109
 tcntsrttnc knarnsarta natnatnggr tt

32

<210> 110
 <211> 27
 <212> DNA
 <213> Unknown: Synthetic construct

<220>
 <221> variation
 <222> 4, 7, 10, 16, 22
 <223> N can be any nucleotide

<220>
 <221> variation
 <222> 1, 9, 13, 19, 25
 <223> r = a or g

<220>
 <221> variation
 <222> 6
 <223> k = t or g

<220>
 <221> variation
 <222> 12
 <223> w = t or a

<220>
 <221> variation
 <222> 11
 <223> s = g or c

<400> 110
 rttncnknarn swrtanatra anggrtt

27

<210> 111
 <211> 886
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 7, 11, 16, 18, 21, 209, 231, 258, 259, 266, 267, 269, 282, 287, 289,
 301, 308, 314, 315, 316, 319, 321, 325, 329, 337, 338, 339, 346, 368, 383,
 385, 393, 398, 412, 413, 416, 417, 420, 439, 440, 442, 447, 453, 459, 474,
 479, 484, 488, 499, 508, 513, 521, 526, 536, 541, 549, 559, 574, 579, 587,
 590, 596, 597, 601, 602, 610, 618, 622, 633, 635, 648, 649, 650, 652, 654,

661, 666, 688, 690, 692, 698, 705, 713, 720, 724, 726, 731, 732, 736, 771, 788, 790, 795, 801, 802, 807, 811, 817, 829, 836, 840, 846, 849, 850, 855, 859, 870, 872, 874, 877, 878, 886
 <223> n = any nucleotide

<400> 111

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ggtcccnlccg ngatatncntt naccctctga tgctgctcga gcggccggca ggggtgatgga 60
tatctgcaga attcgccctt ctgttacgca ggaatatata aaggggttac tgaggaataa 120
ataaatgggt tactgaggaa taaataaatg gggtactgag gaacaaatac ataggggtga 180
aagaactgta aaatagaaaa aggaccttnt gctgctcctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgnng ctgccnntna agagtcccac tntctancng cctcagcccg 300
nctttttntct cacnnnccnt nttntctcnc cctcttnnnc tcttttcttc ctattcccc 360
cccttccnct cctccctttt gcntnaccat tgnccctnat ccctttaatt cnntcnntcn 420
tctccctctc attcctcnn tnttcgnctt cantctctnc ctctttctcc ccnctttct 480
ctctctctct ctctctctng tcatcctngt tcnttctctt ncctanttcc ctctancctt 540
ntcttattnc tctctatnc cctctcatct caentctctt cctctctctn tactttnctc 600
nntcttccn ctccgtctc cnetttctct tcntnaecgc acccctcnnn cntnctctct 660
ntctctctct cactctctcc tctccctnch cntcactntt ctccnctct acntcctatn 720
ctcnctttct nnettnactt tgtcacgctc tctctctctc ctctacgcac nttttatctc 780
ttatctcnch catcnccctc nnttctncac nctattnact cttttctcnc atactntatn 840
ctcctntcnn cttanatcnc ctcccttctn tnancnntc actgcn 886

```

<210> 112

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 13, 31, 36-37, 40, 45-48, 50, 53-54, 61, 63, 67-68, 70, 473, 512, 523, 526, 535, 542-543, 545, 549, 558, 566, 571, 582, 589, 593-594, 603, 612-614, 616, 621, 623-624

<223> n = any nucleotide

<400> 112

```

gctgctcgag cgnccagcgcg tcggcagtggt nagggnnatn tgccnnnnntn gcnnttagat 60
nanaggntn agtatggggg tgaccacagt ggtacataac tgaggctgtt gcacttgagt 120
gtgagttgag ggtggcagca gaactaaggt acacccttag gattgcacca taaaataagg 180
agacaactga gaggtgagat gcacaggtgg aaaatgcctt gtacttcccc tgagctgatg 240
agattgcatg tatggaagaa attatcttag agtaagagta aaggatccca gtcaggggac 300
ctccacccag cagcgcaact gtaaaatata tcaccatgtg attaagaaag ctatcagaac 360
aagcaagttg gatgacctga ttaagttcac agaaaaagtg ggggatttct aaggctgtgc 420
agaaggacag ccgtactacc attagattt gttagcaagga atacagagca ctatgggtcc 480
aggatgccag aaccagcagt cacagagggt gngggtttca tantgnccct gtagngtcag 540
cnnngacna gatggccnca aaccgntctt nggccctcac gncctggna ggnngtttct 600
tantccacca cnnntnttct nannc 625

```

<210> 113

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 6-7, 30, 113, 128, 137, 142, 150, 157, 174, 297, 310, 313, 335, 354, 356, 377, 382, 385, 389, 393, 421, 429, 431, 433, 435, 438, 440, 442-443, 446, 455, 457, 465, 467, 477, 488, 491, 501-502, 504, 508-509, 515, 522, 525-526, 529-530, 542, 557-559, 561, 564, 565, 568, 577, 579-581, 584, 587-589, 591, 596-603, 607-610, 612-613

<223> n = any nucleotide

<400> 113

```
catgcnnag caggctcgag cgccggcagn gtgagggata tctgcagaat tcgcccttcc 60
tatgtacttt ttcctgagcg tatacacaat cccatcatgt actggggaga agncagacca 120
tatcattnac aagctgnctt tngcagatgn actttgnttt ctcattaggc tgcncagagt 180
acttctctct ggcagccatg gcttatgacc gctgtcttgc catctgctat cctttacact 240
acggagccat catgagtagc ctgctctcag cgcagctggc cctgggctcc tgggtgngtg 300
gtttcgcgcn cantgcagcg cccacagccc tcagnagcgg tcttgctctt ctgngncccc 360
cgtgccatta accactnctt tngcngcant gcnccctgca ttgtcttgtc ctgccacca 420
nacagcagna nancntgn gnnttngatc gctgntnecg tctcngntct cactccttcc 480
caccttttnc ntcgcatttc nnttccnnc tcgcnctct gncnntcnn tctcctcttc 540
tnaacgcgtc ctccgannng nctnnatgnt cgtctctnn ntgngcnng ncagcnnnnn 600
nnccannnn tngtgcgcc gctcc 625
```

<210> 114

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 12-13, 20, 23, 188, 375, 399, 402, 416, 443, 460, 472, 474-475, 480, 484, 487-488, 502, 505, 522-523, 529, 532, 537-538, 546, 553, 555, 557, 561, 564-565, 573, 575, 577, 581, 583, 586, 591, 594, 617, 634, 636, 643

<223> n = any nucleotide

<400> 114

```
gnttaagccc tnnccctctn gangcatgct cgagcggccg ccagtgtgat ggatatctgc 60
agaattcgcc cttgttccgc aaacaataga tgaaaggatt aagtgaagga gtgccaccg 120
catagaagag accaaagaac ttgccccctc cttgggcata cggatttttg ggctggaggt 180
agacagcnat gactgagctg tagaagaggg tgaccacagt gagatgggag gagcagggtc 240
caaaggcctt tctccatgct gtggcagagt taatcctcag cactgcctgg gcagtggctc 300
cataagaggg aaggatgagg ctgagaggca caaccacgaa gatgacactg gacacagcca 360
actggatttc attgnaggag gcatctccac aggagagtnc gnatcagaga tgggancctc 420
acataaaaaa gtcattctatc tgntgggtggg gacagaatgn ccatgtggag gntnnatgtn 480
cgtntcnnac ctcttatttt tnttccccct ttctttcgct cnntcccent tntccennet 540
cgccanttcc atnncntctc ntcnnttttt ttntntnacc ntntntcat ntentctctt 600
tattctcttt ctcttgnctc tcccttctct ctentnttcc canctctccc g 651
```

<210> 115

<211> 850

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 3, 15, 279, 288, 292, 295, 296, 299, 307, 309, 317-319, 322, 326-327, 329, 335, 340, 343, 345-346, 354, 362, 367-368, 377, 380-382, 386, 391, 394, 396, 399-400, 410, 412, 415-416, 418, 433, 436, 442, 444, 451, 455, 466, 468-469, 471, 474, 482, 488, 490, 500, 505, 514, 516, 522, 530, 537, 548, 550, 552, 559, 562-565, 569, 570, 571-573, 576, 581, 592, 597, 603, 605-606, 608, 617, 619, 624, 627, 630, 635-636, 643, 647, 653, 661-663, 667, 673-675, 678, 690, 697-698, 709-711, 720, 724, 727, 731, 736, 746, 760, 768, 771, 783-784, 789, 791, 794, 796, 797, 800-801, 808, 810, 816, 818, 821-822, 832, 836

<223> n = any nucleotide

<400> 115

```
ggntctcggt acaanacttg gccctctaga tgcattgctc agcggccgcc agtgtgatgg 60
```

```

atatctgcag aattcgccct tccaatgtat ttattcctgt tatttgagaga cctggagagc 120
ttcctccttg tggccatggc ctatgaccgc tatgtggcca tctgcttccc cctgcactac 180
accgccatca tgagcccat gctctgtctc gccctgggtg cgctgacctg ggtgctgacc 240
acctccatg ccatgttaca cactttactc atggccagnt tgtgcttntg tncennacna 300
ttgttgntnc cccactnnnc tntgtntna gtctnctctn cctnnactg ctctcctct 360
tntccnnga gtcctcnggn nncgtngtcg nttncngenn tcaattgcan tncnnctc 420
atcctttctt tanttntcca tntnttact nattnctctt tatecncnt ntccccctcc 480
anctcctnct tagcttactn tttctgtctc tccngngctc anccctttcn ccataatntc 540
ttctctcncn tntctctcnc tnnnnccenn nntctctcgt ntctctgctc cntcttnacg 600
tctnnncnt tatttantnt ctncncctn tctcngctc cancgngta ccngccctat 660
nnnctctcc ganntgntc atggcatctn cacattngc cctactatnn negatctatn 720
ttcncgncat ntattncaca tccacntgca ctctactcnc ctctctance nccgtacatc 780
gcnnctacng ntgncnntcn nccgtctctn cggccncnat nctccactt tntctnggtc 840
ccccctctccg 850

```

<210> 116

<211> 620

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 451, 479, 501, 533, 542, 550, 553, 561, 572, 582, 585, 600, 604-605

<223> n = any nucleotide

<400> 116

```

gatgcacgt cgagcgcccg cagtgtgat gatatctgca gaattcgccc ttccaatgta 60
ctttttcctg aagaacctct ctgttttgga tctgtgctac atctcagtc ctgtgcctaa 120
atccatccgt aactccctga ctgcgagaag ctccatctct tatcttggt gtgtggctca 180
agcctatctt ttctctgct ttgcatctgc tgagctggcc ttcttactg tcatgtctta 240
tgaccgctat gttgccattt gccacccct ccaatacaga gccgtgatga catcaggagg 300
gtgctatcag atggcagtc ccacctggct aagctgcttt tctacgcag ccgtccacac 360
tggcaacatg ttctggggagc acgtttgcag atccaatgtg atccaccagt tcttccgtga 420
catccctcag gtgttgcccg tggtttctg ngaggtttct tttgtagagc tttgaccng 480
ccctgagcct caatgcttg ntctgggatg ctttattccc atgatgatct ccnattttcc 540
anatcttctn aanggggctc nagaatccct tnaggaccag antcnagcta aaagcctttn 600
cccnnctgct tccccccag 620

```

<210> 117

<211> 628

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 5, 9, 403, 505, 552

<223> n = any nucleotide

<400> 117

```

tggcnctcng atgcacgtc gagcgcccg cagtgtgat gatatctgca gaattcgccc 60
ttccaatgta tttgttctg ttatttgagg acctggagag ctctcctctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgcacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgctgac caccttccac gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagacaa tgtgateccc cactttttct 300
gtgatatgct tctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggtc attcttgcac cccattccta ctatccttg ggtcctatgc 420
aagaattgtc tcttccatcc tcaaggctcc ttcttctaag ggtatctgca aggccttctc 480
tacttggtgc tcccaccctg tctgnggtgt cactgggtct atggaaccgt tattgggtctc 540
tacttatgct cntcagctaa tagttctact ctaaaggaca ctgcatggct atgatgtaca 600

```

ctgtggtgac ccccatgctg aacccctt

628

<210> 118

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 17, 25, 184, 187-188, 199, 202, 206, 212, 214-215, 223, 227-228, 232, 248, 250, 252-253, 255-256, 261-264, 266, 268, 271, 273, 276, 278, 284, 289, 292, 295-296, 298, 300-302, 306, 310, 315-316, 320-322, 325, 329, 333, 337, 340-341, 346, 349, 355, 369, 371, 373-374, 379-380, 383-384, 387-388, 391, 402, 407, 409, 417, 419-420, 436-437, 441-442, 445, 447-448, 450, 456-458, 461, 469, 472, 477-479, 486-487, 490, 493, 503, 510, 512, 517, 530, 540, 542, 544, 552-553, 565, 572, 587, 595, 597-598, 600, 611, 614, 617-618, 622-623, 625, 634-636, 639, 644-645, 646, 652-653, 663, 665, 668, 673-674, 679, 681, 683, 695-696, 699, 706, 710, 712, 716, 725-726, 731-732, 741, 745, 748-750, 763, 771, 774, 776, 772, 774-775, 777-778, 780, 782

<223> n = any nucleotide

<400> 118

```

gatgatgctc gagcggnccg agtgngatgg atatctgcag aattcgccct tcccatgtat 60
ttgttccctga gcaacctctc ctctctggag atttggtata ccacagcagc agtgcccaaa 120
gcactggcca tctactggg gagagacag accatatcat ttacaagctg ccttttgcag 180
atgnacnntg ttttctcant angcctaca gngnncatgt ttncgcngc cntgacttat 240
gacgcgcntn cnnccntatc nnnntntnct ntacnccnac ttctcatna tntgncntn 300
nnttcnctn tggcnnctn nntcncggnc ttncctntgn ncgtentenc ccttnggcct 360
gcattctctc ntntctctnn cncnccnct ntcttctctt cntacctnt ttctgtntnn 420
tccctccctt ctctgntgc nntcnnncn catctnnntg ntctgatenc tntctnnnt 480
ccatcnngtn ctnttctctc gtntctctn cncgcncct gcattactgn gcattatatn 540
cncgtctca tnnctatctt cegtctgtt ccttctctt ctatgcncga cgtctntnn 600
tactatcgct ntctcnnat tnnccctgt tccnngcnc ccgncntcc anntactctc 660
cangntctc ctntctctn ncctgtctta attcnnctnt accgntctn gntctctct 720
cgctnntccc nnttctctc nctcncgnn ccttccagct ntcnanttct antnngnncn 780
cnc

```

783

<210> 119

<211> 674

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 1, 2, 114, 207, 212, 253, 261, 294, 316-317, 325, 327-329, 333-334, 340, 345, 352, 355, 364, 382, 384, 393-394, 397, 414, 418, 424, 426, 431, 440, 447, 449, 452, 455, 462, 467, 474, 482, 486, 492-493, 496, 500, 503, 509, 516, 519-520, 525, 532, 534, 539, 544, 550, 552, 555, 559, 564, 566, 573, 576, 586, 591, 594, 598, 605, 608, 610-611, 618, 626, 629, 635, 638, 644, 660-661, 666, 669

<223> n = any nucleotide

<400> 119

```

nntagatgca tgcctgagcg gcccgccagt gtgatggata tctgcagaat tcgcccttcc 60
tatgtatttc ttctggcca acctgtcctt ctgggagacc tggtagatct ctgngactgt 120
gcccaagtta ctgttagtt ttggtctgc gaacaacagc atctctttca cactctgtat 180
gatacaactg tacttcttca ttgctcncat gngcacagaa tgcgtgcttc tggccgccat 240
ggcctatgac cgntatgtgg ncatctggcg cccactccac tacccaacca taantgagcc 300
atgggctcct gctcnnct cgtntnnna tanngaaccn acagngtagc gncanctccc 360

```

```

tgtncgagaa tctacttcat cntnctgcct tannttntgt gggcccaatg tgcntaanca 420
cttngntctg nggacatttn ctccagnant tnaantctct tntcgcnaca aganactggt 480
cnttancttg annatnttcn ggnacattnt tcctanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngttc tantcngtgc cattcntgtg nctncccntt 600
tcatngcntn ncctcccneg aaagcnaant aagtngnggt cttnactttc gcccccaen 660
ncatncant ggcc 674

```

<210> 120

<211> 643

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 359, 373, 439, 463, 506, 537, 564, 584, 594, 604, 610, 620, 633-634, 636

<223> n = any nucleotide

<400> 120

```

ggccctctag atgcatgctc gagcgggcgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta ttttttctctg ttatttggag acctggagag cctcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggtg gcgctgtcct ggggtgtgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tgnaggggct cattcttgct atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcct cctcaaaggc ccttcttctt aanggggtatc tgcaaggcct 480
tctctacttg gtggctcccc cctgncctgt ggtgtcactg ttctatttgg aaaccgntat 540
tgggactcta cttatgctca tcangctaag agttttactc ttangggaca ctgncaatgg 600
cctntgaagn taccctgggn gtggaccccc atnntngaac ccc 643

```

<210> 121

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 429, 447, 453, 484, 510, 519, 542, 544, 546, 549, 552, 561, 581, 587, 600-601, 613, 618, 620-621, 623, 632, 643, 655-656

<223> n = any nucleotide

<400> 121

```

ggccctctag atgcatgctc gagcgggcgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta ctttttctctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggtg gcgctgtcct ggggtgtgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcac cccattccta ctcaccttg ggtcctatgc 420
aagaattgnc tccttccatc tcaaggncct ttnttctaaa gggatatctgc aaggccttct 480
ctanttggtg ctcccaccct gtcttggtgn tggcactgnt tctaattggga accggtatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
ntcattggct tanggatngn ncnttgggtt cntggaaatc ccnatcatc ttacnng 657

```

<210> 122

<211> 622

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 9, 536, 543, 587, 609, 616, 619, 621-622

<223> n = any nucleotide

<400> 122

```

atgaccctna gatgcatgct cgagcggcgc ccagtgtgat ggatatctgc agaattcgcc 60
cttccaatgt atttgttctt gtccaacctg tcttttttgg atattggctt tatctctaca 120
ataattccca atatgctaga tcatattagc tcaggaatta agctgatttc ttatggggag 180
tgtctgacac aactctatct ctctggccta tttgcagatc tggacaacaa ctttctcctg 240
gctgtgttgg cccttgaccg ctatgtggcc atcagccatc ctctccatta tggcctaacc 300
atgaactccc aacgctgtgt cctgttggtg gctgtgtcat ggggtgatcac tattttacat 360
gccctagtgc ataccctcct agtgaccagg ctttccttct gtgggccaaa tattatccct 420
cacttcttct gtgatctggc cccactcctg aagctggcct gctccagtac ttgtgtcaat 480
gatctgggtg tcactccttg ggcaggaaca ctgctgaatg cgccctttgc tgcattctta 540
tgncctactt ttacattgca ttggccatcc tgagaattga ttcccnagg ggtatgcaaa 600
gggccttnt ccagctcnc nn                                     622

```

<210> 123

<211> 610

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 4, 445, 568-569, 580, 587, 600, 607, 610

<223> n = any nucleotide

<400> 123

```

gcgncgcagt gtgatggata tctgcagaat tggcccttcc aatgtatttg tttctgttat 60
ttggagacct ggagagcttc ctcttgttgg ccattggccta tgaccgctat gtggccatct 120
gcttccccct gcactacacc gccatcatga gccccatgct ctgtctcgcc ctgggtgggc 180
tgtcctgggt gctgaccacc ttccatgcca tgttacacac tttactcatg gccagggtgt 240
gtttttgtgc agacaatgtg atccccact ttttctgtga tatgtctgct ctgctgaagc 300
tggccttctc tgacactcga gttaatgaat ggggtgatatt tatcatggga ggggtcattc 360
ttgtcatccc attctactc atccttgggt cctatgcaag aattgtctcc tccatcctca 420
aggctccctt ttctaagggt atctngcaag gccttctcta cttgcggctc cacctgacct 480
tgggtgtcact gttctatgga accgttattg gtctctactt atgtcatca gccataaagt 540
tttactctaa aaggacactt gtcatggnnt atgatgtacn ctgtggngac ccccatgctn 600
aacccttn                                     610

```

<210> 124

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 469, 477, 482, 484, 493, 500, 509, 524, 527, 530, 536, 542, 549, 553-555, 561, 571, 580, 581, 583, 591, 597, 602, 609, 617-619, 624-625, 627, 636, 638, 642, 645-646

<223> n = any nucleotide

<400> 124

```

ccttggggcc tctagatgca tgctcgagcg gccgccagtg tgatggatat ctgcagaatt 60

```

```

cgcccttctt tattcctgag tgaatatatg aggggggttg cactgctgtt aagagtggac 120
aggaaaatgg aaactagacg aacgtgacaa atccacgtgg atccagaaaa ataggaatca 180
ctgaatgcc aagggcaggt cacagaggag gaagaccagc actctgagca ggatgggtcat 240
gtacagcctg gtcaagggca tcttcgggga tccacaaagg atcctgacca gcagaaccgg 300
gctggaccg cagagaacca cacataaaaa aatcagccat gtgactgtga tgaaatctga 360
tgtttcacac caaacagaat caagcaccac tagacaggaa gccacagaac atccattcca 420
ggatgctctg cagcagggac agggcccaga gcaggacaca cgactgctna ccaggtntr 480
tngngtggct gcnagctctn cttaggatng tccccaagga ttgncnngn ccggtnttt 540
gnttgcttnt cgnnncccta nctatgcct ngctcctgt nngcttgac nattggncct 600
cnccacng gcttaannnt ctcnngncgc atttanancg tnatnntact tccctgtcg 660

```

<210> 125

<211> 632

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 488, 505, 507, 586, 618

<223> n = any nucleotide

<400> 125

```

gnccctctag atgcatgctc gagcgccgc cagtgtgatg gatattctgca gaattcgccc 60
ttcctatgta cttcttcctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgtgac cactttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgtc tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggtc attcttgta tcccatcct actcatcctt gggtcctatg 420
caagaattgt ctctccatc ctcaaggctc cttcttctaa gggatatctg aaggccttct 480
ctacttngg ctcccacctg tcttngngg cactgttcta tgggaaccgg tattggtctc 540
tacttaatgc tcatcaagct aatagttcta ctctaaagga cactgncatg gctatgatgt 600
acactgtggt gaccccnat gctgacccat tc 632

```

<210> 126

<211> 642

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 331, 422, 435, 441, 462, 467-468, 471, 479, 500, 502, 513, 521, 537, 543-545, 549, 551, 563, 565-566, 569, 577, 582-583, 586, 594, 596, 611, 614, 620, 624, 631, 639-640

<223> n = any nucleotide

<400> 126

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tctagatgca tgctcgagcg gccgcagtgt gatggatata tgcagaattc gcccttccaa 60
tgtacttgtt cctggcagcc atggcttatg accgctgtct tgccatctgc tatcctttac 120
actacggagc catcatgagt agcctgtctc cagcgcagct ggccctgggc tctgtgggtgt 180
gtgggttctgt ggccattgca gtgcccacag ccctcatcag tggcctgtcc ttctgtggcc 240
cccggtgccat caaccacttc ttctgtgaca ttgcaccctg gattgccctg gcctgcacca 300
acacacaggg agtagagctt gtggcctttg ngattgctgg tgtgggttatc ctgagttcat 360
gcctcatcac ctttgtctcc tatgtggaca tcatcagcac catccttcag gatccccctt 420
gncagtgccc ggagnaaaag ncttttccac gtgtcctcg cntctcnng nggtgctcna 480
tttgggtatgg gtccacaagn tnttctttca cgncggatt ntccattcaa aagatgncct 540
tgnnntttna ncaaaagctt ggncnncgnc ctgaaanact gnngtngact tcangnttta 600
aaactccttt natntcactn ttanggaac nagggcggn ac 642

```

<210> 127
 <211> 688
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 1, 4, 54, 154, 269, 284, 294, 327, 339, 342, 344, 360, 362, 366, 372-373, 379, 382, 390, 393, 395, 397, 402, 408, 410-411, 417, 425, 428, 433, 435, 442, 446-448, 456, 461, 468, 473, 476, 479, 485, 487, 489, 508-509, 514-515, 526, 532-533, 535, 537, 539, 547, 550-551, 553, 555, 559, 572, 578, 582, 587, 595, 597, 602-603, 609-613, 617, 619, 621, 630, 634, 636, 640, 650, 652, 660, 679, 681, 683-684
 <223> n = any nucleotide

<400> 127
 ntgngccctc tagatgcatg ctcgagcggc cgccagtggtg atggatatct gcangaattc 60
 gcccttccca tgtatttatt ccttagcctg ttggattccc agctgcacag ctggattgtg 120
 ttacacaact caccttcttc aagaatgtgg aaancataaa ttttttttct gtgaccatc 180
 tcaacttctc aaccttgccct gttctgacag catcatcaat aacatattat gtattttaga 240
 tatccctata tttggttttc ttcccattnc agggatcctt ttgncttacc atanaattgt 300
 cctcctccat tccaagaatt ccattgncag acgggacgna tnangccttc tctacctgt 360
 cntctnaccg gnnagtcgnt tntttatctn tgnantnccc tngggcgncn nccctgncct 420
 cagcnttngt canctttctc cncacnnntt cgtcgtgtgt ncccagtnct gtncntctnc 480
 tctentnenc tttctgcctc cctccannng tctnncttct tcagcnccct tnnngncnt 540
 gccagcncn nangntcenc cctctccct cntgtctnct cnetcctntt cttentntec 600
 tnnctcatnn nnncgncnc ncgtctctcn cccntntctn tacgactcen gncgtctctn 660
 cgcctacgac ctccctgtnc ncnncgg 688

<210> 128
 <211> 619
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 10, 46, 60, 322, 365-366, 464, 472, 475, 482, 493, 498, 498, 504, 517, 535, 543, 547, 556, 564, 584, 590, 600, 602, 610
 <223> n = any nucleotide

<400> 128
 gcgtgctgcn agcggggcg gtagtgagc ggatatctgc agaatncgcc cttccgatgn 60
 atttctttct aagcaactta tctttcattg acatctgcta ctcttctgct gtggctccca 120
 atatgctcac tgacttcttc tgggagcaga agaccatata atttgtgggc tgtgtgctc 180
 agtttttttt ctttgtcggc atgggtctgt ctgagtgccct cctcctgact gctatggcat 240
 acgaccgata tgcagccatc tccagccccc ttctctaccc cactatcatg acccagggcc 300
 tctgtacacg catggtgggt gnggcataatg ttggtggctt cctgagctcc ctgatccagg 360
 ccagnnccat atttaggctt cacttttgcg gacccaacat catcaaccac ttcttctgcg 420
 acctccacca gtccctggctc tgtcttgcct tgacaccttc cttnagtcaa gncgncgaat 480
 tntcccgtgg tgntcaentg tcgngaggaa acatcgnntt cctccaaccc cttantctcc 540
 cangggntac catagngtct gcgngtccct gaagaatcct tttngccaan cgggccaatn 600
 gnaagccctn ccaccgcc 619

<210> 129
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 17, 223, 238, 260, 304, 310, 315, 317, 322, 325, 327, 329, 341, 345-347, 350, 351, 356, 361, 369, 373-374, 378, 386, 391, 394, 396, 403, 414, 416, 426, 447-448, 456, 459, 461-462, 469, 473, 475, 477, 482, 488, 493-495, 504, 508, 511, 515, 518, 523, 527, 532-533, 537, 543, 548, 555, 558, 561, 570-571, 578, 580, 587-588, 592, 598-599, 601-602, 606, 608, 613, 619, 622-623, 634-635, 645, 648, 656, 658, 661, 665, 674-675, 682, 685, 687, 694-695

<223> n = any nucleotide

<400> 129

```
gcggcgagcgt gtgatgntat ctgacgaatt cgcccttccg atgtatttat ttctaagcaa 60
cttatctttc attgacatct gctactcttc tgctgtggct cccaatatgc tcaactgactt 120
cttctgggag cagaagacca tatcatttgt gggctgtgct gctcagtttt ttttctttgt 180
cgccatgggt ctgtctgagt gcctctctct gactgctatg gcntacgacc gatatgcngc 240
catctccagc ccccttctcn accccactat catgaccagc ggccctctga cacgcatgga 300
ggtngcgccn tatgntngtt gnetnctnng agctccctga nccannnctn ntcaentatt 360
ntaggetcna ccnntcngc tcccgnctca ncancnaacc cnttcggtc ctgnanactt 420
ctccancagc ttcttggtt ttctgcnct gcctcncgc nnccttatnc ttngantca 480
cncctgancg gcnnttctt ccangecngc ncgncancc cgnctctnct gnngaancct 540
ttncatnct gctcnatnct nctctcatcn ntctctantn ctctcennct cncgctcnnt 600
ncttncnct ctnaacctnt cnatcctca cctnngatat cctcncgntc ttctcngntc 660
nttctctgtc cganntcctc anacnctcc ctanncg 697
```

<210> 130

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 473, 502, 524, 547, 550, 567, 572, 590, 596, 614-615, 619, 623

<223> n = any nucleotide

<400> 130

```
ctctagatgc atgctcgagc ggccgcccagc gtgatggata tctgcagaat tcgcccttcc 60
tatgtattta ttccttagcc acttgcccct cactgacatc tccttttcat ctgtcactgt 120
ccctaagatg ctgatgaaca tgcagactca gcacctagcc gtcttttaca agggatgcat 180
ttcacagaca tattttttca tattttttgc tgacttagac agtttcctta tcacttcaat 240
ggcatataac aggtatgtgg ccactctgaca tcctctacat tatgccacca tcatgactca 300
gagccagtggt gtcctgctgg tggctgggtc ctgggtcatc gcttggtgct gtgctctttt 360
gcgtaccctc ctcttggtcc agcttttctt ctgtgctgac cacatcatcc ctcaactactt 420
ctgtgacctt ggtgccctgc tcaagttggc ctgctcagac acctccctca atnagtttagc 480
aatctttaca ggagcattga cnggcattat gcttccattc ctgngcatcc tgggttctta 540
tgggcanatn tgggggtcac cattctncag anttctttta ccagggcatn tgcaangcct 600
tggccacttg tggnnccncc tcnccg 625
```

<210> 131

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 344, 419, 443, 464, 486, 521, 524, 535, 537-538, 545, 552, 564, 567, 572, 584, 586, 588, 601, 604, 608-609, 611-612, 616, 618, 620, 622, 626, 629-630, 633, 638-639, 643, 645, 655

<223> n = any nucleotide

<400> 131

```

ttggcctcta gatgcattgct cgagcgccgc cagtgtgatg gatattctgca gaattcgccc 60
ttgatacatg attgggttgc ggaaggaata aatcatcggg ttgcggaagg aataaatata 120
tcgggttgcg gaaggaataa atacatcggg ttgcggaagg aataaatata tcgggttgcg 180
gaaggaataa atcatcgggt tgcggaagga ataaatacat cgggttgcg aaggaataaa 240
tacatcgggt tgcgtaagga ataaatcatt ggggttgcgta aggaataaat cattgggttg 300
cgtaaggaat aaatcattgg gttgcgtaag gaataaatca ttgngttgcg taaggaataa 360
atctttgtgc tgggtaccgat ctatcatggg gttacgaaag ggaagaaata cattggaang 420
ggcgaattcc agcacactgc cgnccgctac tagtgggagc cganctcggg accaagcttt 480
gatcgntagc ttgagtattt taacgcccgc aacctaaaat ngcnttggcc ttacnctntg 540
gaccnagctt gnettccttg cgtnaanttt cnttattcct cctntntntc ttctcccccc 600
ncanaatntt nccccngntn ancacncann ttntatannc ctngngctcc cctantc 657

```

<210> 132

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 7, 27, 34, 39, 481, 484, 489, 493, 502, 520, 566, 614, 623-624

<223> n = any nucleotide

<400> 132

```

tgcccncta gatgcattgct cgagcgnccg cagngtgang gatattctgca gaattcgccc 60
ttcctatgta ttatttcctt aatgtcctct cgcttcttga tatttggttac tcttctgttg 120
tcacacctaa gctcttggtc aacttccttg tctctgacaa gtccatctct tttgagggct 180
gtgtgggtcca gctcgcttcc tttgtagtgc atgtgacagc tgagagcttc ctgctggcct 240
ccatggccta tgaccgcttc ctatccatct gtcaaccctt ccattatggt tctatcatga 300
ccagggggac ctgtctccag ctggtagctg tgtcctatgc atttggtgga gccaaactccg 360
ctatccagac tggaaatgtc ttgcccctgc ctttctgttg gcccaaccag ctaacacact 420
actactgtga cataccacc cttctccacc tggcttgtgc caacacagcc acagcaagag 480
nggncctcna tgncttttct gntctggcac cttcttggcn gctgcaggca ttctcacctc 540
taccggcttg ggcttggggg ccaatnggga ggatgcgcct caagaacagg gagggagaaa 600
ggactcccca cttntgcctc ccnn 624

```

<210> 133

<211> 590

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 161, 185, 190, 221, 278, 303, 320, 337, 348, 360, 371, 387-388, 390, 393, 395, 402, 407, 409, 413-414, 423, 437, 449, 455, 459, 461, 464, 466-467, 468, 471, 475, 482, 484, 487, 489, 491, 493-495, 499, 500, 503-504, 510, 515, 519-520, 528, 538, 540, 541, 543, 546, 548, 555-556, 558, 563, 566, 568, 572, 575, 584-586, 588

<223> n = any nucleotide

<400> 133

```

ggagttgata tgaacgggtt aagtgaagga gtgcccactg catagaagag accaaagaac 60
ttgcccctcc cttgggcata cggatttttg ggctggaggt agacagcaat gactgagctg 120
cagaagaggg tgaccacagt gagatgggag gagcagggtcc naaaggcctt tctccatgct 180
gtggnagagn taattctcag cactgcctgg gcagtcggct ncataagagg caaggatgag 240
gctgagaggg acaaccacga agatgacact ggacacangc caactgtatc cattgttaga 300
ggnatctcca caggagagtn gaatcagaga tgggacnttc acattaanaa gttatttatn 360
tgctggcggg nacagatgcc caagcggnan gngntatgg tntctggncna ttnnttcgtc 420

```

canacccatt atctcangcc acatgtatnt cagcntttna ntcncntnt nagtntagtc 480
 tngntgntnt ncnntattnn ccntcttttn tccntcann tatcattntc attccttncn 540
 ncnanantt atggnnncnc cgnacncnct cngtnactcc cctnnngncg 590

<210> 134
 <211> 655
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 2-3, 5-11, 17485, 506, 512, 514, 518, 525, 543, 578, 590-592, 602, 609, 612, 616, 637, 646

<223> n = any nucleotide

<400> 134

gnntnnnnnn ntgttancct cgtccctcta gatgcatgct cgagcggccg ccagtgtgat 60
 ggatatctgc agaattcgcc cttccgatgt atttatttct acacagacac agtgacaatc 120
 tgatctctct tgcctttccc cacacactgc aacctctgcc tccacattca agtgattctc 180
 ctgcctcagc ctcttgagta gctggaatta cagatgtgag ccaccatgcc tggcctgtcc 240
 agatgttttt gaaacaaccc ccaccagcac tggagggagt caaggggaaga caagccaggc 300
 atctgagctc ctctgtctct gcctttcctt ctcactgtcc ccagggtaac ccgtcaccac 360
 ccccatcacg aacccttcca tctacacatt acgtaacaag ggccaattcc agcacactgg 420
 cggccgttac tagtggatcc gagctcggtta ccaagcttga tgcatagctt gagtattcta 480
 acgntcacc taaatagctt ggcgtnatca tngncccnag cttgntttct gtgtgaaatt 540
 tgntatccgc tcacaaattc cacacaacat acgagccnga agcaataagn nntaaagcct 600
 gnggtgccna angagngagc taactcacia ttaattncgt tggctnactt gcccc 655

<210> 135
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 4, 449, 480, 499, 510, 519, 524-525, 536, 543, 547, 550-551, 557-558, 564, 574, 581, 602, 615, 518, 621, 623, 627, 636, 639

<223> n = any nucleotide

<400> 135

ttgngccctc tagatgcatg ctcgagcggc cgccagtggt atggatatct gcagaattcg 60
 cccttccatg gtacttggtt ctaagcaacc tctccttctt ggagatttgg tataccacag 120
 cagcagtgcc caaagcaccg gccatcctac tggggagaag tcagaccata tcatttacia 180
 gctgtctttt gcagatgtac tttgttttct cattaggctg cacagagtac ttcctcctgg 240
 cagccatggc ttatgaccgc tgtcttgcca tctgtctatcc tttacactac ggagccatca 300
 tgagtgcctt gctctcagcg cagctggccc tgggctcctg ggtggtgtgg tttcgtggcc 360
 attgcagtgc ccacagccct catcagtggc ctgtccttct gtggttcccg tgccatcaaa 420
 cacttcttct gtgacattgc accctggant gccctggcct gcaccaaacac cacaggcagn 480
 aagagcttgt ggcctttgng aatcgccctg tggggctanc cttngtcat gccctnatca 540
 ccntttntcn nctatgnngt acantcatta agncccaatc nctcatggga tccccctttg 600
 cnagtggccc ggcgngcnaa ngncctnctc cccgtncn 639

<210> 136
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 3, 108, 186, 216, 221, 252, 322, 329, 339, 344, 346, 350, 370, 376, 379, 385, 388, 391, 398-400, 404, 409, 418, 422, 428-429, 433, 437, 455-456, 462, 465, 474-476, 493, 496, 498, 503, 506, 515, 521, 527, 538, 540, 542, 548, 554, 561, 563, 565, 586, 595, 598, 612, 628, 639, 646

<223> n = any nucleotide

<400> 136

```

tgnccctcta gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccgatgt atttgtttct agccaacctg tcattaactg atgcttgntt cacttctgcc 120
tccatcccca aaatgctggc caacattcat acccagagtc agatcatctc gtattctggg 180
tgtctngcac agctatattt cctccttatg tttggnggcc ntgacaactg cctgctggct 240
gtgatgccat angaccgta tgtggccatt tgccaaccac cccattacag cacatctatg 300
agtccccagc tctgtgcact antgctgcnc gtgtgctgng tgcnanccan ttgtctgcct 360
gctgcacatn ctgttncnc cccnccngg nctctttnnn ccgnaccnc cctacaantc 420
cntatcannt tcnctnccc tttcttctcc ccccnnttct tncnccttc ctcnnnccta 480
ctttctctc tcnccntnct canatnatca gtcnacctc nccttcttt cttcactnan 540
tnctctcnct cccnctcacc ngntngtcta gtctgcccgc gcccctcgc tatcnctncc 600
ccccctccg cntccccga tegtctngt ctaccctcnc catctnatcc ctcc 654

```

<210> 137

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 334, 346, 350, 352, 357, 360, 369, 376-379, 389, 394, 397, 400, 401-402, 411, 414, 421, 435, 438, 447-449, 460, 466-467, 474, 476, 480, 486, 500, 504, 510, 512-513, 515, 517, 521, 525, 528, 543, 551, 554-555, 557, 559, 569-570, 572-573, 585, 587, 591, 593-594, 600-601, 606-607, 612, 615, 617, 621, 623, 628-629, 631, 633, 636-637, 640, 655

<223> n = any nucleotide

<400> 137

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ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60
aatgtatttt ttctaaagca acctctcctt cctggagatt tggatatacca cagcagcagt 120
gccc aaagca ctggccatcc cactggggag aagtcagacc atatcattta caagctgtct 180
tttgcagatg tactttgttt tctcattagg ctgcacagag tacttctctc tggcagccat 240
ggcttatgac cgctgtcttg ccactctgta tcttttacac tacggagcca tcatgagtag 300
cctgctctca gcgcagctgg ccctgggctc ctggncgtgn ggcttngtgn cnttgcnngn 360
ctcctagenc tcatgnnnnc cttgccttnt gggncctnng nnatcaccct nttntctctgt 420
nacacttgta cctcncgnet tgccctnnnc tgcttctaan tccctnngtt gtantnccctn 480
gccttntctc cccttegcctn gttnatcttn anntnctgc ntctntgncc ctctccttcg 540
ttngaccct ntannncnc tcttctctnn anntccctc tatcncnccg ntannccctcn 600
ntgtcnnccg antangntac ntntcacnt ntntcnctn ctctcctaac tcttnccg 658

```

<210> 138

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 342, 347, 358, 376, 383, 401, 403, 409, 448, 451, 455, 463, 470, 474, 478, 481-482, 484, 487, 489-490, 492, 499, 511, 514, 516, 518, 522, 525, 534,

536, 548, 556, 565, 577, 581, 585, 587, 589, 592, 598, 604, 607-609, 624-626, 628, 636, 639, 645, 651, 655, 660, 661-663, 667-668

<223> n = any nucleotide

<400> 138

```

ggccccctag atgcatgctc gagcggggcgc cagcgtgatg gatatctgca gaattcgccc 60
ttcccatgta tttgttttcta agcaacccct ccttcctgga gatttggtat accacagcag 120
cagtgcctcaa agcactggcc atcctactgg ggagaagtca gaccatatca ttacaagct 180
gtctttttgca gatgtacttt gttttctcat taggctgcac agagtacttc ctctggcag 240
ccatggctta tgaccgctgt cttgccatct gctatccttt acactacgga gccatcatga 300
gtagcctgct ctacgcgcag ctggccctgg gctcctgggt gngtggnttc gtggccantg 360
tagtgcctcac agccentatc agnggcctgt ccttttggg ncncctgtnc catcaacccc 420
ttctttctgt gacatttgcc cccctgcntt nccctggcc ctncaccaan cacngcangg 480
nngnttnenn gnetcggcnc cccctttgac ntantncntt gntgngcgt tatnctgcg 540
tttaatgncc ttaatnaaac tctnctctt catgttnttc nttntntng gnaccaantc 600
ttcnaannna ccttttttcc catnnncng tctacntcnc tctnccttc ntcngttn 660
nnngtcnnc 670

```

<210> 139

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 303, 314, 331, 339, 341, 360, 373, 379, 386, 395, 400, 406, 416, 419, 423, 433, 435, 452, 456, 463, 473, 480-481, 487, 490, 493, 499, 501, 504-505, 509, 511, 514, 517, 519, 522, 523, 534, 535, 543, 544, 554, 560, 563, 565, 567, 579, 584, 593, 596-597, 599, 605-608, 611-612, 619-620, 624, 632, 634

<223> n = any nucleotide

<400> 139

```

gatgcatgct cgagcgggccc ccagtgtgat ggatatctgc agaattcgcc cttccgatgt 60
atTTTTTct aagcaacctc tccttcctgg agatttggtta taccacagca gcagtgcctca 120
aagcactggc catcctactg gggagaagtc agaccatata atttacaagc tgtcttttgc 180
agatgtactt tgTTTTctca ttaggctgca cagagtactt cctcttggca gccatggctt 240
atgaccgctg cttgccatct gctatccttt acactacgga gccatcatga gtagcctgct 300
ctnagcgcag ctgncctggg ctctgggtg ngtgggtcng ngccattcag cgccacagn 360
cttcatcagt ggncttgtn cttctgngccc ccgncatcn aaccantttc ttctgngana 420
atngtaccgc tgnanttgcc ctggccttgt anccancaca tangctcgta tngcttctn 480
ntggcncn tgnctgcnt ngtnnccgnc ntancngnc tnnacgtcct ttcnnacact 540
ttnctctat gttntcaacn tcnngncta ttcgctcang atanccactc ttncannnt 600
cggannnnta nctttccnn accntcttcc cntnc 635

```

<210> 140

<211> 709

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 357, 369, 379, 382, 414, 430, 441, 458, 462, 468, 474, 481, 486, 494, 505, 507-509, 514, 520, 533, 546, 551, 555-556, 563, 570, 574, 589, 600, 602, 606, 613, 615-616, 622-623, 628, 638, 644, 653, 669, 671, 677, 679, 680-681, 689, 691, 696-698

<223> n = any nucleotide

<400> 140

```

atgacctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60

```

```

ccttcctatg tatttatttc taagcaacct ctccttcctg gagatttggg tataccacag 120
cagcagtgcc caaagcactg ggccatccta ctggggagaa gtcagaccat atcatttaca 180
agctgtcttt tgcaga+gta ctttgtttcc tcattaggct gcacagagta cttcctcctg 240
gcagccatgg cttatgaccg ctgtcttgcc atctgctatc ctttacacta cggagccatc 300
atgagtagcc tgcctcagc gcaagctggc ctgggctcct ggggtgtgtg tttcggnggc 360
cattgcagng cccacagunc tnatcagtgg gctgtccttt ctgtggggcc ccnggcccat 420
tcaacccacn tttctttttg nggatattgg caaccccntg gnatttgnc cctnggccct 480
ngcacncaaa ccancaccag ggtcngnna caanctttgn cgggcccctt ttntgaaatt 540
ggcctnggtg ngggnnntaat tcnctttggn tttnaatgcc cttccaatna acctttttgn 600
cnttctatg gngnncct tnmattcnag caccacanc ttangggaa cnccttttt 660
gtcaagtng nccggtmann naaaagccnt ntccnnntg cccccccg 709

```

<210> 141

<211> 671

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 1, 18, 368, 374, 375, 386, 392, 404, 405, 414-415, 420-422, 445-446, 449-450, 452, 460, 467-468, 471, 484, 488, 490, 512, 514, 531, 536-537, 541-542, 549, 562, 568, 572, 574-575, 577, 585, 588, 592-593, 595, 599, 617, 619, 627, 636, 639, 647, 658-659, 661-662, 665-667, 669

<223> n = any nucleotide

<400> 141

```

ntgggcccctg agatgcangc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60
ccttcccatg tatttttttc taagcaacct ctccttcctg gagatttggg ataccacagc 120
agcagtggcc aaagcactgg ccacccactt ggggagaagt cagaccatat catttacaag 180
ctgtcttttg cagatgtact ttgttttctc attaggctgc acagagtact tcctcctggc 240
agccatggct tatgatcgct gtcttgccat ctgctatcct ttacactacg gagccatcat 300
gagtagcctg ctctcagcgc agctggccct gggctcctgg gtctgtggtt tcgtggccat 360
tgaagtgncc acanngcctc atcagntggc cntgtccttc tgcnnccccc cgtnncattn 420
nncacttctt tcgtgacatt gccannctnn tnttgccctn gtccttnncc natcatccat 480
ggcngttngn gctgttggcc ctttcgctca cncngctgc gccattctc nctgtnncaa 540
nngcctcent ctactctctg cnttctant antnnncct ctttncctnc tnnantctnt 600
cctcgatctc ctttcangnc tccgctncac tgcctcctna acgtccnttt cttccctnnt 660
ntcnnntnc g 671

```

<210> 142

<211> 739

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 5-6, 23, 232, 235, 349, 353, 358, 374, 397, 400, 406, 423-424, 427, 431, 434, 436-437, 440, 445, 448, 450, 452, 467, 471, 477, 488-489, 497-498, 506, 510-512, 518-520, 525, 528, 547, 550, 557-558, 560, 562-563, 566, 569, 590-591, 604-605, 613, 619, 631, 638-639, 642, 646, 649-650, 654, 660-661, 664, 670, 677, 679, 687, 690, 692, 694-695, 701, 714, 716, 722, 725, 731, 739

<223> n = any nucleotide

<400> 142

```

gggcnncttt gggatgcct tgncccttag atgcatgctc gagcggccgc cagtgtgatg 60
gatatctgca gaattcgccc ttccaatgta cttatttcta gccaacctgt cattaactga 120
tgctgtttc acttctgcct ccaccccaa aatgctggcc aacattcata ccagagtgca 180
gatcatctcg tattctgggt gtcttgaca gctatatttc ctccttatgt tngnggccct 240

```

```

tgacaactgc ctgctggcgtg tgatggcata tgaccgctat gtggccatct gccaacact 300
ccattacagc acatctatga gtccccagct ctgtgcaacta atgctgtgng tngctgngt 360
gctaaccaac tggmctgccc tgatgcacac actgttnctn atcccngcgc tttcttggtc 420
ccnntangcc nctnctnctn ttccttntn tntctctacc tctccctcg ngctctnccc 480
cttccccntt cttcctnntg tactnctan nctgttnnn cccctctntt ctctctctcc 540
ttctctnctn ctttcgmnctn tnnctnctnc tcttgccct acctgtccn ntcatacctt 600
ttcnaatcg ctncatctnc cgcctatagt ncaattcnn tncctnctnn attncctacn 660
nccntcctn ccatcantnc taacctnctn cntnntctct ntctctgtcc tcanctctc 720
gncnatttc ntttcccn 739

```

<210> 143

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 497, 528, 536, 540, 543, 551, 557, 563, 565, 570, 582, 589, 600, 605

<223> n = any nucleotide

<400> 143

```

gatgcattgt cgagcggcgc ccagtgtgat ggatatctgc agaattcgc cttgatagat 60
aattgggttc agcatggggg tcaccacagt gtacatcata gccatgacag tgccttttag 120
agtagaacta ttagctgatg agcataagta gagaccaata acggttccat agaacagtga 180
caccacagac aggtggggag cacaagtaga gaaggccttg cagataccct tagaagaagg 240
gaccttgagg atggaggaga caattcttgc ataggacca aggatgagta ggaatgggat 300
gacaagaatg agccctccca tgataaatat caccattca ttaactcgag tgcagagaa 360
ggccagcttc agcagagcag acatatcaca gaaaagtgg gggatcacat tgtctgcaca 420
aaaacacaac ctggccatga gtaaagtgtg taacatggca tggaaggtgg tcagacacca 480
ggacagcgcc accaggncga gacagagcat ggggctcatg atggcgngt agtgcngggg 540
gangcagatg nccacantag tgntnatagn ccattggtcac angggaggna gctttcagg 600
ctttnaataa c 611

```

<210> 144

<211> 641

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 242, 263, 289, 315, 353, 357, 360, 372, 376, 385, 392, 397, 407, 416, 420, 422, 425, 429, 431, 433, 439, 446-449, 454, 465-466, 471, 479, 485, 492, 499, 501, 512, 516, 524, 528-529, 532, 534, 539, 543, 545, 547, 549, 561, 563, 565, 572-573, 575, 578, 582, 584-586, 596, 602, 604, 613, 615, 617, 622, 627-628, 632, 636-637, 639

<223> n = any nucleotide

<400> 144

```

gcgtgctcga gcggccgcca gtgtgatgga tatctgcaga attcgccctt gttgcgcaaa 60
gagtacatga aggggttaag tgaaggagtg cccactgcat agaagagacc aaagaacttg 120
cccctccctt gggcatacgg atttttgggc tggaggtaga cagcaatgac tgagctgtag 180
aagagggtga ccacagttag atgggaggag cagggtccaa aggcctttct ccatgctgtg 240
gnagagttaa tcctcagcac tgnctgggca gtggctccat aagaggcang gatgaggctg 300
agaggcacia ccacngaaga tgacactgta cacagccaa tgtattttat tgnaggnggn 360
atctccacag gngagnccaa tcagntgatg gntcccnccc atttcanaag tcactntatn 420
tntnttgnc ngncacgang gtccnnnnng agcngttctt gtccnntctt nactatcgnt 480
tacctccct cntccctcnt nttttcttcc cncctncctc ttenttttnc cntntccnt 540
gtncnctnt atcttcccta ntntctctt tntnctntt tngnnncctt cctctntctt 600
tntntccctc tcnantat cncctgnnc cncnntnc c 641

```

<210> 145
 <211> 837
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 8-9, 12, 330, 350, 364, 367, 387, 390-391, 393-395, 398, 399-400, 403, 406, 409, 411, 413, 416, 428-429, 438, 449, 454, 464-465, 475, 481, 486, 488, 492, 500-501, 504, 506-507, 515, 523, 532, 538, 548, 556, 562, 565, 567, 573-575, 578, 582-583, 589, 592, 598, 599-600, 604, 608, 612, 629, 637-639, 643, 645, 647, 652, 663, 666, 668, 672, 679, 686-687, 689-690, 693, 699, 710, 715, 717, 719, 721-722, 724, 732-734, 748-751, 763-764, 772-773, 780, 783, 791, 811, 818, 828, 834, 836
 <223> n = any nucleotide

<400> 145
 ggttgccnnc gnttaggcat tgggccctct agatgcatgc tcgagcggcc gccagtgtga 60
 tggatatctg cagaattcgc ccttccgatg tatttggttc taagcaacct ctcttctctg 120
 gagatttggt ataccacagc agcagtgcc aaagcactgg ccacccact ggggagaagt 180
 cagaccatat catttacaag ctgtcttttg cagatgtact ttgttttctc attaggctgc 240
 acagagtact tcctcctggc agccatggct tatgaccgct gtcttgccat cctgctatcc 300
 tttacactac ggagccatca tgagtagccn tgctctcagc tgcagctggn cctgggctcc 360
 tggntgngct ggtttctcgc cctattnttn ncnnnacnnn ccntantcng ncnctnctct 420
 ctttcttntt tccctttncc tcaactcatnc ctcnctctct tttntgtcc tcttnataac 480
 nttgtntntc gnttctcccn ntentnctt ctctnttget tcnctctcct cntttcgnat 540
 ccctttgntc tctacnctct tncgnantca ctnnnatntc tnntcacng cntcctcnnn 600
 gatnttcncc tncctactgc tactctctnc tatactnnnc ttntntnecat anttcgtctg 660
 ctacnante tntcactent tcccanncn tcnctgtcnt ctgactctcn cctentntnt 720
 nntnctcac cnnntacatg gtccctnnn ntccatctcg tcnntctctc cnnatacgn 780
 ttncatactc nctaacttct ctccatcacc ntcacctntc tttctttntc cctngnc 837

<210> 146
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 16, 340, 379, 394, 401, 425, 428, 433, 435, 437-438, 446, 457, 463-464, 487, 504-505, 508, 510-511, 517-518, 529, 542, 546-547, 549-550, 552-553, 555, 561, 567, 569, 573, 576, 582, 584-586, 590, 594, 597, 599-600, 604, 611, 618, 623, 631, 634, 636
 <223> n = any nucleotide

<400> 146
 gatgatgctc gagcgnegca gtgtgatgga tatctgcaga attcgccctt ccaatgtatt 60
 tatttctagg caccactgac ttcttctctt tggccgtcat gtctctggat cgttacctgg 120
 caatctgccg accactccgc tatgagaccc tgatgaatgg ccatgtctgt tcccaactag 180
 tgctggcctc ctggctagct ggattcctct gggctccttg cccactgtc ctcatggcca 240
 gctgcctttt ctgtggcccc aatgggtatt accacttctt tcgtgacagt tggcccttgc 300
 tcaggctttc ttgtggggac accacactgc tgaactggn ggctttcatg ctctctacgt 360
 tgggtgtact gggccacng gctctgacct cagntttcta ngcccgatt cttgccactg 420
 ttctnagngc ccncnangc ttgcengagc gaagcanaag atnnttttca cattgcgcac 480
 tcggaantta aagggggtgg cgcnnancn nctgggngc ttcattctnt ctttttactt 540
 tnccanngnn tntngctca ntccctntc tcntcncaat cntnnngcn ctentgntnn 600
 gtanactgcc nttaattnga ccncttctcc nacnncac 639

<210> 147

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 347, 411, 415, 418, 435, 441-442, 445, 451, 466, 482, 506, 508, 513, 515-516, 526-527, 531-532, 534, 536, 552, 561, 564, 571, 574, 581, 583, 586-588, 591-592, 616

<223> n = any nucleotide

<400> 147

```

catagatgca tgctcgagcg gccgcagtgat gatggatata tgcagaattc gcccttccga 60
tgtaagttct ttctaggcac cactgacttc ttctctctgg ccgtcatgtc tctggatcgt 120
tacctggcaa tctgccgacc actccgctat gagaccctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttctctctgg tcctttgccc cactgtcctc 240
atggccagcc tgcctttctg tggccccaat ggtattgacc acttctttcg tgacagttgg 300
cccttgctca ggctttcttg tggggacacc cacctgctga aactggnggc tttcatgtct 360
tctacgttgg tgttactggg ctcaactggc ctgacctcag nttcntange ctgcattctt 420
gtcactgtct caggncacct nnagntgctg ngcgaaggaa agcgcntttc acttgcgctt 480
cnatcttaca ggggtggcat catctnangg ggnngntgca tccttnncta nntnncnagg 540
tcccagctat antccaaagt nctnaaaaca ngancctcgg nanganntct nntattctac 600
ccttctctgt aacctncc                                     618

```

<210> 148

<211> 633

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 11, 33-34, 36, 38, 346, 352, 370, 406, 412, 414, 417, 420, 423-424, 427, 434, 437, 440, 449, 452-453, 474-475, 477, 486-487, 491, 496, 499-500, 505-506, 515, 517-518, 533, 535, 537, 540, 543, 547, 549, 556, 558, 563, 568, 570, 571, 575, 577, 580, 588, 590, 593-594, 598, 607, 612, 623, 626

<223> n = any nucleotide

<400> 148

```

cntagatgca ngctcgagcg ggcgccagcg tgnngnanat ctgcagaatt cgcccttcca 60
atgtattttt tctcactaac ttgtctttcc tagatctctg cttcaccacc agttctatcc 120
cccagctgct tttcaatcta ggcagccag gcaagactat cagccacacg ggctgtgcca 180
tccagctctt catgttcctg ggcctgggtg gcaagagtgt attctcttgg cagccgtggc 240
ctatgaccgc ttcatgcaa tctgcaagcc ccttcaactat tctgtcatta tgcacctca 300
gctgtgctgg aagtgtgtgt ctgtggcccg ggggtgttgg actccncagt tntctaggta 360
tgccctcctg gactatgaag cttgtcacga tgcggaagat gtaagnttgc ancnttnccn 420
ttntngngat gccngcnten tataaaaanc annctgggcg ggtcacagt cttnngnata 480
gcattnngtc nccttnatnn catcnnattt gcctngnngt ccctcggttc cantntncan 540
tcnttcntng gcttancntt ctncaccngn ncttnctntan ctactccntn ttnnttcntc 600
cttctanctc tncatctttc ttncntccca tcc                                     633

```

<210> 149

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 433, 456, 511, 513, 516, 533, 541, 543-544, 557-558, 561-562, 567, 573, 582, 597, 604, 606, 609, 617, 619

<223> n = any nucleotide

<400> 149

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgttccta 60
agactataca tgaatgggtt tagcatcggg ttgaaagaac tgtaaaatag aaaaaggacc 120
ttctgctgct cctcaggatg gcgggactta ggggccatgt acatgacgat ggcgctgcca 180
aagaagagtc ccactacgca gaggtgggag gaggcagggtg agaaggcctt tctgcggccc 240
tccccagact ggatcctcag gatggccgcc aggatgtgtg agtaggagac cagcaccagg 300
cagagtggtc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360
gtatcagcac aggccagcct gaggacagac aggatttcac aagaagaagt ggttgatttc 420
acgaggccca canaaagggc agtcttagga tgaggntcac atggaccata gccaggaggg 480
agccacattg tcccaggaag ngntgnccag agtgatgcag acttttcagg tcntgatgat 540
ngnnttattc ggagagnntg nnagacnggt cancgttccc gntcgtagga caattancac 600
ccancnggng ccttcantna tgtc                                     624

```

<210> 150

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 449, 480, 506, 555, 578-579, 601, 608, 610-611

<223> n = any nucleotide

<400> 150

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccaatgt 60
atttatttct ctctgacctc tccttcttgg acctctgctt taccacaagt tgtgtccccc 120
agatgctggt caacctctgg ggcccaaaga agaccatcag cttcctggga tgctctgtcc 180
agctcttcat ctctctgtcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240
ttgaccgata cgtggctgtc tgccagcccc tccactatgc caccatcatc ccccccgcc 300
tgtgctggca gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360
catcatccac cctccacttg cccttctgtc cccaccagca gatagatgac tttttatgtg 420
aggtcccatc tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagttgn 480
ctgtgtccag tgtcatcttt ggtggntgtg cctctcagcc tcatccttgc ctcttatgga 540
gccactgccc aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggctctt 600
nggacctngn n                                     611

```

<210> 151

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 415, 417, 427, 516, 524, 536, 544-545, 558, 561, 575, 580, 582, 584, 590, 607, 610, 615

<223> n = any nucleotide

<400> 151

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc ctttctttat 60
ttcgaagagt atacactagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120
gcacactggc ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180
agtattctaa cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg 240
tgaaattggt atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300

```

```

gcctgggggtg cctaattgagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcgngnaga 420
ggcgggnttg cgtattgggc gctcttccgc ttctcgctca ctgactcgct gcgctcggga 480
cgtccggctg cggcgagcgg tatcagctta ctcaanggcc gtantacggt tattcncagg 540
aatnnggggt taacgccngg naaagaacat tgtgngccan angncaagcn taatgcccag 600
gaaccgntan aacgntccc

```

<210> 152

<211> 959

<212> DNA

<213> Homo sapiens

<220>

<221> variation

```

<222> 139, 203, 209, 211-213, 216, 221, 225, 234, 243, 245, 248, 253, 255,
261, 277-279, 287, 296, 302, 311, 318, 321, 344, 348, 350, 353, 376, 379,
381, 383, 395, 397, 402, 406-407, 414, 420, 429, 436, 438, 448, 450, 452,
463, 476, 481, 483, 496, 499, 502, 517, 520, 523, 527, 530, 535, 537, 539,
542, 549, 550, 558, 570, 571, 579, 580, 584, 587, 596, 605, 609, 634-635,
637-638, 640, 644, 648-649, 663, 665-666, 671, 675, 677, 681, 692, 699, 705,
715, 718, 721, 736, 745, 750, 758, 766, 778-779, 791, 793, 797, 811, 816,
821, 829, 831, 832, 837, 839, 840, 843, 846, 846, 851, 858, 883, 889, 892,
895, 897, 898, 917, 923, 928, 935, 945, 956

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<223> n = any nucleotide

<400> 152

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ctcgagcggc gcagtgtgat ggatatctgc agaattcgcc cttectatgt attattttctc 60
cataatttat ctattgccga tatctgcttc tttccatca cagcgcccaa ggttctggcg 120
gaccttctgt ctgaaagana gaccatctcc ttcaatcatt gctccactca gatgtttcta 180
ttccacctta ttggaggggc ggntgtatnt nnnccntggt ncccnatgcg cctncttttc 240
cctntctntt tcnantcttt ncgcctcttc tcatgcnnnc ccttccntct tattcntgtc 300
gnaatacgct ntctccgnet nctgtctgct catccttgct gttncgtntn canctcatcg 360
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ccctcactnc tctttncntg ctcttctntn cncctgtgtc tancctcttg cctgntacg 480
nncgcgcgct catatncgng tncgtgtatc cctctnatn ttnttctcn cctcntntnc 540
cntctcacnn acttctcngt ctctctccan ncttcgacnn ctncctnate tccacnacgc 600
actntctnt ctatatccgc tcttaccgct ctennnnan cacncttnc tctgcatac 660
agntnntctc ncacnncat nttcttcta cnetctcnc tgtcncacag atctntcnet 720
nctctgtctc cgttgntccc cctgncactn cgcaatcnca catatncgct tctcttcnnt 780
cgccacttat ntngcanctt tctctgcgtt nctctncgat ntccctcnc nntctcenn 840
ctnatnatcg nttattcnaa tcatactcgg tactgtttct gtncctctnt cntgncnct 900
agcttctctc tattcantct acnttctntt cgtntctat ccacnctct cactencct 959

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<210> 153

<211> 375

<212> DNA

<213> Unknown (H38g1 nucleotide)

<220>

<223> Synthetic construct

<400> 153

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ttggcctgtg ctgacacatc cttagcccgagggtgagct tccccgacgt tggcctcata 60
tctcttctgt gctttctgct aattctttta tctacacta gaatcacaat atctatctta 120
agcattcgta caactgaggg ccgtcgccgt gccttctcca cctgcagtgc tcacctcatt 180
gccatctctt gtgcctatgg gccatcatc actgtctacc tgcagccac acccaacccc 240
atgctgggaa ccgtgggtaca aattctcatg aatctggtag gaccaatgct gaaccttttg 300
atctatacct tgaggaataa ggaagtaaaa acagccctga aaacaatatt gcacaggaca 360
ggccatgttc ctgag

```

<210> 154
 <211> 965
 <212> DNA
 <213> Unknown (H38g2 nucleotide)

<220>
 <223> Synthetic construct

<400> 154
 cacacagagc cacggaatct cacagatgtc tgagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcaaccggt cctcgctttg ctctccctgt cctgtccat gtatctgggc 120
 acggtgatga ggaacctgct cagcatcctg actgtcagct ctgtctctcc cctccacacc 180
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggttcac ctcgccacg 240
 gttccacga tgattgtgga catgcagtcg catagcagag tcatccctca tgcgggctgc 300
 ctgacgcaga tgtatttctt ggtctttttt gcatgtatag aaggcatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt cgcctctgtc actaccagct catcgtgaat 420
 cctcacctct gtgtcttctt cgttttggtg tccttttttc ttagcctgtt ggattcccag 480
 ctgcacagtt gaattgtgtt acaattcaac atcatcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaaaact gcctgttctg acagcgtcat caatatcatt 600
 ttcataatatt tcgatagtac tatgtttgct tttcttccca tttcagggat cctatggctt 660
 actataaaat cgtccctctc attctaagga tttcatcgtc agatgggaag tataaatcct 720
 tctccacctg tgctctcac ctagcagttg tttgctgatt tgatggaaca ggcattggca 780
 tgtacctgac ttcagctgtg tcaccacccc ccaggaatgg tgtggtggcg tcagtgatgt 840
 acgctgtggt cacccccctg ctgaaccttt tcatctatag cctgagaaac aggaacatac 900
 aaagtgcctt gcggaggctg cgcagcagaa cagtcgaatc tcatgatctg ttccatcgtt 960
 tttct 965

<210> 155
 <211> 936
 <212> DNA
 <213> Unknown (H38g3 nucleotide)

<220>
 <223> Synthetic construct

<400> 155
 atggatggag ataaccagag tgagaactca cagttccttc tcctggggat ctccagagagt 60
 cctgagcagc agcggatcct gttttggatg ttctgttcca tgtacctggt cacggtgctg 120
 ggaaatgtgc tcatcatcct ggccatcagc tctgattccc acctgcacac ccccatgtac 180
 ttcttctctg ccaacctctc ctctactgac ctcttctttg tcaccaacac aatccccaag 240
 atgctgggtga acttccagtc ccagaacaaa gccatctcct atgcagggtg tctgacacag 300
 ctctacttcc tggctctcctt ggtgacctg gacaacctca tcctggccgt gatggcgtat 360
 gatcgctatg tggccacctg ctgccccctc cactatgtca cagccatgag ccctgggctc 420
 tgtgtcttgc tcctctcctt gtgttggggg ctgtctgttc tctatggcct cctcctcacc 480
 ttctcctga ccagggtgac cttctgtggg cctcgagaga tccactacct cttctgtgac 540
 atgtacatcc tgctgtggct ggcattgtcc aacacccaca tcattcacac agcgttgatt 600
 gccactggct gcttcatctt cctcaccccc ttaggggttca tgaccacatc ctatgtacgt 660
 attgtcagaa ccatccttca aatgcccccg gcctctaaga aatacaaaac cttctctacc 720
 tgtgcctccc atttgggtgt ggtctccctc ttttatggga cgcttgctat ggtgtacctg 780
 cagccccctc atacctactc catgaaggac tcagtagcca cagtgtatga tgctgtgctg 840
 acacctatga tgaaccttt catctacagg ctgaggaaca aagacatgca tggggctccg 900
 ggaagagtcc tatggagacc ctttcagagg cctaaa 936

<210> 156
 <211> 914
 <212> DNA
 <213> Unknown (H38g4 nucleotide)

<220>
 <223> Synthetic construct

<400> 156

atgaggaatc	acacattgct	gaatgaattc	attctacggg	gaataacctca	gacagagggga	60
ctggaggctg	tactctgtgc	tgtcttctca	tccatctacc	tcttcaccct	acttggaat	120
ttactcatcc	ttatagcgat	tgtttcttca	cactcctatg	tatttcttct	tgggacgcct	180
gtctactttt	gacatattgt	tcccatctgt	aacatgtccc	aagatgctat	tgtatctctc	240
tggccagc	ccagtcattt	cttttaaggg	atgtgcttca	cagctcttct	tctatcagtt	300
gctgggttct	gctgaaggct	gcctctatc	tgtgatgtct	tatgatcgct	ttgttgccat	360
acatcacaca	ctgagatata	tgctcatcat	gaagcctgga	gtctgtgtcg	gcttggtcgt	420
ggtgccgggt	tgggtgggtg	tcttcacgcc	accattctga	cctcctttac	ctttcagttg	480
tcctactgtg	gccccaatca	ggtggactac	ttcttctgtg	acattcctgc	tgttttaccc	540
ctggcttgta	ctgacagtgc	cctggcccag	aggggtgggt	ccataaatgt	tggctttctg	600
gctttaacac	ttttgatcag	tgtctgtgtc	tgctacacta	gcattgggat	tgccatcttg	660
agaatccgct	catcagaggg	caggcagaaa	gccttctcca	cctgcagtgc	tcaccttggt	720
gcaatcctct	gtgcctatgg	acctgtaatc	atcatctatc	tgaagtccac	acccaacccc	780
ttgcttggtg	ccaggtgcaa	atattaaata	atgttgtctc	acccatgctg	aactcgtaa	840
tctattcctt	aaggacaag	gaagtgaata	ggtccttgaa	aagagtattc	tgaaatgttt	900
tacttactgt	ttgt					914

<210> 157

<211> 951

<212> DNA

<213> Unknown (H38g5 nucleotide)

<220>

<223> Synthetic construct

<400> 157

atgggaacag	ataaccagac	ttgggtgagt	gaatttattc	tcctcggcct	gtccagtgc	60
tgggacactc	gggtctccct	gtttgtcctg	ttcttgggtc	tgtatgtggg	gaccgtgctg	120
gggaactgtc	tcattgtcct	tctgatcaga	ctggacagcc	gactccacac	tcccatgtat	180
ttctttctca	ccaacctctc	ccttgtcgat	gtctcctatg	ccacaagtgt	agtcctcag	240
ctgctggcac	attttcttgc	agaacataaa	gccatcccat	tccagagctg	tgcagcccag	300
ttatttttct	ccctggcctt	gggtgggatt	gagtttggtc	tcctggcggt	gatggcctat	360
gaccgctatg	tggctgtgtg	tgatgccctg	cgatactcgg	ccatcatgca	tggagggctg	420
tgtgctaggt	tggccatcac	atcctgggtc	agtggcttca	tcagctctcc	tgtgcagact	480
gctatcacct	ttcagctgcc	catgtgcaga	aacaagttta	ttgatcacat	atcctgtgaa	540
ctcctagctg	tggtcaggct	ggcttgtgtg	gacacctcct	ccaatgaggt	caccatcatg	600
gtgtctagca	ttgttcttct	gatgacaccc	ttctgcctgg	ttcttttgtc	ctacatccag	660
atcatctcca	ccatcctaaa	gatccagtcc	agagaaggaa	gaaagaaagc	tttccacacg	720
tgtgcctctc	acctcacagt	ggttgcctctg	tgtatgggtg	tggccatttt	cacttacatc	780
cagccccact	ccagtcctc	tgtccttcag	gagaagtgtg	tctctgtctt	ttatggcatt	840
ttaacaccaa	tgtctgaaccc	catgattttac	agcctaagga	ataaagaggt	gaagggggcc	900
tggcagaaac	tattatggaa	attctctggg	ttaacatcaa	agctggcaac	t	951

<210> 158

<211> 1025

<212> DNA

<213> Unknown (H38g6 nucleotide)

<220>

<223> Synthetic construct

<400> 158

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gateccagaac	tgcagccggg	catcgctggg	ctgttctctgt	ccatgtgcct	ggtcacgggtg	120
ctggagaaac	tgtcatcatc	catggcagtc	agccctgact	tcacacctca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgccct	gacatcggtt	tcacctccac	acgggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcattctc	ctatgcagge	tgcctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tgggaagagag	acatgtctct	gagcgtgatg	360
gcctacgacc	agtttgttagc	catctgtcac	cctcccatat	cgttcagcca	tcttgaaccc	420

gtgtttctgt	ggcttccaag	atttggtgtc	cctgtttttt	tttctttttt	tttttttttc	480
ctcaggcttt	tagactccca	gctgcataac	ttgattgcct	tacaaatgac	ctgcttcaag	540
gatgtggaaa	tttctaattg	cttctgggaa	ccttctcaac	tccccatct	tgcattgtgt	600
gacaccttca	ccaggaacat	caacctgtat	ttccctgctg	ccgtattggg	ttttcttccc	660
atctcgggga	cgctttttct	ttactgtaaa	attgtttcct	ccattctgag	ggtttcatca	720
tcagggtggga	agtataaacc	ttctccacct	gtgggtctca	cctgtctgct	gtttgtctgat	780
tttatggaa	aggcgttggg	gggtatctcg	gttcagatgt	gtcatcttcc	ccgagaaaaga	840
gtgcagtggc	ctcagtgatg	tatacgggtg	tcacccccat	gctgaacccc	ttcatctaca	900
gcctgagaaa	cagggatatg	aaaagtgtcc	tgcggcgggc	gcacagcagc	acggtctaata	960
ctcaatatct	tcttatctgt	tccattcctt	ttgtagggtg	ggttaaaaaa	ggcagcaagg	1020
tcaaa						1025

<210> 159

<211> 936

<212> DNA

<213> Unknown (H38g7 nucleotide)

<220>

<223> Synthetic construct

<400> 159

atggtaaaag	gaaatcattc	cacgggtgact	gaatttaate	tcgctggggt	aacagacaaa	60
ccagagctcc	agctgcctct	tttctctctc	ttcctgggaa	tctatgtggt	cacagtgggtg	120
ggcaacctga	gcattgatcac	tctaataagg	ttcagttctc	acctgcacac	ccccatgtac	180
catttctctc	gcagtcctgtc	cttcattgat	ctctgccagt	cttctgtcat	tacccccaaa	240
atgctgggga	attttgtgtc	agagaggaat	attatctcct	acctcagcatg	catgactcag	300
ctctacttct	tccttgttct	tgtcatatct	gaatgtcaca	tgttggtctg	aatggcttat	360
gaccactaca	ttgccatatt	taaccacctg	ctttaccatg	tcgccatgtc	ttatcagggtc	420
tgctcctgga	tggtagtgtg	gggtgatttt	atgggcttta	ttgggtgctac	gtgctcacac	480
agtctgcatg	ctaagagtgc	ttttctgtaa	ggctgatgta	atcaaccatt	acttctgtga	540
tcttttccca	ctactggagc	tctcccgtct	cagtatttct	atcaatgaaa	tagtagtttg	600
tgcttcagtg	catttaatat	ccttttccgc	agcctcacca	tccttagctc	ttacatcttc	660
atcggttgga	gcattcctctg	cattcgctcc	actgagggca	ggtcacaaaac	cttcagcact	720
tgcagctccc	acatctcggc	tgtttctgtt	ttctttgggt	ctgcagcatt	catgtacctg	780
cagccatcat	ccgtcagctc	catggaccag	gggagtgtct	tctgtgtttt	atgctactgt	840
tgtgcccatg	ctgaaccccc	aatctacagc	ctgaggaata	aagatgtcaa	agttgcctta	900
attaagttcc	ttgaaaaaag	aagtttccctg	tgaaaag			936

<210> 160

<211> 985

<212> DNA

<213> Unknown (H38g8 nucleotide)

<220>

<223> Synthetic construct

<400> 160

atgggtcagg	aaaataaaaa	ccagacatgg	gtgagtgagt	tcattctgct	ggggatttcc	60
agtgattggg	gcattcaggt	atccctcttc	gccctgatcc	tggccatgta	tttggtgact	120
attttaggaa	acaccctcat	tcttcttctg	atcagactgg	acaacaggct	tcataccccc	180
atgtacttct	cccttagtgt	tctgtcattt	gtggactttt	gttatacaaa	gagtattgtc	240
ccacaaatgc	tgtcccaact	gctctcagcc	cgaaagtcca	tcccattcta	cagttgtgtg	300
ctccagctct	atgtttctct	ggcatttgtt	gggtctgagt	tcttcctgct	gggggccatg	360
gcctatgacc	gctacgtggc	cgtgtgccac	ccactgcact	acacgggtcat	catgcatgga	420
gggctgtgcc	tggggctggc	ggccagccgc	ctgggtggctg	gcttctcaaa	ttccctgatg	480
gaaacaatta	tcaccttcca	gcttctgtgt	tcacgggtgt	atcaatcact	ttgtctgtga	540
gaccttagca	gtgctacagc	tagcctgtgt	ggatgtcccc	ttcaacaagg	tcattggtggc	600
catctcaggg	tttctgggtg	tcttgccttc	ctgttccctg	gttctattct	cctatgcttg	660
catagttgcc	accattttgt	gcattcgttc	taccaggtga	cgctgcaaag	cctttggggac	720
ctgtgcctct	cacctcattg	tggtttgcat	gtgctttggg	gtaccatct	gcacctacct	780
ggggccacag	ttggcctcct	cagcagagga	agagaagatg	attgctctct	tctatggagt	840

ggtgtcaccc atgttgaacc ccttgatcta cagcttgagg aataaggaag ttacggctgc	900
tgtccggaag gttttagaaa gatgcagata aagggtcaag actctaagaa cctcttgta	960
tctatcatca aaacaaaaa ggaga	985

<210> 161
 <211> 954
 <212> DNA
 <213> Unknown (H38g9 nucleotide)

<220>
 <223> Synthetic construct

<400> 161	
atggacaaa gcaattatag ttctttacat ggttttattc tgcttggtt ctctaaccat	60
ccaaaaatgg agatgaccc gtcaggagtt gtcgccatct tctacttaac tacattggtg	120
ggtaacacag ccatcattct tgcattcttc ctggattccc agcttcatac accaatgtac	180
tttttcctca gaaatttatc ttccctagat ctatgtttca caaccagcat catccctcag	240
atgctggtca acttggtggg acctgataag accatcagct atgtgggttg tatcatccaa	300
ctctatggtt acatgtggtt gggctcagtt gaggctctc tcttggtgt tatgtcctat	360
gacgttttta cagctatatg taagcccttg cattattttg tagtcatgaa cccacatcta	420
tgcttaaaga tgattatcat gatctggag attagtttg ccaattctgt agtattatgt	480
acactcactc tgaatttgcc cacatgtgga aacaacattc tggatcattt cttgtgtgag	540
ttgccagctc tgggtcaagat agcttggtga gacaccacaa cagttgaaat gtctgttttc	600
gctttaggca ttataattgt cctcacacct ctcatcctta ttcttatatc ctatggctac	660
attgccaaag ctgtgctgag aacgaagtc aaagcaagcc agcgaaaagc aatgaatacc	720
tgtggatctc atcttactgt agtgtctatg ttctatggaa ctattatcta catgtacctg	780
caaccaggtc acagggcttc caaagaccag ggcaagttcc tcaccctctt ttacaccgtc	840
atcactcaa gtctcaacc gtcattttac accttaagaa ataaggacat gaaggatgcc	900
ctgaagaaac tgatgagatt tcaccacaaa tctacaaaaa taaaggaggaa ttgc	954

<210> 162
 <211> 970
 <212> DNA
 <213> Unknown (H38g10 nucleotide)

<220>
 <223> Synthetic construct

<400> 162	
cacacagagc caggaatct cacaggtgtc tgagaattcc tctcctggg actttcagag	60
gatccagagc tgcagtcggt cctcgctttg ctgtccctgt cctgtccac gtatctggcc	120
acgggtgtga ggaacgtgct caacatcctg gctgtcagct ctgactccc cctccacacc	180
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gttcccaaga tgattgtgga catgcagtcg tatagtagag tcatctctca tgagggtgc	300
ctcacacaga tgtctttctt ggtccttttt gcatgtatag aaggcatgat cctgactgtg	360
atggcctatg actgctttgt agccatctgt cgccctctgc attaccagc catcgtgaat	420
cctcacctct gtgtcttttt cgttttggtg tctttttcc ttagcctgtt ggattcccag	480
ctgcacagtt gaattgtgtt acaattcaac atcatcaaga atgtggaaat ctctaatttt	540
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ttcacgtatt tccatagtag tatgtttggt tttcttccca tttcagggt cttttttct	660
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ttctccacct gtgactctca cctagcagtt gttgtctgat tttatggaac aggcattggc	780
atgtacctga cttcagctgt gtcaccaccc ccaggaatgg ttagtggtgc tcaatgatgt	840
acgtgtggt caccctcatg ctgaacctt tcatctacag cctgagaaac agggacatac	900
aaagtgcct gcggaggctg ctgagcagaa cagtcgaatc tcatgatctg ttccatcgtt	960
tttcttgtgt	970

<210> 163
 <211> 933
 <212> DNA
 <213> Unknown (H38g11 nucleotide)

<220>

<223> Synthetic construct

<400> 163

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ttgagtatgc	gggcagccat	gtttctgata	ttccttgtagg	cctatatattct	gacagtggct	120
gaaaacgtga	tcatcatcct	attggtgctg	caaaatcggc	cactgcacaa	gcctatgtac	180
ttcttcctgg	ccaacctgtc	cttcttgtag	acctgggtaca	tctctgtgac	tgtgcccgaag	240
ttactgttta	gttttttggtc	tgtgaacaac	agcatctctt	tcacactctg	tatgatacaa	300
ctgtacttct	tcattgctct	catgtgcaca	gaatgtgtgc	ttctggccgc	catggcctat	360
gaccggtag	tggccatctg	tgcgccactc	cactacccaa	ccataatgag	ccatgggctc	420
tgtctccgcc	tgcgtcttgg	ttcctggggc	attggctttg	gcatctccct	ggcgaagatc	480
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atcctggcac	tgggtcatctt	cctattccca	ctctttatta	ctgtcctgtc	ctacggatgc	660
attctggcca	ccatattatg	catgccacaa	ggaaagcaga	aagcgttctc	cacttgtgcc	720
tcccatcttg	tgggtggtcac	cattttctat	tcagccatta	ttttcatgta	tgtctgacct	780
cgagttatcc	atgccttcaa	catgaacaaa	attaattcca	tcttctatgc	cattgtcact	840
ccttctctca	accctttcat	ttattgccta	agaaaccgag	aggtcaagga	agctctgaag	900
aaactggcat	attgccaggc	cagcagatct	gac			933

<210> 164

<211> 939

<212> DNA

<213> Unknown (H38g12 nucleotide)

<220>

<223> Synthetic construct

<400> 164

atggagcaag	tcaataagac	tgtggtgaga	gagttcgctg	tcctcggtct	ctcatccctg	60
gccaggctgc	agcagctgct	ctttgttata	ttcctgctcc	tctacctggt	cactctgggc	120
accaatgcaa	tcattcattc	caccattgtg	ctggacagag	cccttcatac	tcccatgtac	180
ttcttccttg	ccatcccttc	ttgctctgag	atttgctata	cctttgtcat	tgtacccaag	240
atgctgggtg	acctgctgtc	ccagaagaag	accatttctt	tcctgggctg	tgccatccaa	300
atgttttctt	tcctcttctt	tggctcctct	cactccttcc	tgtctggcagc	catgggctat	360
gatcgctata	tggccatctg	taaccactg	cgctactcag	tgtctatggg	acatgggggtg	420
tgtatgggac	taatggctgc	tgcctgtgcc	tgtggcttca	ctgtctccct	ggtcaccacc	480
tccctagtag	ttcatctgcc	cttccactcc	tccaaccagc	tccatcactt	cttctgtgac	540
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atgcttggtg	tatttgcctt	ggtcattcct	ctgtacttta	tcctagtctc	ctacatccgc	660
atcatctctg	ccattctaaa	aatcccttcc	tccgttggaa	gatacaagac	cttctccacc	720
tgtgcctccc	atctcattgt	ggtaactggt	cactacagtt	gtgcctcttt	catctactta	780
aggcccaaga	ctaattacac	ttcaagccaa	gacaccctaa	tatctgtgtc	atacaccatc	840
cttaccctcat	tgttcaatcc	aatgatttat	agtctgagaa	ataaggaatt	caaatcagcc	900
ctacgaagaa	caatcggcca	aactttctat	cctcttagt			939

<210> 165

<211> 954

<212> DNA

<213> Unknown (H38g13 nucleotide)

<220>

<223> Synthetic construct

<400> 165

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cttttgggaa	atgttatatt	caggaccctt	gtttgttcct	tgggatttca	cacatcatgc	180
atgtattttt	ttccttgaaa	aatatcattg	tgattggcat	gagtttgtct	tcaattattg	240

ctttaccttc	aacgcagaaa	tgagccatca	atgttcaggg	tgctgctgtc	catgttttct	300
cctttccttg	cctgtactgc	cccagatct	tcttgcatte	actgacacag	tgccaccctt	360
ttattgccat	tggaatccca	ctgcaaggta	tgacacaccat	tacacacaaa	ctgtatatac	420
tgctcaccac	agggccctgg	agaggctgct	agctacatgt	caatctcctg	atgctatatt	480
aggcagctac	cctaatacctg	tgccaacgaa	gttatggctg	tcattcccat	cacattcctg	540
aagtcaaaact	gtgacctatg	caagcatata	ctaagcccta	tgccgggtctc	tctctctgtc	600
tctctcttag	tctctctctc	tctttctctc	tcttttccat	taactccata	tcttatactt	660
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cctgccttgc	tcacctcttt	gctttctcaa	cctgcattgc	tcaacctgca	gtctgcaact	780
ccttggtggc	atggacagaa	gctcagaccg	agagctctct	gcgattctgt	gattcagaga	840
ccgaacttgt	gtgtgaccat	ctccttgaac	tccttgattt	ctagcctgag	aatgaaagt	900
gtgaaacaag	cttcacataa	aatatttaaa	gaacaaactt	tattcatgaa	aata	954

<210> 166

<211> 998

<212> DNA

<213> Unknown (H38g14 nucleotide)

<220>

<223> Synthetic construct

<400> 166

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tgggagatcc	agctcctcct	cctagtgttt	tctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
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atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
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gcctttcatt	tctggctgtt	gcctggaccc	ttggtgtcag	tcactccctg	ttccaactgg	480
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ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactctc	tacatcttca	660
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cagctcacag	cacagcggtc	cttttgttct	ttggtccacc	catgtttgtg	tatacatggc	780
cacaccctaa	ttcacagatg	gacaagtttc	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacaatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 167

<211> 966

<212> DNA

<213> Unknown (H38g15 nucleotide)

<220>

<223> Synthetic construct

<400> 167

cacacagggc	cacggaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccact	cctcactttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acgggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccatgtact	tcttctctc	caacctgtgc	tgggctgaca	tcggtttcac	ctaggccaca	240
gtccccaaga	tgattgtgga	catgcagtcg	catagcagag	tcactctctc	tgcggtctgc	300
ctgatacaga	tgtctttatt	agtccttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	tgccctctgc	actaccagct	catcgatgaat	420
cctcacctct	gtgtcttctt	cgttttgggt	tcctttctcc	ttagcttgtt	ggattccag	480
ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaattct	540
gtctgtgacc	cctctcatct	tctcaaaactt	gcttgttctg	acagcgtcat	caatagcata	600
ttcatatatt	tcgatagtac	tatgtttggg	tttcttccca	tttcagggat	cctatggtct	660
tactataaaa	tcgtcccttc	cattctcagg	atttcatcgt	cagatgggaa	gtataaagcc	720

ttctccacct	gtgcctctca	cctagcagtt	gtttgctgat	tttatggaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaatg	gtgtgggtggc	gtcagtgatg	840
tacgctgtgg	tcacccccat	gctgaacctc	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtggcc	tgcgagggt	acgcagcaga	acagtcgaat	ctcatgatct	gttccatcgt	960
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<210> 168

<211> 837

<212> DNA

<213> Unknown (H38g16 nucleotide)

<220>

<223> Synthetic construct

<400> 168

atgtacctgg	ccactgtcct	ggggaacctg	ctcatcatcc	tggccataag	catagactcc	60
cgccctgcaca	cccccatgta	cttcttcctc	agcaacatgt	cctttgtgga	caactgcttc	120
tccaccaccg	tccccaagat	gctggccaat	cacatactca	ggactcaaac	catctccttc	180
tctggctgtc	tcatgcagat	gtattttatc	agtgagcttg	ctgacatgga	caatttcctc	240
ctggctgtga	tggcctatga	ccgctttgtc	gccgtgtgcc	gccccttaca	ttacacagca	300
aagatgaccc	atcagctctg	tgcctgtctg	gtcactggat	catgggtggg	tgccaactcg	360
aatgctctgc	tgcacaccct	gctgatggct	cgactctcat	tctgtgcaga	caacaccatc	420
ccccacatct	tctgcgatgt	gactcccttc	ctgaaactct	cctgttcaga	cacacacctc	480
agtgaagtga	tgattcttac	tgaggetgcc	ctagtcaaga	tcacccatt	tctttgcctc	540
ctggcttctc	atatgcacat	cacctgcgtt	gtcctgaggg	tcccatccac	aaagggaaga	600
tggaaagcct	tctccacctg	tggctcccac	ctggctgtgg	ttctcctctt	ctatggcacc	660
atcatgtctc	catatttcag	aacttcaccc	tcccactcag	ctcagagaga	tatagcagct	720
gctgtgaggt	tcacagtggg	gactcccggt	atgaatcctt	tgatctacag	cctgaggaac	780
aaggacataa	aaggggctct	tgtaaaagtg	gttgctgtga	aatttttttc	tgttcaa	837

<210> 169

<211> 770

<212> DNA

<213> Unknown (H38g17 nucleotide)

<220>

<223> Synthetic construct

<400> 169

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cttggtgctt	atctctgcat	actggtggac	aacatctcaa	ttattgtggg	accagggga	120
tatttttaggg	gagcaccaaa	tgcatcattt	tagctgtgac	gtctttggat	ccttacattg	180
ccatctgcaa	acacttgagg	taccagcta	tcatgcatca	gcaactctgt	gtcctcctag	240
tggccatggc	atggctaagc	agtttggcca	actctacttc	agtcatccct	tgccgtccag	300
ctgccactag	gcggttaaaa	ggtggacgac	tttctgtgtg	aggtctcagc	gatgatcaag	360
atatcacgtt	ttgacaccac	attcaatgta	tctatgctct	ccattgtgag	gatatttttag	420
tccctcgttc	tctaataaat	tatctttgct	tactgtggat	tcattgtagc	tactgtgctg	480
aggattcagt	cctcaggggg	aaagaaggag	gtcttcaaca	catgtgggtc	tcataattgta	540
tctctcctct	atgggcctgt	aattagcatg	tatgtacagc	cctctgcca	ctcccaggac	600
aaaaacaaat	tcatgtccct	gttctacagt	ttggtgactc	ctatgcttaa	cccttttatc	660
tacactttga	gcaacaggga	cataaaaggg	gcaatgagga	ggcttcttgt	ctttttgtat	720
caccaggaag	agaacaaaag	taattatttt	tatactccac	attcttcata		770

<210> 170

<211> 1003

<212> DNA

<213> Unknown (H38g18 nucleotide)

<220>

<223> Synthetic construct

<400> 170

tctacagacc	cacagaatgt	aacggatgtc	tctcgattcc	tcctcctcaa	actctcagag	60
gatccagaac	tgcagccggt	ccttgctggg	ctgttctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	cacttccatg	180
tactttcttc	tctccaacct	gtccttgcc	gacatcggtt	tcccctcccc	cacgggtcccc	240
aagatgggtg	tggacatcca	atctcacagc	agtcattctc	tatgcagggt	gcctgactca	300
gatgtctctc	tttgccattt	ttggaggcat	ggaagagaca	catgctcctg	aatgtgatgr	360
cctatgtccg	gtttgtagcc	atctgtcacc	ctctatatca	ttcagccatc	atgaaccctg	420
gtttctgtgg	cttcttactt	ttgttgtctt	ttttttttct	cgggtctttta	gacgcccagc	480
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tctgtgatcc	ttctcaacte	ccccatcttg	catgttgtga	caccttcacc	aataacatca	600
tcattgtatt	ccctgtctgc	gtatttgggt	tccttcccat	ctcggggacc	cttttctctt	660
actctaaaat	tggttctctc	attctgaggg	tttcgtcatc	aggtgggaag	tataaacctt	720
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caagatggtc	acccccatgc	tgaaccctc	catctacagc	ctgagaaaca	gggatattaa	900
aagtgtcctg	cggcagccgc	acggcagcac	ggtctaattc	caagaccttc	ttatctgttc	960
cattcctttt	gtagtgtggg	ttaaaaaagg	cagcaagggtc	aaa		1003

<210> 171

<211> 998

<212> DNA

<213> Unknown (H38g19 nucleotide)

<220>

<223> Synthetic construct

<400> 171

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tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtatt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
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atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtgggtg	gagatgggtc	tgctcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccctctc	actatctgac	cattatgagc	ccaagaatgt	420
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ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttcttg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 172

<211> 1018

<212> DNA

<213> Unknown (H38g20 nucleotide)

<220>

<223> Synthetic construct

<400> 172

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gatccagaac	tgcagccggt	cctcgctggg	ctgttctgt	ccatgtgcct	ggtcacgggtg	120
ctcaggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tactttcttc	tctccaacct	gtcctttctc	gacagtcgtt	tcacctccac	cacagtcctcc	240
aagatgattg	tggacatcca	gtctcacagc	agagtcattc	cctatgcagg	ctgcctgact	300
cagatgtctc	tctttgccat	ttttggagac	atggaagaga	gacatgttcc	tgagtgtgggt	360

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ggcctatgac cggttttag ccatctgtca ccctttatat cgttcagcca tcttaaacc 420
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tcaccaggaa catcaacctg tatttccctg ctgccatatt tggttttctt cccatctcgg 660
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aaacggggat attaaaagt tcttgcgga gccgcacggc agcacagtct aatctcaata 960
tcttcttate tgttccatc cttttgtagt gtgggttaaa aaaggcagca aggtcaaa 1018

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<210> 173

<211> 942

<212> DNA

<213> Unknown (H38g21 nucleotide)

<220>

<223> Synthetic construct

<400> 173

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ccagagctcc agctttttct gttcctgtct tgcctcatca tgtacatgat aatcctcctg 120
ggaaatagcc tctcattat catcaccatc ttggattctc gcctccatac tcccatgtat 180
ttctttcttg gaaacctctc attcttggac atctgttaca catcctcatc cattcctcca 240
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gaccactatg tggccatctg caaccactg aggtactcca tcatcatgaa cggagtgtctg 420
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aaacccaagt caaagaacac taatacatct gatgagatta ttgggctgtc ttatggagtg 840
gtaagcccaa tgttaaattc catcatctat agcctcagga ataaagaggt caaagaggct 900
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<210> 174

<211> 958

<212> DNA

<213> Unknown (H38g22 nucleotide)

<220>

<223> Synthetic construct

<400> 174

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atggagaaaag tcatgtttgc agtatTTTTG gttctttaca tgataacact ttcaggcaac 120
ctgtcctctg tggttacaat taccaccagc caggctctta gctcccccat gtacttcttc 180
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gaagaacaca tttttggtgc tactgagatc atcctgctga cagtgtatggc ctgtgacaac 360
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ctcctagtgg tagtggcctg gataggagga tttctccatg caaatattca gattctattt 480
acagtatggc tgccttctg tggccccaat gtcatagacc acttcatgtg tgactgtgtc 540
cctttgttaa aacttgtttg cctggacact catacccttg gtctctttgt tgcctgccaac 600
agtgggttca tctgcttatt aaacttctt ctctaggtgg tatectatgt gatcatcttg 660
agatgtttta agaactatat cttggagggg aggggtaaaag ccctctccac ctgtatttct 720
cacatcataa tagttgtctt attctttgtg ccttgtatat ttgtgtatct gcacccagtg 780
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aaatcctttg atctacacac tcagaaatgc tgaggtaaaa agtgcaataa ggaagctttg 900
gagaaaaaaa gttatttcag ataatgacta aataagacca ttgagcactc atcataga 958

<210> 175.

<211> 933

<212> DNA

<213> Unknown (H38g23 nucleotide)

<220>

<223> Synthetic construct

<400> 175

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gtgggctca	tgccctcag	ctgtttcctt	ctcctcctca	cctcctacag	tggcatcgtc	660
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ctgaaccctt	taatctacag	tctcaggaat	aaggaggtga	aattatcact	aaggaaggtc	900
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<210> 176

<211> 906

<212> DNA

<213> Unknown (H38g24 nucleotide)

<220>

<223> Synthetic construct

<400> 176

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gtacagagag	ttctctttgt	ggtctttttg	ctgatctatg	tggtcacggg	ttgtggcaac	120
atgctcattg	tggtcactat	cacctccagc	cccacgctgg	cttcccctgt	gtattttttc	180
ctggccaacc	tatcctttat	tgacaccttt	tattcttctt	ctatggctcc	taaactcatt	240
gctgactcat	tgtatgaggg	gagaaccatc	tcttatgagt	gctgcatggc	tcagctcttt	300
ggagctcatt	ttttgggagg	tggtgagatc	attctgctca	cagtgatggc	ttatgaccgc	360
tatgtggcca	tctgtaagcc	cctgcacaat	actaccatca	tgaccaggca	tctctgtgcc	420
atgctttag	gggtggcttg	gcttgggggc	ttcctgcatt	cattgggttca	gctcctcctg	480
gtcctttggt	tgcccttctg	tgggccaat	gtgatcaatc	actttgcctg	tgacttgtag	540
cctttgctgg	aagttgcctg	caccaatacg	tatgtcattg	gtctgctggg	ggttgccaac	600
agtggtttaa	tctgcctggt	gaacttcctc	atgctggctg	cctcctacat	tgctatcctg	660
tactccttga	ggtccacag	tgagatggg	agatgcaaag	ccctctccac	ctgtggagcc	720
cacttcattg	ttgttgctt	gttctttgtg	ccctgtatat	ttacttatgt	gcattcattt	780
tctactttac	ctatagacaa	aaatatggca	ttattttatg	gtattctgac	acctatgttg	840
aatccactca	tttataccct	gagaaatgaa	gaggtaaaaa	atgccatgag	aaagctcttt	900
acatgg						906

<210> 177

<211> 798

<212> DNA

<213> Unknown (H38g25 nucleotide)

<220>

<223> Synth tic construct

<400> 177

atgatcacac	tgattgggct	cagttctcac	ctgcacacac	ctatgtacta	tttcctcagc	60
agtctgtcct	tcattgactt	ctgccattcc	actgtcatta	cccctaagat	gctgggtgaac	120
tttgcgacag	agaagaacat	catctcctac	cctgaatgca	tggtcagct	ctattttatc	180
agtatttttg	ctattgcaga	gtgtcacatg	ttggctgcaa	tggtgatga	ctgttatgtt	240
gccatctgca	gccccttgct	gtacaatgtc	atcatgtcct	atcaccactg	cttctggctc	300
acagtgggag	tttacatttt	aggcatcctt	ggatctacaa	ttcataccag	ttttatgttg	360
agactctttt	tgtgcaagac	taatgtgatt	aaccattatt	tttgtgatct	tttcctctc	420
ttggggctct	cctgtctccag	cacctacatc	aatgaattac	tggttctggg	cttgagtgc	480
tttaacatcc	tgatgcctgc	cttaaccatc	cttgcttctt	acatctttat	cattgccagc	540
atcctccgca	ttcactccac	tgagggcagg	tccaaagcct	tcagcacttg	cagctccac	600
atcttggctg	ttgtgtttt	ctttggatct	gcagcattca	tgtacctgca	gccatcatct	660
gtcagctcca	tggaccagag	gaaagtgtcg	tctgtgtttt	atactactat	tgtgcccag	720
ctgaaccccc	tgatctacag	cctgaggaat	aaagatgtca	aacttgccgt	gaagaaaatt	780
ctgcatcaga	cagcatgt					798

<210> 178

<211> 954

<212> DNA

<213> Unknown (H38g26 nucleotide)

<220>

<223> Synthetic construct

<400> 178

atgggaaact	ctaatacagtc	tttcatgaca	gaatttgtcc	tgctggggct	ttctggctac	60
ccagagctag	aggccattta	ctttgtgctg	gtcctatgta	tgtatttggg	gatcctgttg	120
ggaaatggag	tcatacatcat	tgtgagtgtt	tatgacaccc	acttgcacac	ccccatgtac	180
tttttctca	gtaacttatc	attcttggac	atctgtctaca	ctagttcatc	tattccacta	240
tttctcagca	gcttcttaac	gtcaaagaaa	actatttctc	tctctgggtg	tggtgtgcaa	300
atgtttctct	cttttgctat	gggagcaaca	gagtgtgtcc	ttctaagtat	gatggcggtt	360
gactgctatg	tggccatctg	taaccctcta	tgatacccta	tcatacatgag	caaggcttca	420
tacatgtcca	tggctgcggg	gtcctggatt	ggaggaggca	tcaattctgt	gttgcaaacc	480
tcccttgcaa	tgcggcttcc	tttctgtgga	gataacgtca	ttaatcattt	tacttgtgaa	540
atcttggctg	tcttaaaaatt	ggcctgtgct	aatatctcca	taaaatattat	tagcatgggt	600
gttgctagta	tgatttttct	tgtagggccca	gtacttttta	tttttgttac	atatgttttt	660
attctctcca	ccatcctgag	aattccttct	gcagaaggaa	ggcacaagc	ctcctccacc	720
tgctctgccc	acctaacagt	gggtgattata	ttctacagaa	ccatcctttt	catgtatgca	780
aagcccaagg	ctaaagactc	ttctggtgca	gacaaaagaa	aagtcacaga	caaaatcatc	840
tccctgttct	atggagtggg	gacacctatg	cttaatcctc	ttatctatag	tttgaggaac	900
aaagacgtga	aggcagctgt	gaagagtata	ctgtgacaaa	aatgcttctt	ggaa	954

<210> 179

<211> 984

<212> DNA

<213> Unknown (H38g27 nucleotide)

<220>

<223> Synthetic construct

<400> 179

aaatctatga	aaaagatgaa	caatgtaata	gaattcatac	tgctgggcct	cactcacaat	60
ccagaactgc	agaaattctt	gtttgttatg	tttttaataca	cctacttgat	cacattggca	120
ggtaacctgt	tcatactcagt	catcatcttc	atcagcccgag	ccctggggtc	ccccatgtac	180
tcttttccgt	cctatttgtt	cattatagac	attttctgct	cttcttccat	agccccataa	240
atgaactttg	acttgatctc	tgaaaagaac	accatacctc	tcaatggctg	catgactcag	300
ctcttcacag	aacatttctt	tacagaacat	ttctttgagg	cagctgagat	catcttatta	360
agtgtcatgg	cctatgacca	ctatgtggcc	atccgtaagc	ccttgacta	tgcaaccatc	420
atgagccaac	ctatgtgtgg	attcctgatg	gtgggtggctg	ggattctggg	atttgtgcat	480

ggagggatcc	agactttgtt	catagcccag	ttaccattct	gtggcccca	tgatcatcaac	540
cactttatgt	gtgatttagt	acctcttctg	gagctggcct	gcacagacac	tcacaccttg	600
gggcctctga	ttgtcgccaa	cagtgggtca	ctgtgtttcc	tcattttttc	catgctgggt	660
gcttcctatg	tcacatcctt	gtgcttcctg	aggactcata	gctctgaagg	gcgtcgcaaa	720
gctctgtcta	gttgtgcctc	tcatatcttc	attgtcatct	tattctttgt	ccctttttca	780
tacctgtatc	taagacctaa	cctccttccc	cactgacaaa	gctgtgactg	tggtttgcac	840
cctatttaca	cctatgttga	accctttaat	ctacaccctc	aaaaataaag	aagtgaaaaa	900
tgatcattaag	aagctctgga	agcaataaat	gacaactgat	gataaataag	tcttgtgaca	960
caaacattta	ggcaagaata	tctg				984

<210> 180

<211> 954

<212> DNA

<213> Unknown (H38g28 nucleotide)

<220>

<223> Synthetic construct

<400> 180

atggaatggg	aaaaccacac	cattctgggtg	gaattttttc	tgaagggact	ttctgggtcac	60
ccaagacttg	agttactctt	ttttgtgctc	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcctc	ttggaccctc	accttcacac	ccctatgtac	180
ttctttctgg	ggaacctctc	cttcttggac	atctgtaca	ccaccacctc	tattccctcc	240
acgctagtga	gcttcctttc	agaaagaaag	accatttccc	tttctggctg	tgagtgagc	300
atgttctctg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caaccctctg	agatatccca	tcacatgag	taaggatgcc	420
tatgtaccca	tggcagctgg	gtcctggatc	ataggagctg	tcaattctgc	agtacaatca	480
gtgtttgtgg	tacaattgcc	tttctgcagg	aataacatca	tcaatcattt	cacctgtgaa	540
attctggctg	tcattgaaact	ggcctgtgct	gacatctcag	acaatgagtt	catcatgctt	600
gtggccacaa	taattgtcat	attgacacct	ttgttattaa	tcattgtctc	ttacccttta	660
atcattgtga	gcattctcaa	aattagctct	tccgagggga	gaagcaaagc	ttcctctacc	720
tggtcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtacatg	780
aagcccaagt	ctaaagagac	acttaattcg	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atgggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aagaggcagt	aaaacaccta	ctgaacagaa	ggttcttttag	caag	954

<210> 181

<211> 792

<212> DNA

<213> Unknown (H38g29 nucleotide)

<220>

<223> Synthetic construct

<400> 181

atggtagaca	acctaatacat	tgtggtgaca	atcaccacca	gcccagccct	ggactccccc	60
gtgtattttt	ttctgtcttt	cttttccttc	atagatggct	gctcctcttc	taccatggcc	120
cccaaaatga	tatttgactt	actcactgaa	aagaaaacta	tttccttcag	tgggtgcatg	180
acccagctct	ttgtagaaca	tttctttggg	ggagttgaga	tcattctgct	cgtggtgatg	240
gcctatgact	gctatgtggc	catctgcaag	cccctgtact	acctgatcac	aatgaacagg	300
caggtatgtg	gcctcctggg	ggccatggca	tgggtcgggg	gatttcttca	cgctctgatt	360
caaatgcctt	taatagcttg	gctgcccctc	tgtggcccca	atgtcattga	ccatttcac	420
tgtgaccttt	tccctctgct	aaaactctcc	tgactgaca	ctcacgtctt	tggactcttt	480
gttgccgcca	acagtgggct	gatgtgtatg	ctcatttttt	ctattcttat	tacctcttac	540
gtcctaatac	tctgtccaca	gcggaaggct	ctctctacct	gcgccttcca	tatcactgta	600
gtcgtcctat	tctttgttcc	ctgtatatgt	gtgtaccttc	gacccatgat	caccttccct	660
attgataaag	ctgtgtctgt	gttttatact	gtggtaaacac	ccatgttaaa	ccctttaatc	720
tacacctca	gaaacacaga	ggtgaaaaat	gccatgaagc	agctctggag	ccaaataatc	780
tgggtaaca	at					792

<210> 182

<211> 936
 <212> DNA
 <213> Unknown (H38g30 nucleotide)

<220>
 <223> Synthetic construct

<400> 182
 atgtggccca atattactgc agcccccttt ttgctgactg gttttccagg gctggaggca 60
 gctcatcaact ggatctccat ccccttcttt gctgtttatg tgtgcatcct tctgggcaat 120
 ggcatgctcc tctacctcat caagcatgac cacagtcttc atgagcccat gtactacttc 180
 ctcaccatgc tggcaggcac agacctcatg gtgacattga ccacgatgcc tactgtaatg 240
 ggcatcctat gggatgaatca caggagatt agcagtgtgg gctgcttcct acaggcttac 300
 tttattcact ccccttctgt tgtggaatca ggttccctcc tggcaatggc atatgatcgt 360
 ttcattgcca tccgcaatcc tttgagatat gcttccattt tcaccaatac tagagtcata 420
 gcgttaggag tgggagtgtt tctaaggggt tttgtatcca tcctgcctgt aattttgcgt 480
 cttttttcat tttcatattg caaatctcat gttatcacac gtgctttctg cctccaccaa 540
 gaaatcatga gactggcttg tgctgacata actttcaata gactttaccc tgtaattttg 600
 atctctttta caatcttctt agactctctg atcatcctct tctcctatat tctaattctt 660
 aatactgtca taggcattgc ctctggtgaa gagagagcca aagccctcaa tacctgtatc 720
 tcccacatta gttgtgttct tatcttctat gttacggtga tgggtttgac attcatttac 780
 agatttgagg agaattgtgcc agaggttgtc cacattatca tgagttacat ctacttcctc 840
 tttctcctt taatgaacct tgcatctac agcatcaaaa ccaagcaaat acaatatggc 900
 attatccgcc ttttatctaa acataggttt agtagg 936

<210> 183
 <211> 854
 <212> DNA
 <213> Unknown (H38g31 nucleotide)

<220>
 <223> Synthetic construct

<400> 183
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 gatccagaac tgcagcccat cctcgctggg ctcttctgtt ccatgtacct ggtcacgggtg 120
 ctggggaacc tgctcattat cctggccatc ggctctgact cccacctga ccccccatg 180
 tacttcttcc tctccaacct gtcttgcct gacatcggtt tcacctcggc cacgggtcccc 240
 aagatgattg aggagatgca atcgcatagc agagtcattt accatgggga ctgctgacac 300
 agatgtcttt ctttgtcctt tttgcatgta aggatgacat gatcctgact gtgatggcct 360
 atgactgggt tgtggccatc tgtcaccctc tgaactaccc aggcacatg aatcctcacc 420
 tctgtgtctt attagtctt gtgcctttt tccttagcct gttggattcc cagctgcaca 480
 atttgattgt gttacaattc atctgcttca agaattgtga aatctctaatt ttttctgtg 540
 acccgtttca acgtctcaac cttgcctgtt ctgacagtga catcaataac atatacatat 600
 atttagatag tactatattt ggttttcttc gcatttcagg gatcctttt tgttactata 660
 cagttgtctt cccattctta agaattccat cctcagatgg gaattataaa gccttctcca 720
 cctgaggctc tcgcctggca gttgtttgtt tattttatgg aacaggcatt ggcgtgtacc 780
 tgacttcgcg tgtgtcatca tccccagga atgatgtggt ggcgtcagta atgtacgctg 840
 tgggtgtcac cccc 854

<210> 184
 <211> 951
 <212> DNA
 <213> Unknown (H38g32 nucleotide)

<220>
 <223> Synthetic construct

<400> 184
 atgggtgaga ttaaccagac acttgtgtca gaatttcttc ttctgggtct ttctggatac 60
 ccaaagattg agattgttta ctttgctctc attctagtta tgtacctagt gattctaatt 120

ggcaatggtg	ttctaatacat	agccagcacc	tttgattctc	attttcacac	accaatgtac	180
ttcttcctgg	gcaacctctc	tttctgggat	atctgctata	catcctcctc	tgttccctca	240
acattggtga	gcttaatactc	aaagaaaaga	aacatttctc	tctctggatg	tgcagtgcag	300
atgttctttg	gggttgcaat	ggggtcaaca	gaatgtctgc	ttcttggcat	gatggcattt	360
gatcggtatg	tggccatctg	caacccactg	agatacccca	tcacctctgag	caaggtggcg	420
tatgtattga	tggcttctgt	gtcctggctg	tccggtggaa	taaattcagc	tgtgcaaaca	480
ttacttgcca	tgagactgcc	tttctgtggg	aataatatta	tcaatcattt	cgcagtgtgaa	540
atattagctg	tcctcaagct	ggcctgtgct	gatatatccc	tcaatattat	caccatgggtg	600
atatcaaata	tggccttctc	ggttcttcca	ctgatgggtca	ttttttctc	ctatatgttc	660
atcctctaca	ccatcttgca	aatgaattca	gccacaggaa	gacgcaaggc	attttccacg	720
tgctcagctc	acctgactgt	ggtgatcata	ttttacggta	ccatcttctt	tatgtatgcg	780
aaaccgaagt	ctcaagacct	gattggggaa	gaaaaattgc	aagcattaga	caagctcatt	840
tctctgtttt	atggggtagt	gacacccatg	ctgaatccta	tactctatag	cttgagaaat	900
aaggatgtaa	aagctgctgt	aaaatatttg	ctgaacaaaa	aaccaattca	c	951

<210> 185

<211> 927

<212> DNA

<213> Unknown (H38g33 nucleotide)

<220>

<223> Synthetic construct

<400> 185

atgggtgcc	agaacaatgt	gactgagttt	gttttatttg	gcctttttga	gagcagagag	60
atgcagcata	catgctttgt	ggtattcttc	ctctttcatg	tgctcactgt	cctggggaaac	120
cttctggtca	tcataccat	caatgctaga	aagaccctga	agtctcccat	gtattttcttc	180
ctgagccagt	tgtcttttgc	tgacatatgt	tatccatcca	ctaccatacc	caagatgatt	240
gctgacactt	ttgtggagca	taagatcatc	tccttcaatg	gctgcatgac	ccagctcttt	300
tctgcccact	tctttggtgg	caatgagatc	ttcctcctta	cagccatggc	ctatgaccgc	360
tatgtggcca	tctgtaggcc	cctgcactac	acagccatca	tggattgccg	gaagtgtggc	420
ctgctagcgg	gggctcctcg	gttagctggc	ttcctgcatt	ccatcctgca	gacctcctc	480
acggttcagc	tgcttttttg	tgggccaat	gagatagaca	acttcttctg	tgatgttcat	540
ccctgctca	agttggcctg	tgcagacacc	tacatggtag	gtctcatcgt	ggtggccaac	600
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ctgaacctaa	gaagccagtc	atctgaggac	cggcgtaagg	ctgtctccac	atgtggctca	720
cacgtaatca	ctgtcctttt	ggttctcatg	cccccatgt	tcatgtacat	tcgtccctcc	780
accaccctgg	ctgctgacaa	acttatcatc	ctctttaaca	ttgtgatgcc	acctttgctg	840
aaccctttga	tctatacact	aaggaacaac	gatgtgaaaa	atgccatgag	gaagctgttt	900
aggggtcaaga	ggagcttagg	ggagaag				927

<210> 186

<211> 987

<212> DNA

<213> Unknown (H38g34 nucleotide)

<220>

<223> Synthetic construct

<400> 186

gctacttgcc	acttgtgaac	acacaatgcg	gctccttttt	tgtctgctgg	cttttcagta	60
ctggaggcaa	cttatcactc	gatctccatc	cccttctttg	ctgtttatgt	gtgcgtcctt	120
cttggaatg	gcaagctcct	ctacctcatc	aagcatgacc	acagtcttca	cgaacccatg	180
tactgtttcc	ttgccacact	gaggcaagac	ctcatggtga	aattgaccat	gatgccctct	240
gtaatgggcg	tcttgtggat	gaatcacaaa	gaggttatcc	atggggcctg	cttcttgcag	300
gtttacatta	tccactccca	ttatccactt	gcagaatcag	gtattctcct	gtcaatggcc	360
tatgaccgtt	tcattatcat	ccacatgctt	ctcaggtata	actctatttc	tactaaatct	420
tgggtgaaga	tagaactgtg	gctattttatg	agggaacttt	tatccctcgt	gcctccaatt	480
ctgccactcc	attgtctccc	atattgtcat	tcccatgttc	tcttccacac	ctttttcttc	540
catcaagatg	tctgaaact	tgctgtgct	gatattacat	tcaatcactt	ataccagct	600
attctgggtg	ctttgatttt	cttcttagac	gctctgatca	ttgtcttttc	ttatatcctg	660

atccttaaaa	cagttatagg	tattgcctcc	agaaaagagc	aagccaaagc	tctcaacatg	720
tgtgtctccc	atatcagctg	tgtctttgga	tttcacatca	ccgtgatcag	tgagactttc	780
attcacaggt	ttgggaacaa	tgcaccacat	gtgggtgcaca	ttaccgtgag	ctaatagactc	840
attttctttt	cctccattca	tgaaccctat	tatatacagc	atcaaaccac	gcagatccaa	900
agaagcattg	ttcgcctatt	ttctgggcac	agaatggctt	gagccctttt	ttcagaattt	960
tgtgatcttc	atgattttctg	ggcctttt				987

<210> 187

<211> 887

<212> DNA

<213> Unknown (H38g35 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(887)

<223> n = A,T,C or G

<400> 187

ctgctgctcc	tggtgctcct	gctgcccacg	ttcctgctga	gtcttntggg	gaacntgctc	60
atcatctcca	ctgtgctgtc	ctgctcccgc	ctccacaccc	ccatgacttc	ttcttgtgca	120
acctctctat	cctggacatc	ctcttcacct	cagtcattctc	tccaaaagtg	ttggccaact	180
taggatctag	ggataaaaacc	atctcctttg	ccggatgtat	caccagtgct	tattttctact	240
ttttcttggg	cacagttgag	ttcctcctgc	tgacgggtcat	gtcctatgac	tgctatgccg	300
ccatctgctg	ccccctgagg	tacaccacca	tcatgagacc	ttatgtctgc	attgggaccg	360
ttgtgttttc	ttgggtggga	ggcttcctgt	ctgtgctctt	tccaaccatc	ctcatctccc	420
agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	ggacccttgc	480
tggccctggc	ctgtgcagac	accactgcca	tcgagctgat	ggattttatg	ctttcttcca	540
tggtcatcct	ctgtgcata	gtcctcgtgg	cctatttcta	tacgtacatc	atcttgacca	600
taatgcgcac	tccttctgca	agtggaaagga	agaaggcctt	taataacctgt	gcttcccacc	660
tgaccatagt	catcatttct	agtggcatca	ctgtgtttat	ctatgtgact	ccctcccaga	720
aagaatatct	ggagatcaac	aagatccctt	cggttctgag	cagtttggtg	actccattcc	780
tcaacccttt	tatatatact	ctgaggaatg	acacagtgc	gggagtcctc	agggatgtgt	840
gggtcagggt	tcgaggaggt	ttcgaaaaga	ggatgagggc	agtgtctg		887

<210> 188

<211> 930

<212> DNA

<213> Unknown (H38g36 nucleotide)

<220>

<223> Synthetic construct

<400> 188

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ggcactcttc	ttgtcctcat	ttggaatgat	cacagcctcc	atgagcccat	gtactacttc	180
ctggctatgc	tggcagacac	ggaccttggg	atgacattca	ctacaatgcc	cacagtcctg	240
ggtgtcctgc	tgctagacca	gagggagatt	gcccatgctg	cctgtttcac	ccaatccttc	300
attcattcac	tggccattgt	agaatcaggt	atcttgcttg	ttttggccta	tgactgtttc	360
attgccatcc	gcacaccact	gaggtacaac	tgcattctta	ccaattcccg	agtgatgaac	420
ataggactgg	gggtactgat	gagagggttt	atgtccattt	tgcccataat	tctttcactc	480
tactgtacc	catattgttg	ttcccgtgcc	ctcttgacac	cattttgcct	ccatcaagat	540
gtcataaaac	tcgcctgtgc	tgatatacag	tttaatcaca	tatatccaat	tattcagact	600
tctttgactg	tctttttaga	tgctctaate	atcatctttt	cttatatact	aatccttaag	660
acagtgatgg	gcattgcgtc	tggacaagag	gaagctaaat	ctctcaacac	ttgtgtctcc	720
catattagct	gtgtcctagt	atttcacatc	actgtgatgg	gactgtcatt	cattcacagg	780
tttgggaaac	atgcacctca	tgtgggtccc	attaccatga	gctatgtcca	ttttctcttt	840
cctccattcg	tgaatcctat	catttatagc	atcaagacca	agcagattca	aagaagcatt	900
attcgcctat	tttctgggca	gagtagggct				930

<210> 189
 <211> 996
 <212> DNA
 <213> Unknown (H38g37 nucleotide)

<220>
 <223> Synthetic construct

<400> 189
 cacacagagc cacggaatct cacaggtgtc tgagaattcc tcctccttgg actcccagag 60
 gatccagaac tgcagccggt tctcgttttg ctctccctgt ccctgtccat gtatctggtc 120
 acggtgctga ggaacctgct catcatcctg gctgtcagct ctgtctctcc cctccacacc 180
 cccatgtact tcttctcttc caacctgtgc tgggctgaca tcggtttcac ctcgccacag 240
 gttcccaaga tgattgtgga catgcagtcg catagcagag ccatctctca tgcgggctgt 300
 ctgacgcaga tgtcttttct gttccttttt gcatgtatag aaggcatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt cgccctctgc actaccagc catcgtgaat 420
 cctcacttct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggattgtgtt acaattcacc atcttcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaaactt gcctgttctg acggcgctcat caatagcata 600
 ttcatatatt ttgatagtac tatgtttggt ttccttccca ttccagggat cctatggtct 660
 tactataaaa tcgtcccttc cattctaagg atttcatcgt cagatgggaa gtataaagcc 720
 ttctccacct gtggctctca ccaggcagtt gtttctgat tttatagaac aggcattggc 780
 atgtacctga cttcagctgt gtcaccaccc cccaggaatg gtgtggtggc atcattgata 840
 tacgctgttg tcactcccat gctgaacctt ttcactetaca gcctgagaaa cagggacata 900
 caaagtgcc tgcggaggct gtcagcaga acagtcgaat ctcatgatct gttccatcct 960
 ttttcttggt gggtagagaa gggcaaccac attaaa 996

<210> 190
 <211> 930
 <212> DNA
 <213> Unknown (H38g38 nucleotide)

<220>
 <223> Synthetic construct

<400> 190
 atgggagaca atataacatc catcagagag ttctcctac tgggatttcc cgttggccca 60
 aggattcaga tgctcctctt tgggctcttc tccctgttct acgtcttcac cctgctgggg 120
 aacgggacca tactggggct catctcactg gactccagac tgcacgcccc catgtacttc 180
 ttctctcac acctggcggt cgtcgacatc gcctacgcct gcaacacggt gccccggatg 240
 ctggtgaacc tcctgcatcc agccaagccc atctcctttg cgggcccgcg gatgcagacc 300
 ttctgtttt ccacttttgc tgtcacagaa tgtctcctcc tgggtggtgat gtccatgat 360
 ctgtacgtgg ccacttgcca cccctccga tatttgcca tcatgacctg gagagtctgc 420
 atcacctcgc cggtgacttc ctggaccact ggagtccttt tacccttgat tcatctgtg 480
 ttacttctac ctttaccctt ctgtaggccc cagaaaattt atcacttttt ttgtgaaatc 540
 ttggctgttc tcaaacttgc ctgtgcagat accacatca atgagaacat ggtcttggcc 600
 ggagcaattt ctgggctggt gggacccttg tccacaattg tagtttcata tatgtgcac 660
 ctctgtgcta tccttcagat ccaatcaagg gaagttcaga ggaaagcctt ccgcacctgc 720
 ttctcccacc tctgtgtgat tggactcgtt tatggcacag ccattatcat gtatgttgg 780
 cccagatatg ggaaccccaa ggagcagaag aaatatctcc tgcgttttca cagcctcttt 840
 aatcccatgc tcaatccctt tatctgtagt cttaggaact cagaagtga gaatactttg 900
 aagagagtgc tgggagtaga aagggtttta 930

<210> 191
 <211> 968
 <212> DNA
 <213> Unknown (H38g39 nucleotide)

<220>
 <223> Synthetic construct

<400> 191

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gatccagaac	tgcagcccg	cctcgctggg	ctgaccctgt	ccatgtacct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgact	cccacctcca	cacctccatg	180
tacttcgtcc	tctccaacct	gcgctgggtt	gacatcggtt	tcacctcggc	cacgggtccc	240
aagatgattg	tggacatgca	gtcgcatagc	agagtcattc	cttatgcggg	ctgcctgaca	300
cagatgtctt	tcttgggtctt	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatgtcc	360
tatgaccaat	ttttggccat	ctgtcacccc	ctgcactacc	cagtcacgt	gaatcctcac	420
ttctgtgtct	tcttagtttt	gggtgccttt	ttccttagcc	tggtggattc	ccagctgcat	480
agatggattg	tgttacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcaa	ccttgccctgt	tctgacagcg	tcataaatat	catattcata	600
tatttagata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaatgtgcc	cctccattct	aaggatgtca	ttgtcagatt	tgaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttttttgc	ttattttacg	gagcaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	accttccggc	aatgggtgtg	tggcttcagt	gatgtacact	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaagt	900
gccccgtgga	ggctgcgag	cacaacagtt	gaatctcatg	atctcttcca	tcctttttct	960
tggtgtctg						968

<210> 192

<211> 960

<212> DNA

<213> Unknown (H38g40 nucleotide)

<220>

<223> Synthetic construct

<400> 192

cacacagagc	cacagaatct	cacagggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcccat	cctggctgggt	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgacc	cccacctcca	cacccccatg	180
tgcttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	cacgggttct	240
aagatgattg	tggacatgca	gtctcatacc	agagtcattc	cttatgaggg	ctgcctgaca	300
cggatactct	tcttgggtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttcctttt	gggtatactt	ttccttagct	tggtggattc	ccagctgcac	480
agttggattg	tgttacaatt	caccatcatc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gacccctctc	aacttctcaa	acttgccctgt	tctgacagcg	tcataaatag	catattcatg	600
tatttccata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaatcgctc	cctccattct	aaggatttca	tcatacagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacttggc	agttgtttgc	tgattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	acccccagg	aatgggtgtg	tagcgtcagt	gatgtacgt	840
gtggtcaccc	ccatgctgaa	ccttttcatc	tacagcctga	gaaacaggga	catacaaagt	900
gccccgtgga	ggctgctcag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

<210> 193

<211> 980

<212> DNA

<213> Unknown (H38g41 nucleotide)

<220>

<223> Synthetic construct

<400> 193

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gatccagaac	tgcagccggt	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtaagggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	catgggtccc	240
aagatgattg	tggaaatccaa	tctcacagca	gagtcattct	ctatgcaggc	tgccctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaaagagag	acatgtctct	gagtgtgatg	360

gcctatgacc	ggtttgtagc	catctgtcac	cctctatatac	attcagccat	catgaacccg	420
tgtttctgtg	gcttcctagt	tttgctgtct	tttttttctt	tctttttctc	agctgcacaa	480
cttgattgcc	ttaaaaaatga	cctgcttcaa	gaatgtggga	attcctaatt	tcctctgtga	540
cccttctcaa	ctcccccatc	tcacatgttg	tgacaccttc	accaatcaca	taatcatgta	600
tttccccgct	gccatatttg	gttttcttcc	catctcgggg	acccttttct	cttaccatgt	660
aattgtttcc	tccattctga	gggtttcacc	atctgtggga	ggtgtaaaagc	cttccccatc	720
tgtgagttgt	ttgctgatat	tatggaacag	gctttggagg	gtacctcagt	tcagatgtgt	780
catcttccct	gagaaaggct	gcagtggcct	cagtgatgta	catggtggtc	acacccatgc	840
tgaaccctt	catctacagc	ctgagaaaca	gggatattaa	aagtgtcgtg	cagcggccgc	900
atggcagcac	ggtctaattc	caatatcttc	ttatctgttc	cattcctttt	gtagtgtggg	960
ttaaaaaagg	cagcaaggtc					980

<210> 194

<211> 939

<212> DNA

<213> Unknown (H38g42 nucleotide)

<220>

<223> Synthetic construct

<400> 194

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attcgaatat	ctctcttcgt	ggttcttggt	gtaacttaca	cattaacagc	aacaggaaac	120
atcaccatca	tctccctgat	atggattgat	catcgccctgc	aaactccaat	gtacttcttc	180
ctcagtaatt	tgtcctttct	ggatatctta	tacaccactg	tcattacccc	aaagtgtgtg	240
gcctgcctcc	taggagaaga	gaaaaccata	tcttttgctg	gttgcatgat	ccaaacatat	300
ttctacttct	ttctggggac	ggtggagttt	atcctcttgg	cgggtgatgtc	ctttgaccgc	360
tacatggcta	tctgcgaccc	actgcactac	acggtcacat	tgaacagcag	ggcctgcctt	420
ctgctggttc	tgggatgctg	ggtgggagcc	ttcctgtctg	tgttgtttcc	aaccattgta	480
gtgacaaggc	taccttactg	taggaaagaa	attaatcatt	tcttctgtga	cattgcccct	540
cttcttcagg	tggcctgtat	aaatactcac	ctcattgaga	agataaactt	tctcctctct	600
gcccttgtca	tcctgagctc	cctggcattc	actactgggt	cctacgtgta	cataatttct	660
accatectgc	gtatccccct	cacccagggc	cgtcagaaaag	ctttttctac	ctgtgcttct	720
cacatcactg	ttgtctccat	tgcccacggg	agcaacatct	ttgtgtatgt	gagacccaat	780
cagaactcct	cactggatta	tgacaagggt	gccgtgtccc	tcatcacagt	ggtgaccctt	840
ctcctgaacc	cttttatcta	cagcttgagg	aatgagaagg	tacaggaagt	gttgagagag	900
acagtgaaca	gaatcatgac	cttgatacaa	aggaaaact			939

<210> 195

<211> 737

<212> DNA

<213> Unknown (H38g43 nucleotide)

<220>

<223> Synthetic construct

<400> 195

atgggaaata	tcaacataag	tcttgaaaat	tactttattc	tactgggtct	ttctaattga	60
cctcctctgg	aaatagttat	ttttgtagtt	ctcttgatat	tctgcttcat	gacactgata	120
ggcaagctgt	tcagcatcat	tctgtcatat	ctggactccc	atccccacac	tctcggctact	180
tattctcttt	tctggatttc	tgctacacca	tcagttccat	cttttaatta	cagtacaatc	240
tctggggccc	acagaagaac	atctcttatg	ccagtgggat	gattcaaatt	tattttgttc	300
tcacactggg	aaccatggat	tgcgctctac	tggtgggtgat	gtccaggact	gtgatgcagc	360
tggacacaga	cacttgccct	atactgttgt	tatggctgtg	gctttttggg	taagtagctt	420
taccaactca	gcatttgatt	ccttttttac	cttctgggta	accctgtgtg	gacatcacta	480
ttatgcttac	atctttatat	ttacatcatt	gttagtataa	agatggttca	ttaacagaaa	540
gaaacagtct	gtgttctcac	tgaatcatgc	agctttatta	acattatctt	ttccattata	600
aatgactgc	ttccaggaga	ttgaaaagaa	catgttaaga	aaagcacagc	attggagaaat	660
ctgaaagcat	gtgatcttgt	tcaattaaac	caagtatcaa	aaacatgcat	ttttatgaga	720
ctatttttagg	aaattca					737

<210> 196
 <211> 949
 <212> DNA
 <213> Unknown (H38g44 nucleotide)

<220>
 <223> Synthetic construct

<400> 196
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 cagcttcaaa tttccctttt ggcagtcctc tggtttactt atatgcttac tctaacagga 120
 aacgttgcca tcatttccct aacatgtgcg aatcatcgcc tccaaacccc aatgtacttc 180
 ttccctcagta attgggtcaat ttgggacatt tttttcacca cctcagttat cccaaagcta 240
 ttagcctgtc tcctgcagga caagaagacc atatcttttg ctgggtgcat cacccaaact 300
 tatttcccttg gttttctggg ggacagtggg gtttatectc tgggcagtga tgtcctttga 360
 ctgctacgtg gccatctgtg accccctgca ctacaccatt atcatgaaca gcagggcctg 420
 cctcctacta gttctgggct gctgggttg agccttcctg tctgtgttgt gcccaaccat 480
 tgtgggtgtc agattgcctt tctgttacaa ggaaattagt cacttcttct gtgacatcac 540
 ccctctgcta catgtgtcct gtatagacac tcatttcac gagatgataa acttctctct 600
 atcttccctc atcctcctga cctcactggg gtcaccact gtgtcctaca tctacatcat 660
 ttctaccatc ctgcacatcc cctcagccca aggacgtcgg aaggcctttt ccacgtgcgc 720
 ttcccacatc accgtcattt ccatcgctta tataagcaac atcttcaggt atgtgaggcc 780
 cagccagagt cattcaatgg gttttgacaa ggtgacagct gtccccacaa tgggtgacccc 840
 tcttctgaat cccttcactt atagtctaag aaatgaaaag gtaaaggcag tcttgaaaga 900
 agcagtcagc aaaattatgt cctcatggca caggagaact taaaacttt 949

<210> 197
 <211> 930
 <212> DNA
 <213> Unknown (H38g45 nucleotide)

<220>
 <223> Synthetic construct

<400> 197
 atggaaccac agaaccacac acaggtatca atgtttgtcc tcttaggggtt ttcacagacc 60
 caagagctcc agaaattcct gttccttctg ttctgttag tctatgttac caccattgtg 120
 ggaaacctcc ttatcatggt cacagtgaact ttgactgcc ggctccacac acccatgtat 180
 tttctgctcc gaaatctagc tctcatagac ctctgctatt ccacagtcac ctctccaaag 240
 atgctgggtg acttccctcca tgagaccaag acgatctcct accagggctg catggcccag 300
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 tgtgtggggc tggtagtagc cgcctgggtg gggggctttg tccactccat tgtccaactg 480
 gctctgatac ttccactgcc cttctgtgac cccaatatca tagataactt ctactgtgat 540
 gttccccaaag tactgagact tgctgcact gatacctccc tctggagtt cctcatgatc 600
 ttcaacagtg ggctgctagt tatcatctgg ttctctctcc ttctgatctc ttatactgtc 660
 atcctggtga tgctgaggtc ccactcggga aaggcaagga ggaaggcagc ttccacctgc 720
 accaccacaca tcatcgtggt gtccatgatc ttcatctcct gtatctatat ctatacctgg 780
 cccttccccc cattcctcat ggacaaggct gtgtccatca gctacacagt catgaccccc 840
 atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900
 ttaggcaagt gcctagtaat ttgcagggag 930

<210> 198
 <211> 932
 <212> DNA
 <213> Unknown (H38g46 nucleotide)

<220>
 <223> Synthetic construct

<400> 198

gaccaagaaa	atcagacttc	tgaagtcacc	ttcatcctct	tgggcttctc	agaatatcca	60
gaccttcaga	cgccctgtt	cctgggtgtc	ctgaccatct	acacagtcac	tgtgctgggg	120
aatctgggca	tgatcatagt	catcaggatc	agccccaac	tccacacccc	catgtgcttt	180
ttcctcagcc	acttgtcctt	tgttgatttc	tgttattcca	ccacaattac	acccaaactg	240
ctggagaact	tggttgtgga	agatagaact	atctccttca	caggatgcac	catgcagtta	300
ttctttgtct	gcataattgt	agtaacagaa	acattcatgc	tggcagtgat	ggcctatgac	360
cgatatgtgg	cgggtgtgta	ccctcttctc	tacacagttg	caatgtacca	gaggctttgc	420
tccttggttag	tggctacatc	atactgttgg	gggtagtctt	gttccttgac	acttacctag	480
tttctactgg	aattatcctt	cagaggaaat	aatatcatta	ataactttgt	ctgtgagcac	540
gctgccattg	ttgctgtgtc	ttgctctgac	ccctgtgtga	gccaggagat	cacttttagtt	600
tctgccacat	tcaatgaaat	aagcagcctg	cttcctatgc	tttcattttt	atcactgtca	660
tgaagacgcc	ttccactggg	gggcgcaaga	aagcgttctc	cacgtctgcc	tcccacttga	720
cggccattac	cattttccat	gggactatcc	ttttcctcta	ctgtgttctt	aactccaaaa	780
gttcgtggct	catgggtcaag	gtggcctctg	tcttttacac	agtggtcatt	cccatgctga	840
acccttgat	ctatagcctc	aggaacaaag	atgtaaaaga	gacagttagg	aggttactca	900
ttaccaaat	attatgtctc	atattataaa	at			932

<210> 199

<211> 1000

<212> DNA

<213> Unknown (H38g47 nucleotide)

<220>

<223> Synthetic construct

<400> 199

tatgcagacc	cacagaatct	aacagatgtc	tctatatctc	tcctcctaga	agtctcaggg	60
gatccagaac	tgacgccagt	ccttgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgattg	tggacatcca	gtctcacagc	agagtcactc	cctatgcagg	ctgcctgact	300
cagatgtctc	tctttgccat	ttttggaggc	atggaagaga	gacatgctcc	tgagtgtgat	360
ggcctatgac	tggtttgtag	ccatctgtca	cccgtatat	cattcaccat	catgaacccg	420
tgtttctgtg	cctttctagt	tttgttgtct	tttttttct	cagtctttta	gactcccagc	480
tgcacaactt	gattgcctta	caagtgcct	gcttcaagga	tgtggaaatt	cctaatttct	540
tctgtgaccc	ttctcaactc	tcccatcttg	catgttgtga	caccttcacc	attaacataa	600
tcatgtatct	ccctgctgcc	atatttggtt	ttcttcccat	cttggggacc	cttttctctt	660
tctctaaaat	tgtttctctc	attctgaggg	tttcttcac	aggtgggaag	tataaagccc	720
tctccacctg	tgggtctcgc	ctgtcagttg	tttgtctagt	ttatggaaca	ggcgttggag	780
ggtacctcag	ttcagatgtg	tcatcttccc	ccagaaaggg	tgcagtggcc	tcagtgatgt	840
acacactgg	cacccccatg	ctgaccccc	tcatctacag	cctgagaaac	agggatatga	900
aagggtcct	gcggcagccg	cacggcagca	cagtctaate	tcaatatctt	atctgttcca	960
ttcctttgta	gtgtgggttc	aaaaaggcag	caaggtcaaa			1000

<210> 200

<211> 921

<212> DNA

<213> Unknown (H38g48 nucleotide)

<220>

<223> Synthetic construct

<400> 200

atggaaacag	ggaacctcac	gtgggtatca	gactttgtct	tcctggggct	ctcgcagact	60
cgggagctcc	agcgtttcct	gtttctaatg	ttcctggttg	tctacatcac	cactgttatg	120
ggaaacatcc	ttatcatcat	cacagtgcac	tctgattccc	agctccacac	acccatgtac	180
tttctgctcc	gaaacctggc	tgtcctagac	ctctgtttct	cttcagtcac	tgctcccaaa	240
atgctagtgg	acctcctctc	tgagaagaaa	accatctctt	accagggctg	catgggtcag	300
atcttcttct	tccacttttt	gggaggtgcc	atgggtcttct	tcctctcagt	gatggccttt	360
gaccgcctca	ttgccatctc	ccggcccttc	cgctatgtca	ccgtcatgaa	cactcagctc	420
tgggtggggc	tggtggtagc	cacctgggtg	ggaggctttg	tccactctat	tgtccagctg	480

gctctgatgc	tcccaactgcc	cttctgtggc	cccaacattt	tggataactt	ctactgtgat	540
gttccccaaag	tactgagact	tgcttgcact	gacacctcac	tgctggagtt	cctcaagatc	600
tccaacagtg	ggctgctgga	tgctgtctgg	ttcttccctcc	tcctgatgtc	ctacttattc	660
atcctgggtga	tgctgagggtc	acatccaggg	gaggcaagaa	ggaaggcagc	ttccacctgc	720
accacccaca	tcategtggt	ttccatgata	ttcgttccaa	gcatttacct	ctatgcccgg	780
cccttcactc	cattccctat	ggacaagctt	gtgtccatcg	gccacacagt	catgaccccc	840
atgctcaacc	ccatgatcta	taccctgagg	aaccaggaca	tgcaaggcagc	agtgagaaga	900
ttagggagac	accggctggt	t				921

<210> 201

<211> 947

<212> DNA

<213> Unknown (H38g49 nucleotide)

<220>

<223> Synthetic construct

<400> 201

cacacagagc	cacagaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gateccagaac	tgacagccgt	cctcgctttg	ctctccctgt	ccctgtccat	gtatctgggc	120
atggtgctga	ggaacctgtc	cagcatcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccacctgtg	ctgggctgac	atcggtttca	ccttggccac	ggttcccaag	atgattgtgg	240
acatgcagtc	gcatagcaga	gtcatctctc	atgcgggctg	tctgaagcag	atgtctttct	300
tcctcctttt	tgcatgtata	gaaggcatgc	tcctgactgt	gatggcctat	gactgctttg	360
tagccatctg	tcgcccctctg	cactaccag	tcctcgtgaa	tcctcacctc	tgtgtcttct	420
tcgttttggg	gtcctttttc	cttagcctgt	tggaattccca	gctgcacagt	tgaattgtgt	480
tacaattcac	catcatcaag	aatgtggaaa	tctctcattt	ttctctgtgac	ccctctcaac	540
ttctcaaat	tgccgtgtct	gacagcgtca	tcaatagcat	attcatatat	ttcgatagta	600
ctatgtttgg	ttttcttccc	atttcaggga	tcctatgggc	ttactataaa	atcatccctc	660
ccatttctaag	gatttcatca	tcatatggga	agtataaagc	cttctccaca	tgtgcctctc	720
acctagcagt	tgtttgctga	ttttatgtaa	caggcattgg	catgtacctg	acttcagctg	780
tgtcaccacc	ccccagcaat	ggtgtagtgg	cgtcagtgat	gtatgctgcg	gtcactccca	840
tgctgaaccc	tttcatctac	agcctgagaa	acagggacat	acaaagtgcc	ctgcggagggg	900
tgctcagcag	aacagtcgaa	tttcatgata	tgttccatcc	tttttct		947

<210> 202

<211> 369

<212> DNA

<213> Unknown (H38g50 nucleotide)

<220>

<223> Synthetic construct

<400> 202

atgtctgggt	ccccactca	actgacagca	ggccccagga	cagccagtgg	ctgtgtcatc	60
atgatctgct	ttgccctcac	tgtcctctct	tacatccgca	tcttggccac	agtggttcag	120
atccgttcag	cagccagccg	cgggaaggcc	ttctccacct	gttcttccca	cctgggcatg	180
gtgctcctgt	tctatggcac	cggcagctcc	acctacatgc	gaccaccac	ccgctactcc	240
ccgctggaag	ggcgcttggc	tgctgtcttc	tactccatcc	tcataccac	cctgaatccg	300
ctcatctaca	gcctgaggaa	ccaggacatg	aagagagccc	tgtggaagct	ctatctccag	360
gtgccatac						369

<210> 203

<211> 1068

<212> DNA

<213> Unknown (H38g51 nucleotide)

<220>

<223> Synthetic construct

<400> 203

atgatcaatg	atagccactt	cagtgggtttt	atactccttg	gattcacagg	gcagcctcag	60
cttcagatga	tgatctctgg	ggttgtcttt	ttcttctaca	ctattgcctt	catgggaaat	120
atggccatca	tcctattgtc	tttccctagat	gaccatctcc	aagtcctccat	gtactttcttc	180
cttagaaatt	tggccatctt	ggatctctgt	tataccacaa	atatagtccc	acaaatgttg	240
gtcagtatct	ggggcaaaga	caaaagaatt	accttttggtg	ggtgtgcctt	tcaacttttc	300
attgatgtgg	cactgtactc	agttgaatgc	atccttctgt	ccatgatgtc	atatgatcga	360
ctcaatgcta	tctgcaagcc	tctgcatcat	atgaccataa	tgaacctcca	actctgccag	420
ggccttgtgg	tcctctctctg	ggtagttggt	gtgattaatt	gcatcatacc	ttcccccttat	480
gccacgagtc	ttcctcgatg	taggaaccac	cacctagacc	acttttttgt	gtgtgtgaaa	540
tgtctgcaat	gatcaagatt	caagattgca	tgtgtggaca	ccacagccat	ggaggtaacc	600
acatttgcca	tgtgcctgat	tatagttctt	gttcctcttc	ttcttattct	tgtgtcatat	660
ggtttcattg	ctgtggctgt	actcaagatc	aagtctgcag	caggaagaca	aaaagcattt	720
gggacctgtt	cctccccatct	cgttgtggta	tccatcttct	gtgggacagt	tacatacatg	780
tatatacagc	caggaaacag	tccaaatcag	aatgagggca	aacttctcag	tatatattac	840
tccattgtta	ctcccagctt	gaacccatta	atttatacgg	taaggaataa	ggagttcaag	900
ggggccatga	agaggctaac	tggaaaagaa	aaagattgca	tggaaaaaag	aggacattga	960
ttcttctctc	cagcaatttc	taatatggca	attgatcttc	ccaatctaaa	atgtagacaa	1020
tttattttgt	aaataaattg	tctacacctg	agataaagat	aatatcca		1068

<210> 204

<211> 949

<212> DNA

<213> Unknown (H38g52 nucleotide)

<220>

<223> Synthetic construct

<400> 204

atgatcaatg	atagttactt	tggttggctt	atgctccttg	ggttccctgg	gaagcctcag	60
ctggagatga	tcctctctgg	ggttgtcttt	ttcttctatg	caatttcttt	gatgggaaat	120
atggctctta	tcctgctgcc	attactggat	aaacatctcc	aaacccccat	atatttcttt	180
cttagaaatc	tggctatctt	ggatctttgt	tacaccacaa	atatagtccc	acagatgttg	240
gtcaatgcct	ggggtaaaga	caagaaaatc	acttttggtg	gctgtgcttt	tcaacttttc	300
actaatgtga	cgctatgcac	ggttgaatgt	atgcttcttg	ctgtgatgtc	atatgacca	360
ttcaatgctg	tctgcaagcc	tctggactat	atgaccataa	tgaaccccc	actctgtcaa	420
ggcctgggtg	ccatgacctg	gttaattggt	gtcactaatt	gcatgatact	ttccccctgt	480
cctgtgagtc	ttcctcgatg	cggagaccac	cacctggatc	actatttttg	tgaatatatct	540
gcaatgggtca	aaattgcatg	tggggctacc	acagtcatgg	aggaaaaaac	ttatttgcac	600
tgtgttgttg	ttgttgtttt	cattttcctt	gcatcacttc	ttctcattct	tgtgtcatat	660
ggcttcattg	ctgtggctgt	actcaagatc	aagtctgcag	caggaagaca	aaaagcattt	720
gggacctgtt	tctcccatct	cattgtggta	tccatcttct	atgggactgt	tagatatatg	780
tatatagagc	caggaaacag	tccatctcag	gatgagggca	aacttctcca	tatatattac	840
tccattgtta	ctcccacett	gaacccatcc	cactaaggaa	taaggagttc	aagtgggcca	900
tgaaaaggct	tattggaaaa	gaaaaagggt	ctggagacac	aatagggtca		949

<210> 205

<211> 936

<212> DNA

<213> Unknown (H38g53 nucleotide)

<220>

<223> Synthetic construct

<400> 205

atggttaacc	aaagctccac	accgggcttc	ctccttctgg	gcttctctga	acaccagggg	60
ctggaaagga	ctctcttctg	ggttgtcttc	acttctctacc	tcctaaccct	agtgggcaac	120
acactcatca	tctgctgtgc	tgcgctggac	cccaagctcc	actctccaat	gtactttttc	180
ctctccaacc	tctcttctt	ggacctctgt	ttcaccacga	gttgtgttcc	ccaaatgttg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttctctg	actgctctgt	ccagatcttc	300
atcttctctg	ccctggggac	aactgagtgc	atcctcttga	cagtgtatgg	ttttgatcgc	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccg	cctgtgctgg	420

cagctggcat	ctgtggcctg	ggtcattggg	ctagtggagt	cagtgggtcca	gacaccatcc	480
accctgcacc	tgcccttctg	ccccgatcgg	caggtggatg	attttgtctg	tgaggtccca	540
gctctaattc	gactctcctg	tgaagacacc	tcctacaatg	agatccaggt	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcatccttg	tctcttacgg	agccattacc	660
tgggcagtgc	tgaggattaa	ctctgcaaaa	gggcggagga	aagcttttgg	gacctgtccc	720
tcccatctca	ctgtggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccct	atgccaaga	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttcactta	accctctcat	atacaccctg	aggaacaagg	aggtaaccag	ggcattcagg	900
agattgctgg	ggaaggaaat	ggggctcaca	caaagc			936

<210> 206

<211> 1030

<212> DNA

<213> Unknown (H38g54 nucleotide)

<220>

<223> Synthetic construct

<400> 206

atgggtaacc	aaagctccgc	accaggcttt	ctccttctgg	gcttctctga	acaccagca	60
ctggaaagga	ctctctttgt	agttgtcttc	acttctacc	tcctaacc	ggaggactca	120
tcactctgct	gtctgtgctg	gacccaggc	tcactctcc	aatgtacttt	ttcctctcca	180
acctctcctt	cttggaacctc	tgtttcacca	taagtgtgt	ccccgggatg	ctgggtcaacc	240
tctgggagcc	aaagaagacc	atcatcttac	tgggctgctc	tgtccagttc	ttcatcttcc	300
tgtccctggg	gaccactgag	tgcatectcc	tgacgggtgat	ggcctttgac	cgctacatgg	360
ctatcttcaa	gcccctgcgc	catgccacca	tcgtccacct	ctgcctgtgc	tggcagctgg	420
catctgtggc	ctgggtcatt	gggctggtag	agtcagtggg	ccagacacca	tccaccctgc	480
gcctgccttt	ctgcccccat	cagcagggtg	atgattttgt	ctgtgagggtc	ccagctctaa	540
ttcgactctc	ctgtgaagac	acctcttaca	atgagatcca	gatggctggt	gccagtgctc	600
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ctaaggacta	actgcaaaag	ggcagaggaa	agcttttggg	acctgtctct	cccactctac	720
tgtgggtcacc	ctcttctaca	gctcagtcac	tgctgtctac	ctccagccca	aaaatcccta	780
tgcccaagag	aggggcaagt	tctttgggtc	cttctatgca	gtgggcactc	cttcacttaa	840
ccctctcata	tacaccctga	ggaacaagga	ggtaaccagg	gcattcagga	gattgtctggc	900
gaaggaaatg	gggtctatac	aaagttgagg	gagagctgtt	taatgtgctt	tctaaattaa	960
gaagaaatta	tttatccttt	tgtgaacaag	tttgagctcc	caagtatact	acctttcata	1020
caccatcac						1030

<210> 207

<211> 873

<212> DNA

<213> Unknown (H38g55 nucleotide)

<220>

<223> Synthetic construct

<400> 207

atgttcgccc	cccttgctct	cctgtgctac	ctcctgacct	tgacgggcaa	ctcggcgctg	60
gtcgtgctgg	cggtgcgcga	cccgcgcctg	cacacgcccc	tgtactactt	cctctgccac	120
ctggccttgg	tagacgcggg	cttcaactact	agcgtgggtc	cgccgctgct	ggccaacctg	180
cgcgaccag	cgctctggct	gccgcgcagc	cactgcacgg	cccagctgtg	cgcatcgctg	240
gctctgggtt	cgccgaatg	cgctctcctg	gcgggtgatg	ctctggaccg	cgccggccaag	300
aaagtgaagg	gggcagcgag	gaggctgctg	cggagtctgg	ggagaggcca	ggctgggcag	360
agcgctcct	ggctaagcgg	cctcaccaac	tcggttgccg	aaaccgcgct	cctggctgag	420
cgcccgctgt	gcgcgccccg	cctgctggac	cacttcatct	gtgagctgcc	ggcggttgctc	480
aagctggcct	gcggaggcga	cggagacact	accgagaacc	agatgttcgc	cgcccgcgctg	540
gtcatcctgc	tgcgtccgtt	tgccgtcate	ctggcctcct	acgggtgccgt	ggcccgagct	600
gtctgttgca	tgcggttcag	cggaggcccg	aggaggcccg	tgggcacgtg	tgggtccac	660
ctgacagccg	tctgcctgtt	ctacggctcg	gccatctaca	cctacctgca	gcccgcgcag	720
cgctacaacc	aggcacgggg	caagttcgta	tcgctcttct	acaccgtggg	cacacctgct	780
ctcaaccgcg	tcatctacac	cctcaggaat	aagaaagtga	agggggcagc	gaggaggctg	840

ctgcggagtc tggggagagg ccaggctggg cag

873

<210> 208

<211> 921

<212> DNA

<213> Unknown (H38g56 nucleotide)

<220>

<223> Synthetic construct

<400> 208

gagctgatta	cgaattcgag	ctcgggtaccc	tcttgtgagc	ggacaattca	gatcttcctc	60
ttctcactca	taactacaat	atatgcactg	actataacag	gtaatggagc	cattgctttt	120
gccctgtggt	gtgaccggcg	acttcacact	cccatgtaca	tggtcctggg	agatttctcc	180
tttttagaga	tatggtatgt	cttttctaca	gttcccaaga	tggttggtcaa	cttcctttca	240
gagaaaacaa	acatctcctt	tgctggattg	cttttctccag	atctatttct	tcttctcttt	300
gatacatcag	aatgcttgct	tttgactgtg	atggcctttg	atcagaacct	tgctatctgc	360
cggcccttgc	actatcctaa	tatcatgact	gggcatctct	gtgccaaact	ggccatactg	420
tgctggggtt	gtggctttct	gtgggttcctg	atccccatth	tctcatctct	cagatgccct	480
tctgtggccc	aaacattatt	gaccatgttg	tgtgtgaccc	agggccacta	tttgcatagg	540
attgtgtttc	tgcccaaga	atccaactgt	tttgctacac	tctaagctca	ttagttattt	600
ttggtaactt	cctctttatt	attggatcct	atactattgt	cctgaaagtt	gtgttgggta	660
cgccttcaag	cactgggaga	cataaggcct	tctctacctg	tggttctcat	ttggctgtgg	720
tatcactgtg	ctatggctct	cttatgggtca	tgtatgtgag	cccaggactc	ggacattcta	780
cggagatgca	gaaaattgta	actttgttct	atgctatggg	gacctcactc	ttcaatcccc	840
ttatctatag	gcctccagaa	taaggagata	aaggcagcct	tgaggaaagt	tctgggtgagt	900
tccaacataa	tctaaggcat	a				921

<210> 209

<211> 660

<212> DNA

<213> Unknown (H38g57 nucleotide)

<220>

<223> Synthetic construct

<400> 209

gcatgtaagc	atgcatgac	ctgactgtga	tggcctatga	ctgcttagta	gccatctgtc	60
gccctctgca	ttaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	gttttgggtg	120
ccttctcatt	agcatgtagg	ttcccagctg	cacagttgaa	ttgtgttaca	attcaccatc	180
atcaagaatg	tggaaatctc	taattttgtc	tgtgacccct	ctcaatttct	caaacttgcc	240
tgttctgaca	gcgtcatcaa	tagcatattc	acgtatttcc	atagtactat	gttttgggtt	300
cttcccattt	cagggatcct	tttgtcttac	tttaaaatcg	tcaccttcat	tctctggatt	360
tcatcttcag	atgggaagta	taaagccttc	tccacctgtg	actctcacct	agcagttggt	420
tgctgatttt	atggaacagg	cattggcggtg	tacttgactt	cagctctgtc	accaccccc	480
aggaatgggtg	tgatggcgtc	agtgatgtac	gctgtgggtca	cccccatgct	gaaccttttc	540
atctacagcc	tgagaaacag	ggacatacaa	agtgcctgtg	ggaggctgct	cagcagaaca	600
gtcgaatctc	atgatctggt	ccatcctttt	tcttgtgtgg	gtaagggtcaa	ccacattaaa	660

<210> 210

<211> 942

<212> DNA

<213> Unknown (H38g58 nucleotide)

<220>

<223> Synthetic construct

<400> 210

atggccaaga	ataatctcac	cagagtaacc	gaattcattc	tcatgggctt	tatggaccac	60
cccaaattgg	agattccctt	ctttctgggtg	tttctgagtt	tctacctagt	cacccttctt	120
gggaatgtgg	ggatgattat	gttaatccaa	gtagatgtca	aactctacac	cccaatgtac	180

ttcttcctga	gccacctctc	cctgctggat	gcctgttaca	cctcagtcac	cacccctcag	240
atcctagcca	cattggccac	aggcaaaacg	gtcatctcct	acggccactg	tgctgcccag	300
ttctttttat	tcacatctg	tgccaggcaca	gagtgtcttc	tgctggcagt	gatggcctat	360
gatcgctatg	ctgccattcg	caacccactg	ctctataaccg	tggccatgaa	tcccaggctc	420
tgctggagcc	tggtggtagg	agcctatgtc	tgtgggggtgt	caggagccat	cctgcgtacc	480
acttgcacct	tcacctctc	cttctgtaag	gacaatcaaa	taaacttctt	cttctgtgac	540
ctcccacccc	tgctgaagct	tgccctgcagt	gacacagcaa	acatcgagat	tgcatcatc	600
ttctttggca	attttgtgat	tttggccaat	gcctccgtca	tcctgatttc	ctatctgctc	660
atcatcaaga	ccattttgaa	agtgaagtct	tcaggtggca	gggccaagac	tttctccaca	720
tgtgcctctc	acatcactgc	tgtggccctt	ttctttggag	cccttatctt	catgtatctg	780
caaagtggct	caggcaaatc	tctggaggaa	gacaaagtcg	tgtctgtctt	ctatacagtg	840
gtcatcccca	tgctgaaccc	tctgatctac	agcttaagaa	acaaagatgt	aaaagacgcc	900
ttcagaaagg	tcgctaggag	actccaggtg	tccctgagca	tg		942

<210> 211

<211> 941

<212> DNA

<213> Unknown (H38g59 nucleotide)

<220>

<223> Synthetic construct

<400> 211

atgggtgggc	taaaaagaga	caatgcctct	gagatgactg	aactcatcct	tggttgattt	60
gcccaacacc	ctgaaatcca	gactgccttc	ttcttggaac	tactgttttt	ctactagtca	120
cagcgtttga	gaacatcctt	atcgttgctg	tagtgagatg	agattctcga	cttcatactc	180
ctatgggatt	tttttttctt	cagtacctta	tcctcccttg	aaatgtgtta	ctccatcagc	240
tgggagctat	aagtcttggc	tcaatgcctc	aaggacttcc	ccaccatctc	ctataacagc	300
tgttctgttc	agatgatcac	acacctcttt	ctggggatga	cagtgtctcc	tccttgctgg	360
catggcttac	aacaggtttg	ttgaaatctc	ttatctcctc	cattacacta	ttattatgag	420
caatcgggtc	tgtatacagt	tggccttggg	aatctggacc	catgccttct	tagtagcagt	480
cacactaatc	attgcaattc	ctgctagtta	ttatggacac	aatgtcatca	accattttac	540
cttgagatcc	aggccctgct	gaagctcgtc	tgctcagaca	cccttgtcag	cctgattcag	600
ggtctgggtta	tcagtgtgtt	cacactgccc	ctgcccttca	cattcatcct	catctcctaa	660
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atctgactgg	agtcaccata	ttttatgggg	cagccatctg	catgtacttg	aaacctcagt	780
caaagggaac	ccaggaagag	gataaagtgt	tctcaaaact	ttatggagca	gttactccca	840
tggttaaattc	cccaattttac	attcagagaa	ataaggatat	aaaagggtgca	cttagaaagt	900
tagccaaagg	aaatgaaaaa	tcctaacagt	tctcttttaa	c		941

<210> 212

<211> 1049

<212> DNA

<213> Unknown (H38g61 nucleotide)

<220>

<223> Synthetic construct

<400> 212

atggatattc	tggttattga	taatggcagt	gaagtgcacg	agttcatcct	ggtggggttg	60
tacaaccatc	caaaattttca	gattgccttt	tatcgacca	tggtagtggg	ctacctgatc	120
acatttggtg	gtagcagtct	cattattggt	gtgggttaaag	ttgatgggtg	gcttcacact	180
cctatgtgtt	ttttcctaag	caacctgtcc	ttccttgata	tctgctactc	cagcaattca	240
gtaccttttt	tgttgttcaa	tggcttaaga	gactacccca	ccatttccta	taacagctgt	300
tatgcccaga	tgaccagtgc	tttttttctg	gggatgcacg	ggtgtcttct	ccttgctgtc	360
atggcttatg	agagatttgt	tgtgatctcc	aatccccctg	gctacatcat	cattatgaac	420
aataaggtct	gcatacagtt	ggccatgggt	acctgggcca	gtgccttctt	tatgtcatta	480
atacaataat	tgcataata	cattgcaata	atacattaat	tgcaatgatt	gcattgcaat	540
tcctgccccat	ttttgtggac	acaatgtcat	caaccatttt	acctgtgagg	tgcaggaaat	600
gttgaagctt	gtctgtctcag	acatcccagg	cagcctcatc	ctcgggtctag	tcacggcat	660
attcaccttg	tccttgccct	tcaccttgcc	cctgccttcc	accttcatcc	tcttcgccta	720

tgctcacatt	gtggttgctg	tgctgaggat	caactctgca	gaggccagac	tcaaagcttt	780
ctccacctgt	ggatcccatc	tgactgtgat	catcatatct	tatgggacag	ccacctacat	840
gtacttgaaa	cctcagtcac	gggaatccca	agatgagggt	aaagtcatct	ctgtattttt	900
tttgaaagta	gagaagcaac	atcaaaatga	tagcatctct	gtattttatg	gtgttgtagac	960
ccctatgttg	aacccctca	tttacacctt	gagagacaag	gatgcgaaaa	tgctctaaga	1020
aaaataatta	ggaagaaaa	gtcctaaaa				1049

<210> 213

<211> 954

<212> DNA

<213> Unknown (H38g62 nucleotide)

<220>

<223> Synthetic construct

<400> 213

atggacaaga	taaaccagac	atttgtgaga	gaattcattc	ttctgggact	ctctgggttac	60
cccaaacttg	agatcatttt	ctttgctctg	attctagtta	tgtacgtagt	gattctaatt	120
ggcaatgggtg	ttctgatcat	agcaagcatc	ttggattctc	gtcttcacat	gcccattgtac	180
ttcttcctgg	gcaacctctc	tttcctggat	atctgctata	caacctcctc	cattccctca	240
acactgggtga	gcttaatctc	aaagaaaaaga	aacatttcct	tctctggatg	tgcatgacag	300
atgttctttg	ggtttgcaat	gggggtcaaca	gaatgtttcc	tccttggcat	gatggcattt	360
gatcggttatg	tgcccatctg	taacctctctg	agatacccca	tcacatgaa	caagggtggtg	420
tatgtactgc	tgacttctgt	atcatggctt	tctgggtgaa	tcaattcaac	tgtgcaaaaca	480
tcacttgcca	tgcatggcc	tttctgtggg	aacaatatta	ttaatcattt	cttatgagag	540
atcttagctg	tcctaaaatt	agcttgttct	gatataatctg	tcaatattgt	taccctagca	600
gtgtcaaata	ttgcttttct	agttcttctc	ctgctcgtga	tttttttctc	ctatatgttc	660
atcctctaca	ccatcttgcg	aacgaactcg	gccacaggaa	gacacaaggc	attttctaca	720
tgctcagctc	acctgactgt	ggtgatcata	ttttatggta	ccatcttctt	tatgttgca	780
aaacctaaagt	cccaggacct	ccttgggaaa	gacaacttgc	aagctacaga	ggggcttggt	840
tccatgtttt	atgggggtgt	gaccccatg	ttaaacccca	taatctatag	cttgagaaat	900
aaagatgtaa	aagctgctat	aaaatatttg	ctgagcagga	aagctattaa	ccag	954

<210> 214

<211> 957

<212> DNA

<213> Unknown (H38g63 nucleotide)

<220>

<223> Synthetic construct

<400> 214

atgttccccg	caaattggac	atctgtaaaa	gtatttttct	tcctgggatt	ttttcactac	60
cccaaagttc	aggatcatcat	atttgcggtg	tgcttgctga	tgtacctgat	caccttgctg	120
ggcaacattt	ttctgatctc	catcaccatt	ctagattccc	acctgcacac	ccctatgtac	180
ctcttctcca	gcaatctctc	ctttctggac	atctgggtact	cctcttctgc	cctctctcca	240
atgctggcaa	actttgtttc	agggagaaac	actatttcat	tctcagggtg	cgccactcag	300
atgtacctct	cccttgccat	gggtctccact	gagtgtgtgc	tcctgcccac	gatggcatat	360
gaccggatg	tgcccatctg	caacccccctg	agataccctg	tcacatgaa	taggagaacc	420
tggtgacaga	ttgcagctgg	ctcctggatg	acaggctgtc	tcactgccat	ggtggaaatg	480
atgtctgtgc	tgccactgtc	tctctgtggt	aatagcatca	tcaatcattt	cacttgtgaa	540
attctggcca	tcttgaaatt	ggtttgtgtg	gacacctccc	tggtgcagtt	aatcatgctg	600
gtgatcagtg	tacttcttct	ccccatgcca	atgctactca	tttgatctct	ttatgcattt	660
atcctcgcca	gtatcctgag	aatcagctca	gtggaagggtc	gaagtaaagc	cttttcaacg	720
tgacacagccc	acctgatggt	ggtagttttg	ttctatggga	cggtctctct	catgcacctg	780
aagccctccg	ctgtagattc	acaggaaata	gacaaattta	tggttttggt	gtatgccgga	840
caaaccccca	tggtgaatcc	tatcatctat	agtctacgga	acaaagaggt	gaaagtggcc	900
ttgaaaaaat	tgctgattag	aaatcatttt	aatactgcct	tcatttccat	cctcaaa	957

<210> 215

<211> 930

<212> DNA

<213> Unknown (H38g64 nucleotide)

<220>

<223> Synthetic construct

<400> 215

atggcagaga	tgaacctcac	cttggtgacc	gagttcctcc	ttattgcatt	caactgaatat	60
cctgaatggg	cactccctct	cttcctcttg	tttttattta	tgtatctcat	caccgtattg	120
gggaacttag	agatgattat	tctgatccctc	atggatcacc	agctccacgc	tccaatgtat	180
ttccttctga	gtcacctcgc	tttcatggac	gtctgctact	catctatcac	tgccccccag	240
atgctggcag	tgctgctgga	gcatggggca	gctttatctt	acacacgctg	tgctgctcag	300
ttctttctgt	tcaccttctt	tggttccatc	gactgctacc	tcttggccct	catggcctat	360
gaccgctact	tggctgtgtg	ccagccctcg	ctttatgtca	ccatcctgac	acagcaggcc	420
cgcttgagtc	ttgtggctgg	ggcttacgtt	gctggtctca	tcagtgcctt	ggtgcggaca	480
gtctcagcct	tcactctctc	cttctgtgga	accagtgaga	ttgactttat	tttctgtgac	540
ctccctcctc	tggttaaagt	gacctgtggg	gagagctaca	ctcaagaagt	gctgattatt	600
atgtttgcc	tttttgtcat	ccctgcttcc	atgggtggtga	tcttgggtgc	ctacctgttt	660
atcatcgtgg	ccatcatggg	gatccctgct	ggaagccagg	ccaagacctt	ctccacctgc	720
acctcccacc	tcactgctgt	gtcactcttc	tttggatccc	tcactctcat	gtacttgaga	780
ggtaactcag	atcagtcttc	ggagaagaat	cgggtagtgt	ctgtgcttta	cacagaggtc	840
atccccatgt	tgaatccct	catctacagc	ctgaggaaca	aggaagtga	ggaggccctg	900
agaaaaattc	tcaatagagc	caagttgtcc				930

<210> 216

<211> 964

<212> DNA

<213> Unknown (H38g65 nucleotide)

<220>

<223> Synthetic construct

<400> 216

atgggcatgg	agggtcttct	ccagaactcc	actaacttcg	tcctcacagg	cctcatcacc	60
catcctgctt	tcctcgggct	tctctttgca	atagtcttct	ccatctttgt	ggtggctata	120
acagccaact	tggtcatgat	tctgctcatc	cacatggact	cccgcctcca	cacacccatg	180
tacttcttgc	tcagccagct	ctccatcatg	gataccatct	acatctgtat	caactgtccc	240
aagatgctcc	aggacctcct	gtccaaggac	aagaccattt	ccttccctggg	ctgtgcagtt	300
cagatcttcc	tctacctgac	cctgattgga	ggggaattct	tcctgctggg	tctcatggcc	360
tatgaccgct	atgtggctgt	gtgcaaccct	ctacgggtacc	ctctcctcat	gaaccgcagg	420
gtttgcttat	tcatgggtgt	cggctcctgg	gttgggtggt	ccttggatgg	gttcattgctg	480
actcctgtca	ctatgagttt	ccccttctgt	agatcccag	agatcaatca	cttttctgtg	540
gagatcccag	ccgtgctgaa	gttgtcttgc	acagacacgt	caactctatga	gacctgatg	600
tatgcctgct	gcgtgctgat	cgctgcttat	ccctctatct	gtcatctctg	tctcctacac	660
gcacatcctc	ctgactgtcc	acaggatgaa	ctctgctgag	ggccggcgca	aagcctttgc	720
tacgtgttcc	tcacacatta	tggcggtgag	cgttttctac	ggggcagcct	tctacaccaa	780
cgtgctgccc	cactcctacc	acactccaga	gaaagataaa	gtggtgtctg	ccttctacac	840
catcctcacc	cccattgctca	accactcat	ctacagcttg	aggaataaag	atgtggctgc	900
agctctgagg	aaagtactag	ggagatgtgg	ttcctcccag	agcatcaggg	tggcgactgt	960
gatac						964

<210> 217

<211> 933

<212> DNA

<213> Unknown (H38g66 nucleotide)

<220>

<223> Synthetic construct

<400> 217

atggctcaca	caaataatc	gatgggtgtct	gagtttgtac	ttttgggact	ctctaattcc	60
------------	-----------	-------------	------------	------------	------------	----

tggggacttc	aacttttctt	tttcgccatc	ttctctatag	tctatgtgac	atcagtgcta	120
ggcaatgtct	taattattgt	cattatttct	tttgactccc	atttgaactc	tcctatgtac	180
ttcttgtctc	gtaatctttc	tttcattgat	atctgtcagt	ctaactttgc	cacccccaa	240
atgctttag	acttttttat	tgagcgcaag	actatctcct	ttgaggggtg	catggcccag	300
atattcggtc	ttcacagttt	tggtgggagt	gagatgatgt	tgcttgtagc	tatggcatat	360
gacagattta	tagccatatg	taagcctctg	cactacagta	caattatgaa	cggaggctc	420
tgtgtaattt	ttgtgtctat	ttcctgggcg	gtgggcgttc	ttcattctgt	gagccactg	480
gcttttacag	tggacctgcc	attctgtggt	cccaatgagg	tggatagctt	cttttgtgac	540
cttccttgg	tgatagagct	ggcttgcag	gatacatatg	aaatggaaat	tatgacccta	600
acgaacagtg	gcctgatatc	attgagctgt	ttcctggctt	taattatttc	ctacaccatc	660
attttgatcg	gtgtccgatg	caggtcctcc	agtgggtcat	ctaaggctct	ttctacatta	720
actgccaca	tcacagtgg	cattcttttc	ttcgggcctt	gcatttattt	ctatatatgg	780
ccttttagca	gacttcctgt	ggacaaaatt	ctttctgtgt	tctacactgt	ttgtactccc	840
ttgttgaaac	ccatcatcta	ctctctgagg	aatgaagatg	ttaaagcagc	catgtggaag	900
ctgagaaacc	gtcatgtgaa	ctcctggaaa	aac			933

<210> 218

<211> 936

<212> DNA

<213> Unknown (H38g67 nucleotide)

<220>

<223> Synthetic construct

<400> 218

atggatcaga	aaaatggaag	ttcttttact	ggatttatcc	tactgggttt	ctctgacagg	60
cctcagctgg	agctagtcct	ctttgtgggt	cttttgatct	tctatatctt	cactttgctg	120
gggaacaaaa	ccatcattgt	attatctcac	ttggaccac	atcttcacac	tcctatgtat	180
tttttcttct	ccaacctaa	ctttttggat	ctgtgttaca	caaccggcat	tgttccacag	240
ctcctggtta	atctcagggg	agcagacaaa	tcaatctcct	atgggtgggtg	tgtagttcag	300
ctgtacatct	ctctaggctt	gggatctaca	gaatgcgttc	tcttaggagt	gatgggtattt	360
gaccgctatg	cagctgtttg	caggcccttc	cactacacag	tagtcatgca	cccttgtctg	420
tatgtgctga	tggcttctac	ttcatgggtc	attggttttg	ccaactccct	attgcagacg	480
gtgtcatct	tgcttttaac	actttgtgga	agaaataaat	tagaacactt	tctttgtgag	540
gttcctccat	tgctcaagct	tgctgtgtt	gacactacta	tgaatgaatc	tgaactcttc	600
tttctcagtg	tcattattct	tcttgtagct	gttgcatata	tcataattctc	ctatagtcag	660
attgtcaggg	cagtcattgag	gataaagtta	gcaacagggc	agagaaaagt	gtttgggaca	720
tgtggctccc	acctcacagt	ggtttccctg	ttctacggca	cagctatcta	tgcttacctc	780
cagcccgga	acaactactc	tcaggatcag	ggcaagttca	tctctctctt	ctacaccatc	840
attacaccca	tgatcaaccc	cctcatatat	acactgagga	acaaggatgt	gaaaggagca	900
cttaagaagg	tgctctggaa	gaactacgac	tccaga			936

<210> 219

<211> 939

<212> DNA

<213> Unknown (H38g68 nucleotide)

<220>

<223> Synthetic construct

<400> 219

atgtgctcag	ggaatcagac	ttctcagaat	caaacagcaa	gcactgattt	caccctcacg	60
ggactctttg	ctgagagcaa	gcatgtgtcc	ctcctctaca	ccgtgacctt	ccttcttttc	120
ttgatggccc	tactgggaa	tgccctcctc	atcctcctca	tccactcaga	gccccgcctc	180
cacaccccc	tgtacttctt	catcagccag	ctcgcgtca	tggatctcat	gtacctatgc	240
gtgactgtgc	ccaagatgct	tgtgggccag	gtcactggag	atgataccat	ttccccgtca	300
ggctgtggga	tccagatggt	cttcacactg	accctggctg	gagctgaggt	tttctcctg	360
gtgccatgg	cctatgaccg	atatgtgtgt	gtttgcagac	ctctccatta	cccactgctg	420
atgaaccaga	gggtgtgcca	gtcctgtgtg	tcagcctgct	gggttttggg	aatggttgat	480
ggtttgttgc	tcacccccat	taccatgagc	ttcccccttt	gccagtctag	gaaaatcctg	540
agttttttct	gtgagactcc	tgccctgtgt	aagctctcct	gctctgacgt	ctccctctat	600

aagatgctca	cgtacctgtg	ctgcacccctc	atgcttctca	ccccatcat	ggcatctctcc	660
agctcataca	ccctcatcct	gcattctcctc	cacaggatga	attctgcccgc	cggccgcagg	720
aaggccttgg	ccacctgctc	ctcccacatg	atcatagtgc	tgtctgtctt	cgggtgcttcc	780
ttctacacct	acatgctccc	gagttcctac	cacacagctg	agcaggacat	gatgggtgtct	840
gccttttaca	ccatcttcac	tcctgtgctg	aacccctca	tttacagtct	cgcacaacaaa	900
gatgtcacca	gggctatgag	gagcatgatg	cagtcaga			939

<210> 220

<211> 942

<212> DNA

<213> Unknown (H38g69 nucleotide)

<220>

<223> Synthetic construct

<400> 220

atggatgtgg	gcaataagtc	taccatgtct	gaatttggtt	tgtctggggct	ctctaattcc	60
tgggaactac	agatgttttt	ctttatgggtg	ttttcattgc	tttatgtggc	aacaatgggtg	120
ggtaacagcc	tcatagtcat	cacagttata	gtggaccctc	acctacactc	tcctatgtat	180
ttcctgctta	ccaatcttcc	aatcattgat	atgtctcttg	cttctttcgc	caccccaaag	240
atgattacag	attacctaac	aggtcacaaa	accatctctt	ttgatggctg	ccttaccag	300
atattctttc	tcacaccttt	cactggaaact	gagatcatct	tactcatggc	catgtccttt	360
gatagggtata	ttgcaatatg	caagcccctg	cactatgctt	ctgtcattag	tccccagggtg	420
tgtgttgctc	tcgtgggtggc	ttcctggatt	atggggagtt	tgcattcaat	gagtcagggtc	480
atatttgccc	tcacgtttacc	attctgtggt	ccctatgagg	tagacagctt	tttctgtgac	540
cttctgtgtg	tgttccagtt	ggcttgtgtg	gatacttatg	ttctgggcct	ctttatgatc	600
tcaacaagtg	gcataattgc	gttgtcctgt	tttattgttt	tatttaattc	atatgtttatt	660
gtcctgggta	ctgtgaagca	tcattcttcc	agaggatcat	ctaaggccct	ttctacttgt	720
acagctcatt	tcattgttgt	cttctgtgtc	tttgggccat	gcattcttcat	ctacatgtgg	780
ccactaagca	gctttctcac	agacaagatt	ctgtctgtgt	tttataccat	ctttactccc	840
actctgaacc	caataatcta	tactttgagg	aatcaagaag	taaagatagc	catgaggaaa	900
ctgaaaaata	ggtttctaaa	ttttaataag	gcaatgcctt	ca		942

<210> 221

<211> 930

<212> DNA

<213> Unknown (H38g70 nucleotide)

<220>

<223> Synthetic construct

<400> 221

atgggagaca	atataacatc	catcagagag	ttcctcctac	tgggatttcc	cgttggccca	60
aggattcaga	tgtctctctt	tgggctcttc	tcctgtttct	acgtcttcac	cctgtctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgcacgcccc	catgtacttc	180
ttcctctcac	acctggcggt	cgctcgacatc	gcctacgcct	gcaacacggg	gccccggatg	240
ctggtgaacc	tcctgcatcc	agccaagccc	atctcctttg	cgggcccgcat	gatgcagacc	300
tttctgtttt	ccacttttgc	tgtcacagaa	tgtctctctc	tgggtgggtg	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttggcca	tcatgacctg	gagagtctgc	420
atcacccctg	cgggtgacttc	ctggaccact	ggagtccttt	tatccttgat	tcattctgtg	480
ttacttctac	ctttaccctt	ctgtaggccc	cagaaaattt	atcacttttt	ttgtgaaatc	540
ttggctgttc	tcaaaccttg	ctgtgcagat	accacatca	atgagaacat	ggtcttggcc	600
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ttctcccacc	tctgtgtgat	tggactcggt	tatggcacag	ccattatcat	gtatgttggg	780
cccagatag	ggaaccccaa	ggagcagaag	aaatatctcc	tgtgttttca	cagcctcttt	840
aatcccatgc	tcaatccctt	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtctta				930

<210> 222

<211> 969

<212> DNA

<213> Unknown (H38g71 nucleotide)

<220>

<223> Synthetic construct

<400> 222

cacacggagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgctgccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggc	120
atggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	tccacacccc	180
cgtgtacttc	ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cgcccacggt	240
tcccaagatg	attgtggaca	tgcagtcgca	tagcagagtc	atctctcatg	cgggctgcct	300
ggcacagatg	tctttcttgg	tcctttttgc	atgtatagaa	gacatgctcc	tgactgtgat	360
ggcctatgac	agctttgtag	ccatctgtca	ccctctgcac	taccagtcac	tcatgaatcc	420
tcacctctgt	gtcttcttcg	ttttggtgtc	ctttttcctt	agcctgttgg	attcccagct	480
gcacggttgg	attgtgttac	aattcaccat	catcaagaat	gtggaaatct	ctaattttct	540
ctgtgacccc	tctcaacttc	tcaaacttgc	ctgttctgac	agcgtcacca	atagcatatt	600
catataattt	gatagtacta	tgtttggttt	tcttcccatt	tcagggatcc	ttttgtctta	660
gtataaaatt	gtccccctcca	ttctaaggat	gtcatcgctc	gatgggaagt	ataaagcctt	720
caccacctgt	ggctctcacc	tagcagttgt	ttgctgattt	gatggaacag	gcattggcat	780
gtacctgact	tcagctctgt	caccaccccc	caggaatggg	gtggcggcgt	cagtgatgta	840
cgctgtggtc	acccccatgc	tgaacctttt	catctacagc	ctgagaaaca	gggacataca	900
aagtgccttg	cggaggctgc	gcagcagaac	agtggaaatct	catgatctgt	tccatccttt	960
ttcttgtgt						969

<210> 223

<211> 945

<212> DNA

<213> Unknown (H38g72 nucleotide)

<220>

<223> Synthetic construct

<400> 223

atggcctgga	gcaatcagtc	tgcggttaacc	gaattcatac	tacgggggtct	gtccagttct	60
ttagaactcc	agattttcta	cttctgtttt	ttctccatag	tctatgcagc	cactgtgctg	120
gggaaccttc	ttattgtggt	caccattgca	tcagagccac	accttcattc	ccctacgtac	180
tttctgctgg	gcaatctctc	cttcattgac	atgtccctgg	cctcatttgc	cacccccaaa	240
atgattgcag	acttccttag	agaacacaaa	gccatctctt	ttgaaggctg	catgacccag	300
atgttcttcc	tacatctctt	aggggggtgt	gagattgtac	tgctgatctc	catgtccttt	360
gataggtagc	tggctatctg	taagcctcta	cattacctaa	caatcatgag	ccgaagaatg	420
tgtgttgggc	ttgtgatact	ttcctggatt	gtcggcatct	tccatgctct	gagtcagtta	480
gcattttacag	tgaatctgcc	cttctgtgga	cccaatgaag	tagacagttt	cttttgtgac	540
ctcccttttg	tgattaaact	tgcttgtgtc	gcacacatata	ttctgggggt	gttcatgac	600
tcaaccagtg	gcatgattgc	cctgggtgtc	ttcatcctct	tgggtgatctc	ttacactatc	660
atcctgggtca	cgttctggca	gcgttctctt	ggtggatcct	ccaaagccct	ctccacgtgc	720
agtgcacct	ttactgttgt	gaccttttct	tttggcccat	gcactttcat	ttatgtgtgg	780
cctttcacaa	atttcccaat	agacaaagta	ctctcagtat	tttataccat	atacactccc	840
ctcttgaatc	cagtgatcta	taccgttagg	aataaagatg	tcaagtattc	catgaggaaa	900
ctaagcagcc	atatcttttaa	atctaggaag	actgatcata	ctcct		945

<210> 224

<211> 963

<212> DNA

<213> Unknown (H38g73 nucleotide)

<220>

<223> Synthetic construct

<400> 224

atgaaaaagt	acatggaaag	gactaattga	acaactgagt	ttgagttgat	tctcataagt	60
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ctatgagtag	tcataagttg	acaaaaactc	ctttttgtca	catgcttagt	ggtgtatcta	120
gtgaccctct	tggggaacag	aatacagatc	atcccaacac	tccttggttc	ccacctatat	180
ttatgccatg	gcaatccctc	cttccctggat	atcgggctta	cgtccttttt	actccctcta	240
tcctaataaa	cttcctatca	gagggaaaaa	aactctcttt	cacagattgt	attatacaaa	300
tgtctatctt	ctattccatg	gggtccacgg	agtgtgtgct	cctagcagtg	atggcatatg	360
ataactgtgt	ggatcatcag	aaattcctga	gataccctct	catcataaat	aaggtgaata	420
aaataaaaaa	ggtgctttgt	gttttcatgg	ctactgtctc	ttatgaatta	ggattttctca	480
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tcatttttat	aaaatattac	agttaatggc	tctggcttgc	atagatatatt	ccttgaatga	600
gaatataata	atattgggca	aagtaaactt	ttcattttact	ttattactac	catttcagtt	660
ctttatatte	agttttttat	attttcacca	tctatgctgt	attgaaatca	attcagctga	720
aggaaggaaa	aaggtctctt	ccacctgttc	agccacata	acagtggatg	ttgtgtttca	780
cgggacaatc	ctcttcatgt	acataaagtc	aacatctaata	ggcactactt	cagagaaact	840
ggttgacctg	ttctgcgggg	tagtaatgct	catgctcaat	cttatcatct	atagcctggg	900
gaatatggag	gtgcttgggg	ttatgaagaa	attgatcagt	atgagtagac	cctgggtgctg	960
gaa						963

<210> 225

<211> 974

<212> DNA

<213> Unknown (H38g74 nucleotide)

<220>

<223> Synthetic construct

<400> 225

cacacggagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggg	cctcgctttg	ctgtccctgt	ccctgtccat	gtccatgtat	120
ctgggtcacgg	tgtcgaggaa	cctgctcagc	atcctggctg	tcagctctga	ctcccaactc	180
cacacccccca	tgtacttctt	cctctccaac	ctgtgctggg	ctgacatcgg	tttcacctcg	240
cccattggttc	ccaagatgat	catggacatg	cagtcgcata	gcagagtcac	ctctcatgcg	300
ggctgcctga	cacggatgtc	tttcttggtc	ctttttgcat	gtatagaaga	catgctcctg	360
actgtgatgg	cctatgactg	ctttgtagcc	atctgtcgcc	ctctgcacta	cccagtcac	420
atgaatcctc	acctctgtgt	cttcttcggt	ttggtgtcct	ttttccttag	cctgttggat	480
tcccagctgc	acagttagat	tgtgttacaa	ttcactttct	tcaataatgt	ggaaattgct	540
aattttgtct	atgagccatc	tcaactcttc	aaccttgact	gttctgacac	cgctcatcaat	600
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tcttagtata	aaattgtccc	ctccattcta	aggatgtcat	cgtcagatgg	gaagtataaa	720
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ggcatgtacc	tgacttcagc	tgtgtcacca	ccccccagga	atgggtgtgg	ggcgtcagtg	840
atgtacgctg	tggtcacccc	catgctgaac	cttttcatct	acagcctgag	aaacagggac	900
attcaaatgt	cctgcagag	gctgagtagc	agaacagtgg	aatctcatga	tctgttccat	960
cctttttctt	gtgt					974

<210> 226

<211> 957

<212> DNA

<213> Unknown (H38g75 nucleotide)

<220>

<223> Synthetic construct

<400> 226

atgggtaact	ggactgcagc	ggtgactgag	tttgttctgc	tgggggttttc	cctgagcagg	60
gaggtggagc	tgtgtctcct	ggtgtctcct	ctgcccacgt	tcctgtctgac	tcttctgggg	120
aacctgtctca	tcattctccac	tgtgtctgtc	tgctcccgc	tccacacccc	catgtacttc	180
ttctttgtgca	acctctctat	cctggacatc	ctcttcacct	cagtcacttc	tccaaaagtg	240
ttggccaact	taggactctag	ggataaaaacc	atctcctttg	cgggatgtat	caccagtgcc	300
tattttctact	ttttcttggg	cacagttgag	ttctctctgc	tgacgggtcat	gtcctatgac	360
cgttatgccca	ccatctgctg	ccccctgcgg	tacaccacca	tcatgagacc	ttctgtctgc	420
attggggaccg	ttgtattctc	ttgggtggga	ggcttctctg	ctgtgtctct	tccaaccatc	480

ctcatctccc	agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	540
ggacccttgc	tggccctggc	ctgtgcagac	accactgcc	tcgagctgat	ggattttatg	600
ctttcttcca	tggctatcct	ctgctgcata	gtcctcgtgg	cctattccta	tacgtacatc	660
atcttgacca	tagtgcgcat	tccttctgca	agtgggaagga	agaaggcctt	taatacctgt	720
gcttcccacc	tgaccatagt	catcattcct	agtggcatca	ctgtgtttat	ctatgtgact	780
ccctcccaga	aagaatatct	ggagatcaac	aagatccctt	tggttctgag	cagtgtggtg	840
actccatccc	tcaaccctt	tatatatact	ctgagggaatg	acacagtgca	gggagtcctc	900
agggatgtgt	gggtcagggt	tcgaggagtt	tttgaaaaga	ggatgagggc	agtgtg	957

<210> 227

<211> 939

<212> DNA

<213> Unknown (H38g76 nucleotide)

<220>

<223> Synthetic construct

<400> 227

atggaaactg	caaattacac	caaggtgaca	gaatttggtc	tactggcct	atcccagact	60
cgggaggtcc	aactagtcct	atttggtata	tttctatcct	tctatttggt	catcctacca	120
ggaaatatcc	ttatcatttg	caccatcagg	ctagaccctc	atctgacttc	tcctatgtat	180
ttcctgttgg	ctaattctggc	cctccttgat	atttggtact	cttccattac	agccccataa	240
atgctcatag	acttctttgt	ggagaggaag	ataatttcct	ttggtggatg	cattgcacag	300
ctcttcttct	tacactttgt	tggggcttcg	gagatgttct	tgctcatagt	gatggcctat	360
gaccgctatg	ctgctatctg	ccgaccctc	cactatgcta	ccatcatgaa	tcgacgtctc	420
tgctgtatcc	tgggtggctct	ctcctggatg	gggggcttca	ttcattctat	aatacagggtg	480
gctctcattg	ttcgacttcc	tttctgtggg	cccaatgagt	tagacagtta	cttctgtgac	540
atcacacagg	ttgtccggat	tgctgtgcc	aacaccttcc	cagaggagtt	agtgatgatc	600
tgtatagatg	gtctgatctc	tgtggtgtgt	ttcattgctc	tgtaatgtc	ctatgccttc	660
cttctggcct	tgctcaagaa	acattcaggc	tcagatgaga	ataccaacag	ggccatgtcc	720
acctgctatt	cccacattac	cattgtgggtg	ctaattgtttg	ggccatccat	ctacatttat	780
gctcgcccat	ttgactcatt	ttccctagat	aaagtgggtg	ctgtgtttca	tactgttaata	840
ttccctttac	ttaatcccat	tattttacaca	ttgagaaaca	aggaagtaaa	ggcagccatg	900
aggaaggtgg	tcaccaaata	tattttgtgt	gaagagaag			939

<210> 228

<211> 940

<212> DNA

<213> Unknown (H38g77 nucleotide)

<220>

<223> Synthetic construct

<400> 228

atggaaagtc	aaaggaacat	ataaaaattc	atactcatga	gcctttcctc	tatccagaac	60
atacaaatat	ttgtttttgt	gttcttattt	tgtaatgttg	ccatcttggt	gggaaacttt	120
ctgatcctta	tctctatttg	atgtagtcct	ctttttaacc	aaccaatgca	ctatttcttc	180
aggctatatg	aatatctact	atacctcctg	tgtcacaccc	aaaataattg	gtgatctagt	240
agtgggaaga	ataaacatct	cctatgatag	gagtccttcc	catgcacttc	tttggaatca	300
ttgaaatctt	catccttaca	gtcatggctt	ttgatcacta	tgttgccatc	tgcaaacctc	360
cccgtacct	aattatcatg	aataggacaa	aatacaatac	tctaactctg	gttgcttggc	420
tgttggggct	ttccattctt	tgtttcagtt	ttctatgaaa	atctggttgc	ctttctgtgg	480
ctccaacaaa	gttgatgact	aatattaaga	tatttttctc	ttactgaaag	tcgcttgtag	540
tgatacctgc	atcactgggtg	tcctcgtggg	tgccaattct	ggaatgtttg	ccttggtaac	600
cttggtctgt	cgtttggtc	ttatgtcatt	atactattcc	ccttaaaaaa	tcattcagta	660
gaggggaagat	gcaaagccct	ctctacctgt	ggatctcata	tcaccatggg	aatctttttc	720
ttcgaacctt	caatctttgc	ctaccttaga	ccttctcact	tttctgagg	acaaaatatc	780
tgctctggtt	tacactatta	ttgctccaat	gttcaaccac	ctaactcata	acctgagaaa	840
tacagagatg	aaaaaggcca	tgagaaaagt	ttggtaccac	atatcatttt	cagaagaaaa	900
acagctgatt	tgctctactt	agtgactaa	agaactttat			940

<210> 229

<211> 912

<212> DNA

<213> Unknown (H38g78 nucleotide)

<220>

<223> Synthetic construct

<400> 229

atgagaaatg	gcacagtaat	cacagaattc	atcctgctag	gctttcctgt	tatccaaggc	60
ctacaaacac	ctctctttat	tgcaatcttt	ctcacctaca	tattaaccct	tgagggaat	120
gggcttatta	ttgccactgt	gtgggctgag	cccaggctac	aaattccaat	gtacttcttc	180
ctttgttaact	tgtctttctt	agaaatctgg	tacaccacca	cagtcatccc	caaactgcta	240
ggaacctttg	tagtggcaag	aacagtaatc	tgcattgtct	gctgcctgct	gcaggccttc	300
ttccacttct	tcgtgggcac	caccgagttc	ttgatcctca	ctatcatgtc	ttttgaccgc	360
tacctacca	tctgcaatcc	ccttcaccac	cccaccatca	tgaccagcaa	actctgcctg	420
cagctggccc	tgagctcctg	ggtgggtggc	ttcaccattg	tcttttgtca	gacgatgctg	480
ctcatccagt	tgccattctg	tggcaataat	gttatcagtc	atttctactg	tgatgttggg	540
cccagtttga	aagccgcctg	catagacacc	agcatttttg	aactcctggg	cgatcatagca	600
accatccttg	tgatcccagg	gtcactttct	tttaatatga	tttcttatat	ctacattctg	660
tccgcaatcc	tacgaattcc	ttcagccact	ggccaccaaa	agactttctc	tacctgtgcc	720
tcgcacctga	cagttgtctc	cctgctctac	ggggctgttc	tgttcatgta	cctaagaccc	780
acagcacact	cctcctttta	gattaataag	gtgggtgtct	tgctaaatac	tacctcacc	840
ccccttctga	atccctttat	ttatactatt	agaaacaagg	aggtgaaggg	agccttaaga	900
aaggcaatga	ct					912

<210> 230

<211> 963

<212> DNA

<213> Unknown (H38g79 nucleotide)

<220>

<223> Synthetic construct

<400> 230

atgacaattc	ttcttaatag	cagcctccaa	agagccactt	tcttcttgac	gggcttccaa	60
ggtctagaag	gtctccatgg	ctggatctct	attcccttct	gcttcatcta	cctgacagtt	120
atcttgggga	acctcaccat	tctccacgtc	atttgtactg	atgccactct	ccatggaccc	180
atgtactatt	tcttgggcat	gctagctgtc	acagacttag	gcctttgcct	ttccacactg	240
cccactgtgc	tgggcatttt	ctggtttgat	accagagaga	ttggcatccc	tgctgttttc	300
actcagctct	tcttcatcca	caccttgtct	tcaatggagt	catcagttct	gttatccatg	360
tccattgacc	gctacgtggc	cgtctgcaac	ccactgcatg	actccaccgt	cctgacacct	420
gcatgtattg	tcaagatggg	gctaagctca	gtgcttagaa	gtgctctcct	catcctcccc	480
ttgccattcc	tcttgaagcg	cttccaatac	tgccactccc	atgtgctggc	tcattgcttat	540
tgtcttcacc	tggagatcat	gaagctggcc	tgctctagca	tcattgtcaa	tcacatctat	600
gggctctttg	ttgtggcctg	caccgtgggt	gtggactcac	tgctcatctt	tctctcatac	660
gccctcatcc	ttcgcacctg	gctcagcatt	gcctcccacc	aggagcgact	ccgagccctc	720
aacacctgtg	tctctcatat	ctgtgctgta	ctgctcttct	acatcccat	gattggcttg	780
tctcttgtgc	atcgcttttg	tgaacatctg	ccccgcgttg	tacacctctt	catgtcctat	840
gtgtatctgc	tggtaccacc	ccttatgaac	cccatcatct	acagcatcaa	gaccaagcaa	900
attcgccagc	gcatcattaa	gaagtttcag	tttataaagt	cacttaggtg	tttttggaag	960
gat						963

<210> 231

<211> 968

<212> DNA

<213> Unknown (H38g80 nucleotide)

<220>

<223> Synthetic construct

<400> 231

atggggaacc	acaccaccgt	caccgagttt	gtcctgctgg	ggctctcaga	gacctgtgag	60
ctgcagatgc	tcattcttct	ggggctcttc	ctgacctacc	tcctcacact	gctggggaat	120
ctggtcacg	tggatcacac	cctcatggac	aggcgctcc	acaccacat	gtactacttc	180
ctccgcaact	ttgctgtccc	ggagatctgg	ttcacctcgg	tcattcttcc	caaggtgctg	240
gccaacatcc	tcacaggata	caagaccatt	ccctcccagg	ctgcttctctg	caaagtttgc	300
tctatttttt	cttgggcacc	agagctct	tcctcgtggc	ggtgatgtcc	tttgacaggt	360
acgtggccgt	atgtaaccct	ttgcattatg	ccaccatcat	gagcaaaagg	gtctgtgtcc	420
agctagtctt	ctgttagtgg	atgacaggat	tccttctcat	cattattcca	agttttcttg	480
tccttcagca	gccattctgt	ggccccaaca	tcattaacca	tttcttctgt	gacaactttc	540
ccctcttgaa	actcatttgt	gcagacatga	ctctgataga	gtcctcgggt	tttggtatag	600
ccaacgtcag	cttactgggc	actctgtcta	tgacggccac	ttgctatggc	cacatcctcc	660
acgccattct	gcacatcccc	tcagccaaag	agaagcagaa	agccttctcc	gcctgctcct	720
cccacatcat	tgctgtgtct	ctcttctatg	gcagctgcat	cttcatgtac	attcagtcag	780
gcaagagtga	ccagaaggaa	gacaggaaca	aggtggcggc	attgcttaac	accgtggtga	840
ccctgatgct	caacccttc	atctacacc	tgaggaacaa	acaggtgaaa	caggtgttta	900
ggcagcaggt	gagcaaactc	ctcatataaa	gctgtgtaaa	aaaaaaactg	aagctcagca	960
tccccaga						968

<210> 232

<211> 949

<212> DNA

<213> Unknown (H38g81 nucleotide)

<220>

<223> Synthetic construct

<400> 232

gaaataaaga	tagcaaaaca	cacagtagtg	acagaattta	tcctccttgg	tctgactcag	60
tctcaagata	ttcagctctt	ggtcttttgg	ctgatcttaa	ttttctacct	tatcatcctc	120
cctggaaatt	tcctcatcat	tttcaccata	aagtcagatc	ctgggctcac	agcacccttc	180
tatttctttc	tgggcaactt	ggccttcctg	gatgcacct	actccttcat	tgtggctccc	240
cggatgttgg	tggacttctt	ctctgcgaag	aatgtaatct	cctacagagg	ctgcatcact	300
cagctctttt	tcttgcactt	ccttggagga	ggagagggat	tactccttgt	gatgtagcct	360
ttgaccgcta	catcgccatc	tgcgggcttc	tgcactattc	tactctcatg	aacccagag	420
cttgcctatg	aatgatgttg	gctctgtggc	ttgggggttt	tgtccactcc	attatccagg	480
tggctctcat	cctccgcttg	ccttttttgg	gccccaaaca	gctggacaac	ttcttctgtg	540
atgtcccaca	ggtcatcaag	ctggcttgca	ccgacacgtt	tgtggtggag	cttctgatgg	600
tcttcaacag	tggcctgatg	acactcctgt	ctttctgggg	cttctggctt	cctatgcagt	660
catcctgtgc	catgttcgta	aggcagcttc	tgaattgaag	aacaaggcca	tgtccacgtg	720
caccattcat	gtcattatta	tacttcttat	gtttggacct	gctatcttca	tctacatgca	780
ccccttcagg	gcttaccag	ctgacaaggt	ggtttcttcc	tttcacacag	tgatctttcc	840
attgatgaat	cctatgattt	atacccttcg	aaaccaggaa	gtgaaaactt	ccatgaagag	900
gttattgagt	cgacatgtag	tctgtcaagt	ggactttata	ataagaaac		949

<210> 233

<211> 857

<212> DNA

<213> Unknown (H38g82 nucleotide)

<220>

<223> Synthetic construct

<400> 233

gtcatacgaa	accagacaat	ggtaactgaa	ttcaccgggt	ctcccttctt	gctgtccagg	60
agcttcagat	ttggctatgt	gtccttctct	ggctggttca	tatgctcacc	ataacaggaa	120
accttttctg	cattttctta	acgtggacag	ataattgtct	ccaaacccca	atggacttgt	180
tccttagaaa	aaagtcatat	cgttctctgg	ctgcatcacc	caaatatatt	tctacttctt	240
tctagggaca	gtggcggtta	tcccttggc	agtgacatcc	ttcaaact	gcatggcaac	300
ctgtgacccc	ctgtgcagca	ccatcattgc	aaaaagcagg	gcctgcctcc	tgtggctctt	360
gggatgctgg	atgggaacct	tcctggctgt	gttgccgctg	actattgtgg	tgtccagggt	420

gccagactgt	actgaaaaaa	ttagtcctt	cttctgtgac	attgcctctt	tactgcaggt	480
ggcctgtatt	gatattcatt	tcattgagat	gataagcttc	ctttgatcat	ctcttatggg	540
cctgacctcg	ctgggtgctta	atgccacatc	ctacgcctac	atcattttctc	cctcctgtgc	600
atccccctcag	cccaaggatg	tcaggaggcc	ttttccacct	gtgcttcaca	catcaccatc	660
atctttattg	cctgccyaaa	ctccatctcc	acgtgtgtga	ggcctaacct	gaggtattag	720
ctggattttg	achaaagcgac	agctatcctc	actatagtag	tgacttcttt	tctgaatccc	780
cgcattttata	gcttgaggta	aaggaagtat	gaagggagtc	aatttgcaca	atactgtcac	840
cacattccaa	aggaaca					857

<210> 234

<211> 921

<212> DNA

<213> Unknown (H38g83 nucleotide)

<220>

<223> Synthetic construct

<400> 234

atggaaagcg	agaacagaac	agtgataaga	gaattcatcc	tccttgggtct	gacccagtct	60
caagatattc	agctcctggg	ctttgtgcta	gttttaatat	tctacttcat	catcctccct	120
ggaaattttc	tcattatttt	caccataaaag	tcagaccttg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttggc	cttcctggat	gcacccact	ccttcactgt	ggctccccgg	240
atgttgggtg	acttctctct	tgcgaagaag	ataatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcacttctt	tggaggaggg	gagggattac	tccttgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggcctctg	cactatccta	ctgtcatgaa	ccctagaacc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtctctcatc	tccgcttggc	tttttgtggc	ccaaaccagc	tggacaactt	cttctgtgat	540
gtcccacagg	tcataaagct	ggcctgcacc	gacacatttg	tgggtggagct	tctgatggtc	600
ttcaacagtg	gcctgatgac	actcctgtgc	tttctggggc	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagg	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacgtgc	720
atcacccata	tcattgttat	attcttcatg	tttggacctg	gcactttcat	ctacacgcgc	780
cccttcaggg	ctttcccagc	tgacaagggtg	gtttctctct	tccacacagt	gatttttctt	840
ttgttgaatc	ctgtcattta	tacccttcgc	aaccaggaag	tgaaagcttc	catgaaaaag	900
gtgtttaata	agcacatagc	c				921

<210> 235

<211> 927

<212> DNA

<213> Unknown (H38g84 nucleotide)

<220>

<223> Synthetic construct

<400> 235

atggaaaatc	aaaacaatgt	gactgaattc	attcttcttg	gtctcacaga	gaacctggag	60
ctgtggaaaa	tattttctgc	tgtgtttctt	gtcatgtatg	tagccacagt	gctggaaaaat	120
ctacttattg	tggtaaactat	tatcacaagt	cagagtctga	ggcacctat	gtattttttt	180
cttaccttct	tgtccctttt	ggatgtcatg	ttctcatctg	tcgttgcccc	caagggtgatt	240
gtagacaccc	tctccaagag	cactaccatc	tctctcaaaag	gctgcctcac	ccagctgttt	300
gtggagcatt	tctttgggtg	tgtggggatc	atcctcctca	ctgtgatggc	ctatgaccgc	360
tacgtggcca	tctgtaagcc	cctgcactac	acgatcatca	tgagtccacg	gggtgtgtgc	420
ctaagtgtag	gaggggcttg	gggtggggga	tttatgcacg	caatgatata	acttctcttc	480
atgtatcaaaa	tacccttctg	tggctctaata	atcatagatc	actttatatg	tgatttgttt	540
cagttgttga	cacttgcctg	cacggacacc	cacatcctgg	gcctcttagt	taccctcaac	600
agtgggatga	tgtgtgtggc	catctttctt	atcttaattg	cgtcctacac	ggtcatecta	660
tgctccctga	agtcttacag	ctctaaaagg	cggcacaaaag	ccctctctac	ctgcagctcc	720
cacctcacgg	tggttgtatt	gttctttgtt	ccctgtattt	tcttgtacat	gaggcctgtg	780
gtcactcacc	ccatagacaa	ggcaatggct	gtgtcagact	caatcatcac	acccatgtta	840
aatcccttga	tctatacact	gaggaatgca	gaggtgaaaa	gtgccatgaa	gaaactctgg	900
atgaaatggg	aggctttggc	tgggaaa				927

<210> 236
 <211> 933
 <212> DNA
 <213> Unknown (H38g85 nucleotide)

<220>
 <223> Synthetic construct

<400> 236

gtagaggata	tgggtgccatt	ctctatgagg	atttctggca	tttttcaa	cttcatttta	60
cggctatcat	caccttatct	actaatatc	tgtactgaca	tgtgtacat	ttcagtttac	120
atattctcat	atagtaaaat	gttaactgca	aggggaattta	cctcaaacc	aaaccattaa	180
cgtaacttca	gagacaatat	ggattaagat	tatccatgat	ttccttcatg	aacccaagac	240
tatctccttt	gagggctgca	tggcccagat	attcttggtc	catgtctttg	ctgggtggtga	300
gatggtgctc	cttgtagcca	tggcatatga	catatatgta	gccatatgca	aacctctcca	360
ttatgcaacc	atcatgaact	tgtgcacatg	tacaggccta	gtggtaggat	cttgggtcac	420
tggagttatg	cactccctga	gccagttagc	tttcaactgta	agtttgccct	tctgtggccc	480
aaacatagtg	gacagttatt	attgtgacct	tactttggtc	atcaaacttg	cctgtacaga	540
tacttatatc	cctgaagcgt	tgatgctttt	ggacagtggg	cttatggggg	tgacttcatt	600
ttgcttttgc	tgatctccta	cacggtcatt	ctgattactg	tgacgcgacc	ttcctcagca	660
ggtagggcga	aggctggcag	cactctgact	gcccacgtga	ctgtgggtgac	cctgttcttt	720
gggccttgta	tcttcatcta	tgccctggcc	ttcagcaact	taccagtggg	taacattttg	780
tctgtattct	ctacagtttt	cacacctata	ttaaaccccc	ttatctacac	actgagaaac	840
aaagaggtaa	aatcagcaat	tcataacctg	aagacccagt	atgtaacttc	caggctgtct	900
tcacagctct	ctctcatagg	actagatttg	ttg			933

<210> 237
 <211> 629
 <212> DNA
 <213> Unknown (H38g86 nucleotide)

<220>
 <223> Synthetic construct

<400> 237

ttgggaaatg	tctcaacaga	gactactttt	atttttgttt	gtttcacaaa	tggacaacaa	60
ttccagcctg	tatgcttctc	ctcattttta	gtgcttggcc	actcagtgtc	tgggctaagt	120
tctctctcca	acatcctggg	gaacttgtct	tcagcttggt	ttcttttgtt	tttgtttttc	180
agatgtccta	ctcctttgtc	attttaatta	aaatgataat	gaactctata	tctgagaggt	240
acatcaccac	taatttgaag	tgcaagattc	tgcccttggt	tttatctgct	ttgctatcag	300
tgagcactct	aatacttttg	gcttggggtc	actgtgggat	ctgtgtgccc	cagggtctgtt	360
ctctgacgat	gcttggcctg	cactggggta	ggtattgatg	gtgtcatggc	ccaccagag	420
gcaatggcca	gtctgtcttt	ctgtgaccgc	agcatcatca	accactgtgt	gtggcacact	480
tcttttctac	aaactctcct	tagagcacct	gcttcacaag	ctgggtgattt	tgtagtcatt	540
gcgtagtgtg	tgatcatctt	catctctgac	atactatcct	ttccaccatc	ctccattttc	600
tcttttctga	ggcaaaactca	aaagctttt				629

<210> 238
 <211> 822
 <212> DNA
 <213> Unknown (H38g87 nucleotide)

<220>
 <223> Synthetic construct

<400> 238

atgggggaatc	tgggcatgat	catgggtcatc	aggatcaacc	ccaaactcca	cacccttatg	60
tactttttcc	tcagccactt	gtccttttgtt	gatttctgtt	attccaccac	aattacacca	120
aaactgctgg	agaacttggt	tgtggaagac	agaatcatct	ccttcacagg	atgcatcatg	180
caattcttct	ttgctgtat	atttgtgggtg	acagaaacat	tcagtctggc	agcgatgggt	240
tatgacagat	ttgtggcagt	gtgtaaccct	ctgctttaca	cagttgcaat	gtcccagagg	300

ctttgtctct	tgtagtgge	tgcatacat	tcttgaggt	tagttgttc	cttaacatac	360
acatactttc	tgtagacttt	atctttttgt	aggactaact	tcattaataa	ctttgtctgt	420
gagcacgctg	ccattgttgc	tgtytcttg	tctgaccct	acatgagcca	gaaggtcatt	480
ttagtttctg	caacattcaa	tgaataaagc	agcctgggtga	tcattctcac	ttcctatgct	540
ttcattttta	tcactgtcat	gaagatgcct	tccactgggg	ggcgcaagaa	agcgttctcc	600
acgtgtgcct	cccacctgac	cgccatcacc	atcttccatg	ggactatcct	ttttctctac	660
tgtgttccta	actccaaaag	ttcatggctc	atgggtcaagg	tggcctctgt	cttttacaca	720
gtggtcattc	ccatgctgaa	ccccttgatc	tatagcctca	ggaacaaaga	tgtaaaagag	780
acagtcagga	agttagtcat	taccaaatta	ttatgtcata	aa		822

<210> 239

<211> 1041

<212> DNA

<213> Unknown (H38g88 nucleotide)

<220>

<223> Synthetic construct

<400> 239

atgaccaaca	gcagtgtcaa	gggagacttc	atcctgggtg	gtttctctca	tcagccccac	60
ctggaaaaga	tctcttttgt	ggctgttttg	atatacctatc	tccttaccct	tgtgggaaat	120
acagtaatta	ttctgatctg	ctctgtagac	cctaaactca	agacacccat	gtattttttc	180
ttactcacct	ctccttagtt	gatatctgtt	ttaccaccag	tattgtcccc	cagctgctgt	240
ggaacctaaa	aggacctgac	aaaacaatca	cattcctggg	ttgtgtcatc	cagctctaca	300
tctccctggc	attgggctcc	actgagtgtg	tctcctggc	tgtaatggct	tttgatcgct	360
atgctgcagt	ttgcaaacct	ctccactata	ccgccgtaat	gaacctcag	ctgtgccagg	420
ttctggcagg	ggttgcgtgg	ctgagtggag	tgggaaacac	tcttatccag	ggcactgtca	480
ccctctggct	tctcgtctgt	ggacaccgat	tgctccaaca	tttcttcgtg	aggtaccctc	540
catgattaag	cttgcagtgt	tggacatcca	tgataatgag	gttcagctct	ttgttgcttc	600
actggctctt	ctcctcttgc	ccttagtgct	aatactgctg	tcctatggac	atatagccaa	660
ggtggtcata	aggatcaagt	cagtccaggc	ctgggtgcaa	ggcctgggga	catgtggatc	720
ccatttgata	gtagtgtccc	tcttctgtgg	gaccatcaca	gctgtctaca	tccagtccaa	780
cagttcttat	gcccattgct	atgggaagtt	catctccctc	ttctatacag	ttgtgacccc	840
gacctcaat	cctctcatct	acacactgat	gaataatgac	gtgaaaggag	cactgcgatt	900
atttaacaga	gacttaggca	cataaaaaat	gaagcagagt	acacagcgct	caactttttt	960
cacaaagcaa	ctttaagggt	catcttgtat	aattttttcac	tcaagaactt	tgccagtctg	1020
taaaggaaga	gatgtaatct	t				1041

<210> 240

<211> 957

<212> DNA

<213> Unknown (H38g89 nucleotide)

<220>

<223> Synthetic construct

<400> 240

atggataagt	ccaattcttc	agtgggtgtct	gaatttgtac	tggtgggact	ctgtagttct	60
caaaaactcc	agcttttcta	tttttgtttc	ttctctgtgt	tgtatacagt	cattgtgtctg	120
ggaaatcttc	tcattatcct	cacagtgaact	tctgatacca	gcctgcactc	ccctatgtac	180
tttctcttgg	gaaacctttc	ctttgttgac	atttgtcagg	cttcttttgc	tacctctaaa	240
atgattgcag	attttctgag	tgcacacgag	accatatctt	tcagtggctg	catagcccaa	300
attttcttta	ttcacctttt	tactggaggg	gagatgggtc	tacttgtttc	gatggcctat	360
gacaggatag	tagccatatg	caaaccctta	tactatgtgg	tcatacatgag	ccgaaggaca	420
tgcactgtct	tggtaatgat	ctcctgggct	gtgagcttgg	tgcacacatt	aagccagtta	480
tcatttactg	tgaacctgcc	tttttgtgga	cctaagttag	tagacagctt	tttttgtgat	540
cttctctgag	tcaccaaact	tgcctgcctg	gactcttaca	tcattgaaat	actaattgtg	600
gtcaatagtg	gaattctttc	cctaagcact	ttctctctct	tggtcagctc	ctacatcatt	660
attcttggtta	cagtttggct	caagtcttca	gctgcaatgg	caaaggcatt	ttctacgctg	720
gcttcccata	ttgcagtagt	aatattatct	tttggacctt	gcactctcat	ctatgtgtgg	780
ccctttacca	tctctccttt	ggataaattt	cttgccatat	tttacactgt	tttcaccccc	840

gtcctaaacc ccattattta tacactaagg aatagggata tgaaggctgc cgtaaggaaa 900
attgtgaacc attacctgag gccaaaggaga atttctgaaa tgtcactagt agtgaga 957

<210> 241

<211> 935

<212> DNA

<213> Unknown (H38g90 nucleotide)

<220>

<223> Synthetic construct

<400> 241

atgcctgcc	agaactcctc	ctccgtgaca	gcgtttatcc	tctcaggctt	aaccgaccag	60
ccgggactcc	agatcccccgc	cttcttcctg	tttctaggtt	tctacgcggt	cacggtgggtg	120
gggaacctgg	gcttgataat	cctgataggg	ctcaactctc	gcctgcatat	ccccatgtac	180
tttttccctt	tcaacttgct	cttcatagat	tttagttatt	ccactaccct	cgcccctaaa	240
atgctgatga	gctttgtctc	agagaacatc	atttcctatg	cagggtgtat	gactcagctt	300
tttttcttct	gtttctttgt	cttttctgaa	tcctatatcc	tatcagcgat	ggcgtatgac	360
cgctacgtgg	gcactctgtaa	cccactgttg	tacacgggtca	ccatgtctcc	ccagatgtgt	420
ttgtctcctt	tactgggtgt	ctatgggatg	gggattttgg	ggctgtgggt	catatgggaa	480
acataatgtt	tatgtccctt	tgtggagaca	accttgtcaa	tcactatatg	tgtgacatcc	540
ttcctctcct	tgagctctcc	tgcaacagct	cttacataaa	tttgcgtgtg	gtttttatta	600
ttgtgaccgt	tggcattggg	gtgccgattg	tcaccatttt	tctctcttat	ggttttatcc	660
tttccagcat	tctccacatt	agttccacag	agggcagggtc	taaagccttc	agtacctgca	720
gttcccatat	aattgtggta	tcgcttttct	ttgggtcagg	tgctttcatg	tacctcaaac	780
caccttctat	tctacccttg	gaccagggga	aagtgtcctc	cattttttgt	actgctgtgg	840
tgcccatgtt	taaccatta	atctacagcc	tgaggataaa	agatgtcaaa	gttgccctga	900
ggagaacctt	ttgcagaaa	ttagtctctt	aaaaa			935

<210> 242

<211> 1071

<212> DNA

<213> Unknown (H38g91 nucleotide)

<220>

<223> Synthetic construct

<400> 242

atgaattggg	taaataagag	tgtcccacag	gagttcattc	tgtagtttt	ctcagatcaa	60
ccatggctag	agattccacc	ctttgtgatg	tttctgtttt	cctatatctt	gacaatcttt	120
ggcaatctga	caataattct	tgtgtcacat	gtggatttca	aactccacac	ccctatgtac	180
ttttttctta	gcaatctctc	actcctggac	ctttgtcata	ccacaagtac	agttccacaa	240
atgctggtaa	acatatgcaa	caccaggaaa	gtaatcagtt	atggtggctg	tgtggcccag	300
cttttcattt	tcctggcctt	gggttccaca	gaatgtcttc	tcctggccgt	catgtgcttt	360
gataggtttg	tagctatttg	tcggcctctc	cattactcaa	ttatcatgca	ccagaggctc	420
tgcttccagt	tggcagctgc	atcctggatt	agtggcttta	gcaattcagt	attacagtcc	480
acctggacac	ttaagatgcc	actgtgtggt	cacaaagaag	tggatcactt	cttctgtgaa	540
gtccctgctc	tgctcaagtt	gtcctgtgtt	gacacaacag	caaattgaggc	tgaactatcc	600
ttcatcagtg	tgctattcct	tctaataccc	gtgacactca	tccttatatc	gtatgctttt	660
attgtccaa	cagtggtgag	aatccagctc	gctgaagggtc	aacgaaaggc	atttgggaca	720
tgtggctccc	atctaattgt	ggtgtcactt	ttttatggta	cagctatctc	catgtacctg	780
caaccacctt	caccagctc	caaagaccgg	ggaaagatgg	tttctctctt	ctgtggaatc	840
attgcacca	tgctgaatcc	ccttatatat	acacttagga	acaaagagggt	aaaggaagcc	900
tttaaaagggt	tggttgcaaa	gagtccttct	aatcaagaaa	taagaaatat	gcaaatgata	960
agcttttgcta	aagacacagt	gcttacttac	cttactaact	tctccgcaag	ttgtcctatt	1020
tttgtcatta	ctatagaaaa	ctattgtaat	ctccctcaaa	gaaaatttcc	t	1071

<210> 243

<211> 959

<212> DNA

<213> Unknown (H38g92 nucleotide)

<220>

<223> Synthetic construct

<400> 243

cacacagagc	cacggaatct	cacaggagcc	tgagaactcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcccat	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacggtg	120
ctgaggaacc	tcctcatcag	cctggctgtc	agctctgact	cccacctcca	caccccaatg	180
tgtctcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcacctcgge	cacggttccc	240
aagatgattg	tggacatgcg	gtcgcatagc	ggagtcactc	cttatgcgga	ctgcctgaca	300
cggatgtctt	tcttggtcct	ttttgcatgt	gtagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcactgt	gaatcctcac	420
ctctgtgtct	tcttagtttc	gggtgccttt	tccttagcct	gttggattcc	cagctgcgca	480
gttggattgt	gttgcaattc	accttcttca	agaatgtgga	aatctctaata	tttgtctgtg	540
acccatctca	acctctcaag	cttgccctgtt	ctgacagcat	catcgatagc	atgttcataat	600
atttcgatag	tactatgttt	ggttttcttc	ccatttcagg	gacccctttg	tcttactata	660
aaattgtccc	ctccattcta	aggatttcat	cgtcagatgg	gtagtataaa	gccttctccg	720
cctgtggctc	tcacctgcca	gttgtttgct	tattttatgg	aacaggcatt	ggcgtgtacc	780
tgacttcagc	tgtggcacca	cccctcagga	atggtgtggg	ggcgtcagtg	acgtatgctg	840
tggtcacccc	catgctgaac	cctttcatct	acagcctgag	aaacagggac	attcaaagcg	900
ccctgtggag	gctgcgcgag	agaacagtca	aatctcatga	tctgttccat	cctttttct	959

<210> 244

<211> 939

<212> DNA

<213> Unknown (H38g93 nucleotide)

<220>

<223> Synthetic construct

<400> 244

atggaggggt	tcaactgttc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agagattctt	ttttgtggta	ttttctgtct	tctatttaata	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtgcta	tccacctcac	accttcactc	tcccatgtac	180
ttcctgctca	gcaacctgtc	tctcattgac	atgtgcctgt	cctcctttgc	cacaccaaaag	240
atgattatgg	acttttttgc	tctgcgtaag	accatctctt	ttgaaggctg	catttctcag	300
atcttttttt	gcacctcttc	accgggactg	agattgtgct	gctgatctcc	atgtcttttg	360
acaggatat	tgccatatgt	aaacctctcc	attattcaac	aattatgagc	caaagagtgt	420
gtgttgagct	tgtggccggt	tcttggacag	tgggctttct	gcatacaatg	agccaattag	480
cttttaccct	ctatttgccc	ttctgtggct	ccaatgttgt	agagtttttt	ctgtgatctt	540
cctttgggtca	tccagctagc	ttgtatggat	atttatgttc	ttgggatctt	catgatttca	600
actagtgggt	tgattgtctt	tataagtttt	ctgcttttgc	tcacctccta	catcattgtt	660
cttattactg	tcagggaacta	ctcctccaca	ggatcctcca	aggctctttc	tacctgtaca	720
gcacatttta	ttgttgtgtt	aatgttcttt	gggcctgtga	ttttcattta	tgtgtggcct	780
tccacaaact	tcttggtaga	caaaattctc	tctgttttct	ataccatctt	cactcccttt	840
ctgaatccac	ttatctatac	tttgagaaac	caggaagtga	agacagcaat	gaagaagtaa	900
ctgaatattc	agtatttcag	tcttgggaaa	actgctccg			939

<210> 245

<211> 1014

<212> DNA

<213> Unknown (H38g94 nucleotide)

<220>

<223> Synthetic construct

<400> 245

atgatattgc	ctgctagctt	ttcttaagga	acaatggaaa	caagcagtgt	aagttctgga	60
acagatttca	tccttctggg	gttttctgat	cgaccccaat	tagagcacat	catctcagtg	120
gttgtcttca	tcattctatat	tgtgactctg	gtaggaaata	caaccatcat	tcttgtatct	180
tatctagaca	cccagctcca	taccttcatg	tattttttct	tatccaattt	gtctttcttg	240

gacctctgtt	atacaactag	cattatcccc	cagatgctgg	caaataaatg	gggccccaaa	300
aaatctatta	cttatggagg	gtgtgtactc	caattctttt	ttgtccttga	cttggggagcc	360
acagaatgtc	ttctgttggc	tgtgatggcc	tatgatcggt	atgctgctgt	ctgtcaacct	420
cttcactaca	ccttaaaatg	caccctcagc	tttgccactg	cctgggttgag	tggctcttgcc	480
agtgccttaa	ttgtttgctc	cttgactttg	aagttgccaa	gatgtgggca	ccgggaagtg	540
gataattttt	tctgtgagat	gccagcattg	atcaagatgg	cttgtgtcta	ttcaaaagta	600
attgagattg	ttgtctttgc	tttcggagtg	gtatttcttt	tcgtacctct	atcactaatt	660
cttatctcat	atggagttat	cactcaagct	gtaatgagga	tcaagtcagc	aacaagggtg	720
caaaagatcc	ttaatacatg	tggctccac	ctcacagtag	taattctgtt	ttatggaaca	780
atcattttata	tatacatgaa	gccacagaat	accatatccc	aagatgaagg	gaagttcttc	840
actcttttac	acaatcatca	caccagcct	taaccttccc	atctacactt	taagaaacaa	900
agatgtaaag	agtgcactga	agagaatact	gtggatgaaa	aaatcttcag	cagaatcatg	960
aattagatgg	aaaaaagtag	aatgtagagc	actaaagaaa	tattggcatt	tatc	1014

<210> 246

<211> 941

<212> DNA

<213> Unknown (H38g95 nucleotide)

<220>

<223> Synthetic construct

<400> 246

atgcaccaag	gaaattgaac	tactgtctct	aaattctttc	tcctgggaat	cacaacaaag	60
cctaaagagc	agcagtttat	cttcatgctg	tttctatgca	cgtatctggg	cactatggta	120
agaaatttac	ttatcatcct	ggccgttgct	agtgatgctc	acctccatgg	ccccatatat	180
ttcttcttg	ccaatctatc	tttactaac	gtctgcatca	caaccactac	agtccccaaa	240
atcttggcag	atattcaaaag	ccagaattca	accatatcct	ttgaaggatg	ccctgcacaa	300
atgtagtttt	aaatattcct	ggtggatctg	gataatttcc	tattggtaga	catggcatat	360
aattgataca	ttgccatctg	tcacccatta	cactatatgt	ggtagtactg	agtcccaaga	420
actgtgccct	gttggttggtg	actccatggg	ttatctccaa	ccttgtctca	atactgcatc	480
tcagtctgct	aagccactta	actttctgtg	atttcacata	tcttctatga	cctggaaccc	540
attttagggc	ttgcttgctc	agacacccaa	atcaacaact	tgataattac	tgccattggg	600
gaagtagtta	tcttcacccc	ctttaccttc	acattcttgt	ctcctatggc	cttattggca	660
gcactatgct	tggagttcca	tcagccaagg	ggaagtagaa	aacattctct	acatgtgggt	720
cccattctctc	agttgtgccc	caggtcttct	atgggttcat	cattggagtc	tactttctct	780
ccttttttgc	ctactcagca	gaaagggatg	aggtagctgc	tatcatgtat	acaactgtaa	840
ctcacttgat	caaatacttt	atctgtagtc	taaggaaacg	ggacatgaaa	ggagcactga	900
ggagaccact	cagcagacaa	ggtttttctg	gagtgggtgag	c		941

<210> 247

<211> 941

<212> DNA

<213> Unknown (H38g96 nucleotide)

<220>

<223> Synthetic construct

<400> 247

atgatgaaga	agaaccaaac	catgatctca	gagttcctgc	tcctgggcct	tccatccaac	60
ctgagcagcg	gaatctgttc	tatgccttgt	tcttggccgt	gtatcttacc	acctccttgg	120
ggaacctcct	cgtcattgtc	ctcattcgac	tggactccca	cctccacatg	cctatgtatt	180
tgtgtctcag	caacttgccc	ttctctgacc	tctgttttcc	ctcgggtcaca	atgccccaat	240
tgtctgcagaa	catgcagagc	caaaacccat	ccatcccctt	tgcggactgc	ctggctcaga	300
tgtactttca	tctgttttat	ggagttcttg	agagcttccct	ccttgtgggtc	atggcttata	360
actgctatgt	ggctatttgc	tttccctctgc	actacaccac	tatcatgagc	cccaagtgtt	420
gccttgggtc	gctgacactc	tcctggctgt	tgaccactgc	ccatgccacg	ttgcacacct	480
tgcttatggc	caggctgtcc	ttttgtgctg	agaatgtgat	tcctcacttt	ttctgtgata	540
catctacctt	gttgaagctg	gcctgtctca	acacgcaagt	caatgggtgg	gtgatgtttt	600
tcattggggc	gctcatcctt	gtcatcccat	tcctactcct	catcatgtcc	tgtgcaagaa	660
togtctccac	cactctcagg	gtcccttcca	ctgggggcat	ccagaaggct	ttctccacct	720

gtggccccca cctctctgtg gtgtctctct tctatgggac aattattggt ctctacttgt	780
gccattgac gaatcataac actgtgaagg acactgtcat ggctgtgatg tacactgggg	840
tgaccacat gctgaacccc ttcattctaca gcctgaggaa cagagacatg agggggaacc	900
ctgggcagag tcttcagcac aaagaaaatt tttttgtctt t	941

<210> 248

<211> 994

<212> DNA

<213> Unknown (H38g97 nucleotide)

<220>

<223> Synthetic construct

<400> 248

atggctgccg agaactcctc ctccgtgaca gagtttatcc tcgcaggctt aatccaccag	60
ccgggactcc aggtccccgt cttcttctctg tttctagggt tctacgcggt cacgggtggtg	120
gggaacctgg gcttgataat cctgataggg ctcaactctc gcctgcatat ccccatgtac	180
ttttccccct tcaacttgct cctcgtagat tttagtttct ctacgacctt cattcccaaa	240
atgctgatga gttttgtctc aaggaagaac attatttctt tcacagggtg tatgagtcag	300
ttcttcttct tctgtttctt tgtcttttct gagtccttca tctgtcggc gatgggtgtg	360
gaccgctacg tgggcatctg taaccactg ttgtacacga tcaccatgtc tccccagggtg	420
tgtttgctcc ttttactggg tgtctacggg atgggggttt ttggggctgt ggctcataca	480
ggaaatatag tgtttctcac cttttgtgca gacaaccttg tcaatcata catgtgtgac	540
atccttcccc tctttgagct ctctgcaac ggctcttaca taaatgtcct ggtcatcttt	600
attgtttgga ccgttggcat tggggtgccc attgttgccg tttttatctc ttatggtttt	660
attctttcca gcattctccg cgttagttct gctgaggcca ggtctaaagc cttcagtagc	720
tgcagctcct acataattgc agtttctctt ttctttgggt caggagcttt tacgtacctc	780
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gtggtgcccc tgtttaacct attaatctac agcctgagga ataaggatgt caaacttgcc	900
ctgaagagaa ctttttccag aataagcttt tcttgaaaaa aatttttagaa acagaaaaga	960
gatactagga tttttttaaa atcagattgc tttt	994

<210> 249

<211> 942

<212> DNA

<213> Unknown (H38g98 nucleotide)

<220>

<223> Synthetic construct

<400> 249

atgtcgaatg aggacatgga acaggataat acaacattgc tgacagagtt tgttctcaca	60
ggacttacat atcagccaga gtggaaaatg cccctgttct tgggtgttctt ggtgatctat	120
ctcatcacta ttgtgtggaa ccttggtctg attgctctta tctggaatga cccacaactt	180
cacatcccca tgtacttttt tcttgggagt ttagcctttg ttgatgcttg gatattcttc	240
acagtaactc ccaaaatgtt ggttaatttc ttggccaaaa acaggatgat atctctgtct	300
gaatgcatga ttcaattttt ttcttttgca tttggtggaa ctacagaatg ttttctcttg	360
gcaacaatgg catatgatcg ctatgtagcc atatgcaaac ctttactata tccagtgatt	420
atgaacaatt cactatgcat acggctgtta gccttctcat ttttaggtgg ctctctccat	480
gccttaattc atgaagtcct tatattcaga ttaaccttct gcaattctaa cataatacat	540
catttttact gtgatattat accactgttt atgatttcct gtactgacct ttctattaat	600
tttctaattg tttttatttt gtctgggtca attcaggat taccattgt gacagttctt	660
aattcttaca catttgctct tttcacaatc ctaaaaaaga agtctgttag aggcgtaagg	720
aaagccattt ccacctgtgg agcccatctc ttatctgtct ctttatatta tggcccactt	780
atcttcatgt atttgcgccc tgcattctcca caagcagatg accaagatat gatagaactc	840
gtcttttata caatcataat tccttttgcta aatcccatTA tctacagtct gagaaataaa	900
caagtaatag attcattcac aaaaatggta aaaagaaatg tt	942

<210> 250

<211> 939

<212> DNA

<213> Unknown (H38g99 nucleotide)

<220>

<223> Synthetic construct

<400> 250

atggagggga	aaaatctgac	cagcatctca	gaatgtttcc	tcctgggggt	ctctgagcag	60
ctggaggagc	agaagccccct	ctttgggtcc	ttcctgttca	tgtacttggg	cacgggtggca	120
ggcaacctcc	tcattcattct	agtcattcatt	actgacactc	aactccatac	ccccatgtac	180
ttctttctag	ccaacctctc	ccttgacagat	gcctgctttg	tgtccaccac	agtcacctaa	240
atgctggcaa	acatacagat	ccagagtcag	gccatctcct	actcagggtg	tctactacag	300
ttgtattttt	tcattgttatt	tgtgatgctg	gaggcattcc	tcttggcggt	catggcctat	360
gactgctacg	tggccatattg	ccacccactt	cattacattc	tgatcatgag	ccctgggctc	420
tgcattcttc	tcgtgtctgc	atcctggatc	atgaatgccc	tccactccct	tctacacaca	480
cttctgatga	acagcctgtc	cttctgcgca	aaccatgaga	tcccacactt	cttctgtgac	540
atcaatcccc	tcctgagtct	gtcctgcaca	gacccttca	ccaatgagct	gggtgatctt	600
atcactgggg	gtctcacagg	actcatttgt	gtgctttgcc	tgattatctc	ttacacgaac	660
gttttctcga	ccatcctgaa	gatcccatca	gctcagggga	agcggaaagc	cttttccacc	720
tgcagctctc	atctctccgt	ggctctctct	ttctttggga	cttctttttg	tgttgatttc	780
agttctccct	caacccactc	ggcccagaag	gacacagttg	catcagtgat	gtacacagtg	840
gtaactccaa	tgttgaatcc	ctttatctac	agtttgagga	accaagaaat	aaagtcttcc	900
ctgagaaagt	taatctgggt	tcggaaaatt	cattccct			939

<210> 251

<211> 931

<212> DNA

<213> Unknown (H38g100 nucleotide)

<220>

<223> Synthetic construct

<400> 251

atggaagagg	aaaatgcaac	attgctgaca	gagtttggtc	tcacaggact	tttatatcaa	60
ccacagtggg	aaataccccct	gttcctgaca	ttcttggtta	tatatctcat	caccatcatg	120
gggaatcttg	gtctgattgc	tgtcatctgg	aaagaccctc	accttcagat	cccaatgtac	180
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atgctgaata	acttcttagc	taagagtaag	atggatatct	tgctgaaaag	caaaatacag	300
tttttttctg	ttgcaatcag	tgtaccact	gaatgttttc	tcttggcaac	aatggcatat	360
gatcgctatg	tagccatattg	caaaccctta	ctttatccag	ccattatgac	caatggactg	420
tgcattccgg	tatgtagggtg	gtcttcttca	tgctttaatc	catgaaggat	ttttattcag	480
actaaccttc	tgtaaactcca	acgtagtaca	ccacatttac	tgtgacatta	tcccattgtc	540
taagatttct	tgtactgatt	cttctattaa	ttttctaattg	gttttttattt	tctcagggtc	600
aattcaagtt	ttcaccattg	ggactgggtc	tatatcttat	acatttgtcc	tctttacaat	660
cttgaaaaag	aaatctgtca	aaggtataag	aaaagccttc	tccacctgtg	gagctcatct	720
cttatctgta	tctttatacc	atgggccccct	cgacttcatg	tatatgggct	ctgcatcccc	780
acaggctgat	gacgaagaca	tgatggagtc	tctattttac	actgtcatag	ttcctttatt	840
aaatcccatg	acctacagcc	tgagaaacaa	acaagtaata	gcttcattca	caaaaatgtt	900
caaaagaaat	aatatttaga	tctcttactc	a			931

<210> 252

<211> 690

<212> DNA

<213> Unknown (H38g101 nucleotide)

<220>

<223> Synthetic construct

<400> 252

ttctgtttgt	tcccagccac	agtctccaag	gcagtgggtga	aatttttggc	agagacaatt	60
tccttctcct	attatgtgat	acaaatgctg	gtatttttgt	tctttgtgac	tactgaatgc	120
aatcttttag	cctccctggg	caaggacatt	tatatgccaa	tcagacaacc	catgctctat	180

cctgtcacta	tgteccaagt	ttgttgatc	caattagtgg	cttcatgtta	cgggcatgga	240
gttatccata	ctatgttttt	aggaggttca	atctctatat	ttgccttttg	taagttcaaa	300
ccatcatcag	cttttttggt	gacagtttcc	cactcttggt	cctctcctgc	tcagacacct	360
acataatgaa	ttctttgttc	tttttcactg	ggtgcttcat	ttggatgagc	tcttgaccag	420
tcatecttgt	ctcccacatg	ttcatcattg	tcactttctt	gaggatcttc	tcagttgtag	480
ttgaatctaa	agggttttctt	gctttttctt	cacatctaac	tgctatcatt	ctcttctatg	540
gggacattat	atztatatat	gtgacattct	tccaactatt	ttctgaacca	agaccagact	600
gtatccattt	tctacatggt	aagaattctt	ttgttaagcc	ccattatcta	ttgtttaata	660
aaaatgcaag	tgatttggtt	tcttgaaaa				690

<210> 253

<211> 647

<212> DNA

<213> Unknown (H38g102 nucleotide)

<220>

<223> Synthetic construct

<400> 253

cttttttttt	ttgtctgaca	cagcatcctg	acctgatagg	aaggagtaaa	agaaatttgg	60
tactttcagg	aattttctgac	atatccaaga	catagaaaact	cctgtttgtc	tcttctctgca	120
tgtattattc	ctcaagaatt	ttcctaagga	ggacagtaaa	cattctattt	ctgcttaagg	180
ttatctcatt	gctttgttat	gggtcaaaac	tcagtttggt	catttttgtt	gttactgcag	240
aatttttagct	tttggcctcc	aggatctgcc	attgctatat	tattatttgt	aaccctattct	300
ctaccaaat	ctcacattaa	aagcttttaa	tttcaattct	gacggctcat	tacaataaga	360
gagtatgtat	ttcaataaca	acatcaaaca	ctatgtctta	gctcttcttt	ggcagatcca	420
atgtggtgaa	caacttctct	gatcttctct	tgctcttaga	tttatcctgc	acatttgtga	480
gtttctgata	tccatctcag	cttcctgata	atagtcctgg	tccccataat	tttatcattg	540
tggtcaatat	aaagatttag	ttagctgaag	ggaagcacia	agacttctct	atctgtccat	600
tataatttgc	tactgtcagc	aatttttttaa	tggcacacat	acatatt		647

<210> 254

<211> 936

<212> DNA

<213> Unknown (H38g103 nucleotide)

<220>

<223> Synthetic construct

<400> 254

ttcatggaaa	ataggaatat	tgctactgtc	tttattctcc	tgggactttc	tcaaaacaag	60
aacattgaag	tttttttggt	tgtattattt	gtattttgct	acattgctat	ttggatggaa	120
aacttcatca	taatgatttc	tatcatgtac	atttagctaa	ttgaccaacc	catgtatttc	180
ttccttaatt	acctcgcact	ctcagatctt	tgctacatat	ccactgtggc	ccccaaagcta	240
atgattgacc	tactaacaga	aaggaagatc	gtttcctata	ataactgcat	gatacagcta	300
tttatcactc	acttccttgg	agacattgag	atcttcatac	tcaaagcaat	ggcctatgac	360
cactacatag	ccatctgcaa	gcacctgcac	tacaccatca	tcacgaccaa	gcaaagctgt	420
aacaccatca	tcatagcttg	ttgtactggg	ggattttatac	actctgccag	tcagtttctt	480
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tatectctgc	tgaagttggc	tcgcattgat	atatacagaa	ttggtttctt	ggtaattggt	600
aattcaggcc	tgatttcttt	gttggctttt	gtgattttga	tggtgtctta	ttatttgata	660
ttatccacca	tcagggttta	ctctgctgag	agtcatacca	aagctctttc	aacctgtagc	720
tctcacataa	tagttgtggt	cctattcttt	gtgcctgccc	tcttcattta	catcagacca	780
gccataaact	ttccagaaga	taaagtgttt	gttctcttct	gtgccatcat	tgctcccatg	840
ttcagttctc	ttatctacat	gctgagaaag	gtggagatga	agaacgctgt	aaggaaaatg	900
tgggtgtcatc	aattgcttct	ggcaaggaag	taactt			936

<210> 255

<211> 924

<212> DNA

<213> Unknown (H38g104 nucleotide)

<220>

<223> Synthetic construct

<400> 255

atggccatgg	acaatgtcac	aggagtggtt	cagttttctcc	ttattggcat	ttctaactat	60
cctcaatgga	gagacacgtr	cttcacatta	gtgctgataa	tttacctcag	cacattgttg	120
gggaatggat	ttatgatctt	tcttattcac	tttgacccca	acctccacac	tccaatctac	180
ttcttcccta	gtaacctgtc	tttcttagac	ctttgttatg	gaacagcttc	catgccccag	240
gctttgggtg	attgtttctc	tacccatccc	tacctctctt	atccccgatg	tttgggtcaa	300
acgagtgtct	ccttggcttt	ggccacagca	gagtgcctcc	tactggctgc	catggcctat	360
gaccgtgtgg	ttgctatcag	caatccccctg	cgttattcag	tggttatgaa	tggcccagtg	420
tgtgtctgct	tggttgctac	ctcatggggg	acatcacttg	tgctcactgc	catgtctatc	480
ctatccctga	ggcttcactt	ctgtggggct	aatgtcatca	accattttgc	ctgtgagatt	540
ctctccctca	ttaagctgac	ctgttctgat	accagcctca	atgaatttat	gatcctcatc	600
accagtatct	tcacctgtct	gctaccattt	gggtttgttc	tcctctccta	catacgaatt	660
gctatggcta	tcataaggat	tcgctcactc	cagggcaggc	tcaaggcctt	taccacatgt	720
ggctctcacc	tgaccgtggg	gacaatcttc	tatgggtcag	ccatctccat	gtatatgaaa	780
actcagtcga	agtcctaccc	tgaccaggac	aagtttatct	cagtgtttta	tggagctttg	840
acacccatgt	tgaaccccct	gatatatagc	ctgagaaaaa	aagatgttaa	acgggcaata	900
aggaaagtta	tgttgaaaag	gaca				924

<210> 256

<211> 971

<212> DNA

<213> Unknown (H38g105 nucleotide)

<220>

<223> Synthetic construct

<400> 256

atggaagcag	aaaaccttac	agaattatca	gaattcctcc	tcttaggact	ctcagatgat	60
cctgaactgc	agcccgctcct	ctttgggctg	ttcctgtcca	tgtacctggt	catggtgctg	120
gggaacctac	tcatactcct	ggccgtcagc	tctgactccc	acctccacag	ccccatgtaa	180
ttcttctctt	ccaacttgte	ctttgtggag	acctgtttca	tctgcaccac	agtccccaag	240
atgctatgga	acatccaggc	acggagcaaa	gacatctcct	acatgggggtg	cctcactcag	300
gtgtattttt	aaatgatgtt	tgctggaatg	gatactttcc	tactggctgt	gatagcctat	360
gaccggtttg	tggccatctg	ccacccactg	cagtacatgg	tcatacataa	cccccatctc	420
tgtggcctcc	tggttctggc	atcttgggtc	atcattttct	ggttctccct	ggttcatatt	480
ctactgatga	agaggctgac	cttctccaca	ggcactgaga	ttccgcattt	cttctgtgaa	540
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gtggccacgg	cactgctggg	tgtgtttcct	gtagctggga	tcctcttctc	ctactctcag	660
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gtcaccacca	tgctgaacct	cttcatctac	agcctgagga	acaaggatgt	gaagggggcc	900
ctggggagac	tccttagcag	ggcagcctct	tgtctcttac	ggtacacaac	ctcagaacta	960
agaggatgct	a					971

<210> 257

<211> 873

<212> DNA

<213> Unknown (H38g106 nucleotide)

<220>

<223> Synthetic construct

<400> 257

atggaggggt	tcaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattctt	ttctgtgggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtccta	tccacctcac	accttcactc	tcgcatgtac	180

ttcctgctca	gcaacatgtc	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgtc	tgcgtaacac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	gacctcttca	atgggactga	gattgtgctg	ttgatctcca	tgtcttttga	360
caggatatatt	gccatatgta	aacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttggtggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agttttttcc	tctattttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcttttgg	tcattccagtt	agcttgtata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgattgc	tcttataagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcaggga	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcatt	ttattgttgt	gttaatgttc	tttggggcct	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttctcgtt	agacaaaatt	ctctccgctt	tctataccat	cttctactccc	840
tttctgaatc	cacttatcta	tactttgaga	aac			873

<210> 258

<211> 985

<212> DNA

<213> Unknown (H38g107 nucleotide)

<220>

<223> Synthetic construct

<400> 258

tacacagagc	cacagaatct	cacaggtgtc	tcagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctggg	ctgttccgtg	ccatgtacct	ggtcacgggtg	120
ctgggggaacc	tgtcctcat	cctggtgtgc	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttggct	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgattg	tgacatgca	aactcacagc	agagtcactc	cctatgaagg	ctgcctgact	300
cagatgtctt	tttttgcct	ttttgcatgt	atggatgaca	tgctcctgag	tgtgatggcc	360
tatgaccggt	ttgtggccat	ctgtcacccc	ctgcactacc	gaatcatcat	gaaccacgc	420
ctctgtggct	tcttaatctt	gttgtctttt	tttattagtc	ttttggactc	ccagttgcac	480
aatttgatta	tgttacagct	cacctgcttc	aaggatgtgg	acatttctaa	tttcttctgt	540
gaccttcttc	aactcctcca	ccttaggtgt	tccgacacct	tcataatga	aatggtcata	600
tatttcatgg	gtgccatatt	tggtgtcttc	cctatctcag	ggatcctttt	ctcttactat	660
aaaattgttt	ccccattctt	gagagttcca	acatcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacagggct	tgtagggtac	780
ctcagttcag	ctgtgttacc	atcccccagg	aagagtatgg	tggttccagt	gatgtacact	840
gtggtcaccc	ccatgctgaa	ccccttcac	tacagcctga	ggaacaagga	cattcaaagt	900
gcctgtgca	ggctgcatgg	cagaatcatc	aaatctcatc	atctccatcc	tttttgttat	960
atgggataga	aatggcagca	aaatt				985

<210> 259

<211> 976

<212> DNA

<213> Unknown (H38g108 nucleotide)

<220>

<223> Synthetic construct

<400> 259

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ttccctgggc	tggaggcctt	ccacatctgg	atctcaattc	ccttcttctc	tctgagcaca	120
gttgctctct	tagggaacag	catgatccta	ttgggtgtta	ttctggagcc	aaacctccat	180
gaacccatgt	actgttttct	cttcatgctg	tctgccgctg	acctggggct	gacctctctc	240
acaatgcccc	cgacctcag	tgtcctctgg	ttcagtgac	gtgaaatcat	cctcaatgca	300
tgtatcatcc	agctcttttt	cctccacagc	tctggcttta	tggaatcctc	agtactgatg	360
gccatggctt	ttgacgctt	tggtgccatt	tgagacccc	tcagatatgc	taccatcctg	420
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tctccatccc	tctttctcat	taagagactg	tcattttgca	aagtcaatgt	cctttcccat	540
tcttactgct	tccaccctga	tgcgcttaaa	gttgcatgtt	ctgattcaag	gatgaacagc	600
tatggaggct	tagctgttct	cattctggtc	accgggggtg	gtacaccatg	tgttgcgctt	660
tcctacatcc	tgataatcca	ctctgtacta	aacatcatct	cttcagaggg	acggaggaag	720


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gccttcgaca cttgtggatc tcacattggg gcagttgcag tcttctacat tccctggggt 780
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gtccaacatc tatttccttg gccctctctg gctgaacccc atcatatata gtgtgaagac 900
taaacaaatc cgcagggtcta tcttcaaact ctttcaaaca aaatcaaaag aaatgtaatg 960
ggggcttttc ttctctg 976

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<210> 260

<211> 884

<212> DNA

<213> Unknown (H38g109 nucleotide)

<220>

<223> Synthetic construct

<400> 260

```

atccaatgca agggctaata gaagtgaatt aagacattct ctgtaactcc aatattaaat 60
ggaaaccggg aaatagccag attcctctcc aacctgtcct tggctggcat cggtttcccc 120
tccaccatag tctccaagat gattgtggac atccagtctc acagcagagt catctcctat 180
gcgggctgcc tgactcaggt atctcttttt gccgtttttg gatgcatgga agacatgctt 240
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aatgacatag tcatgtattt ccttgctgcc atatttggtt ttcttcccat ttcggggacc 540
ttttcatctt actataaaat tgtttctctc attctgaggg ttctcatcctc aagtgggaag 600
tataaagcct tctccacctg tggctctcac ctgtcagttg ttgtgttatt ttatggaaca 660
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tcagtgatgt acacggtggg tactcccatg ctgaaccctc tcatctacag cctaacaggg 780
aaattaaaag tgccctgagg cagctgcact gcagaatagt ctaatctcat tttcttatta 840
tctgttccat tcttccgta gtgtgagtta gaaaaggcag caag 884

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<210> 261

<211> 959

<212> DNA

<213> Unknown (H38g110 nucleotide)

<220>

<223> Synthetic construct

<400> 261

```

tacacagact cgcagaatct cacaggtgtc ttagaatttc tcttctctggg actctcagag 60
gatccagaac tgcagcccggt cctcggtggg ctgttctgtt ccatgtacct gatcacggtg 120
ctggggaacc tgctcatcat cctggccgct agctgtgact cccacctcca caccctcatg 180
tacttcttcc tctccaactt gtccttggtt gacatcggac tcacctctgc caccatccct 240
aagatgattg ttgatatgca atctcacagc agaatcatct cctatgaggg ctgcctgatg 300
cagatgtctt tatctatatt gtgtgtatga atgacatggg cctgactgtg atggcctatg 360
accagtttgt ggccatttgt caccctctac gctaccaggt catcatgaat ccccatctct 420
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catctcaact tctcaacctt gcctgttctg acagtgtcat caataacata ttcatgtatt 600
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gttcagctgc gtcctctttc cccaggaagg gtgcgggtcac ctgagtgtg tacactgtgg 840
tcatccctat gctgaacccc ttcacttaca gcctgagaaa caggacattt aaaagtgcc 900
tgtggagggt gcacagcaga acagtctaatt ctcatatct gttccatctt ttctgtagt 959

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<210> 262

<211> 955

<212> DNA

<213> Unknown (H38g111 nucleotide)

<220>

<223> Synthetic construct

<400> 262

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gatccagaac	tgcagccact	ccttgctggg	ctgttcctat	ccatgtgcct	ggtcacgatg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	catccccatg	180
tacttcttcc	tctccaacct	gtccttgccct	gacattggtt	tcaccttggc	cacgggtcccc	240
aagatgattg	tagacatgca	atcacatagc	agagtcactc	cccatgcagg	ctgtctgaca	300
cagatacctt	tctttgtcct	ttttgtatgt	atagatgaca	tgctcctgac	tgtgatggcc	360
tatgactgat	ttgtggccat	ctgtcacccc	ctgcactacc	cagtcacatc	gaatcctcac	420
ctctgtgtct	tcttagtggt	gatgtctttt	tccttagcct	gttggattcc	tagctgcaca	480
actggattgt	tacaattcac	ctgcttcaag	aatgtggaaa	tctctaattt	tttctgtgac	540
tgatctcaac	ttctcaacct	tgcctgttct	gactgtcatc	agtaacatat	tcatacattt	600
agatagtact	atatttggtt	ttcttcccat	ttcagggatc	cttttgtctt	actataaaat	660
tgtgccctcc	attctaagaa	ttccattgtc	agatgggaag	tataaagcct	tctccacctg	720
tggctctcac	ctggcaattg	tttgcttatt	ttatggaaca	ggcattggca	tgtacctgac	780
ttcagctgtg	tcaccagccc	ccaggaatgg	tgtggtggca	tcagtgttgt	acgctatggg	840
cacccccatg	ctgaacccct	tcatctgcag	cctgagaaac	aggggcatc	aaagtgcctt	900
gtggaggctg	tgcaggagga	aagtctaata	tcatgatctg	tttcatcctt	tttct	955

<210> 263

<211> 1049

<212> DNA

<213> Unknown (H38g112 nucleotide)

<220>

<223> Synthetic construct

<400> 263

atgtcccaac	tgggaaggga	caacataacc	tgggtgagtg	agttcatcct	aatgggtctc	60
tccagtgaac	ggcagaccca	ggctggactc	tttatcttat	ttggggctgc	ctacctgctg	120
acctgtctgg	gcaatgggct	catcctgctc	ctgatctggc	tggacgtgag	actccacctg	180
cccatgtatt	tcttctctctg	caacctctca	cttgtgaaca	tctgctacac	ctccagcagg	240
gtccctcaga	tgctggtgca	ctgcaccagc	aaagaaagac	catctccttt	gcccgatgtg	300
ggacccagct	ctttttctcc	ctggccctcg	gggggaccga	gtttttgttg	ctggccgcaa	360
tggcctatga	ccgctacgtg	gctgtttgcg	acccccctgtg	ttacatagca	gtgatgagcc	420
caaggctctg	catggcactg	gcagctgtct	cttggctagt	gggcctggct	aattctgcta	480
tggagacggc	actgaccatg	cacctgcccc	cctgtgggca	caacgtgctg	aaccatgtgg	540
cctgtgagac	actggcactg	gtcaggtcgg	cctgctggga	catcaccttc	aatcaggtgg	600
tcatagtggc	ctccagtgtg	gtgggtgctg	tgggtgccctg	ctgcctgggc	tcgctgtcct	660
acaccctcat	tgtagtgtgc	gtcctgcaga	tccactccac	ccaggggcac	cgcaaggcct	720
ttgggacctg	tgcttccac	ctcactgtgg	tctccatata	ctatgggatg	gccctcttta	780
cctacatgca	gcctcgctcc	atggcctcag	ctgagcagga	aaaggatgatg	gtactctctt	840
atgctgtggt	gacccccatg	ttgaatcctt	tcatctacag	tctgcggaac	aaggatgtga	900
aggcagctct	gagtcgagct	ctgatgagga	gctctgaatt	aaaacattag	agagtgggtt	960
gagtaacaag	aaggcctcac	tctgaaaaca	gtgggcattg	gactgtgctc	tccagtataa	1020
cgtgtgtacg	catgtgtgtg	tatgtgtgtg				1049

<210> 264

<211> 955

<212> DNA

<213> Unknown (H38g113 nucleotide)

<220>

<223> Synthetic construct

<400> 264

atggacagtc	ccagcaatgc	caccgtgccc	tgtggctttc	tccttcaagg	cttctccgaa	60
ttcccgaccc	tgagacccgt	gctcttcctt	ttgctgctgg	gggtgcacct	ggccaccctg	120

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ggcggaacc tgcctaccc ggtggccgtg gcctcgatgc caagccggca gccatgctg 180
ctcttcctgt gccagctgtc agccatcgag ctgtgctaca cgctgggtgt ggtgccccgc 240
tccctggctg acctgagcac gccggggcca ccgcaggggc agccctatct ccttcctgag 300
ctgcgccttt agatgcaga tgtttgtggc tctgggcggg gccgagtgt tctgctygc 360
cgccatggct aatgaccgct acgtggccat ctgccaccgc ttgcgctacg cgccgtgggtg 420
acccccgggc tgtgcgcgcg actggctctg gctgctgcct caggggactg gcggtgtcgt 480
ggggctcacg gtgccatctt ccacctgcct ttctgcggct cccgcctgct gctgacttc 540
ttctgcgaca tcacggcgct gctgcacctg gcctgcacgc ggactacgcc gacgagctgc 600
ctctgctggg cgccctgcctg gtgctgctgc tgcctgcctc ggtgctcatc ctggcctcct 660
atggcgccat cgccgcgcgc ctggccgcct gcgctgcccc aaaggccggg gcaaggccgc 720
ctccacctgc gccttgacc tggcagtcac cttcctgcac tacggctgcg ccaccttcac 780
gtacgtgcgg ccaggggcca gctactcccc gcgcctggag cgcaccctgg cgctggtcta 840
caccaacgtc acgccgctgc tgtgccact catctacagc ctgcgcaacc gcgagatcac 900
cgccgcctg agcagggtgc tggggcgccg gcggccaggc caagctccag gcggg 955

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<210> 265

<211> 945

<212> DNA

<213> Unknown (H38g114 nucleotide)

<220>

<223> Synthetic construct

<400> 265

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atgggagact ggaataacag tgatgctgtg gagcccatat ttatcctgag gggttttcct 60
ggactggagt atgttcattc ttggctctcc atcctcttct gtcttgcata tttggtagca 120
tttatgggta atgttaccat cctgtctgtc atttggatag aatcctctct ccatcagccc 180
atgtattact ttatttccat cttagcagtg aatgacctgg ggatgtccct gtctacactt 240
cccaccatgc ttgctgtgtt atggttggat gctccagaga tccaggcaag tgcctgctat 300
gctcagctgt tcttcattca cacattcaca ttcttgaggt cctcagtggt gctggccatg 360
gcctttgacc gttttgttgc tatctgccat ccactgcact accccaccat cctcaccac 420
agtgtaatgg gcaaaattgg tttggcctgt ttgctacgaa gcttgggagt tgtacttccc 480
acacctttgc tactgagaca ctatcactac tgccatggca atgcccctct tcacgccttc 540
tgtttgcacc aggatgttct aagattatcc tgtacagatg ccaggaccaa cagtatttat 600
gggctttgtg tagtcattgc cacactaggt gtggattcaa tcttcatact tctttcatt 660
gttctgattc ttaatactgt gctggatatt gcatctctgt aagagcagct aaaggcactc 720
aacacatgtg tatcccatat ctgtgtgggt cttatcttct ttgtgccagt tattgggggtg 780
tcaatgggcc atcgcttttg gaagcatctg tctcccatag tccacatcct catggcagac 840
atctaccttc ttcttcccc agtccttaac cctattgtct atagtgtcag aacaaagcag 900
attcgtctag gaattctcca caagtttgtc ctaaggagga ggttt 945

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<210> 266

<211> 869

<212> DNA

<213> Unknown (H38g115 nucleotide)

<220>

<223> Synthetic construct

<400> 266

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tttcatggct ggatttccat gcccttttgc tgtatttact tgatgcctct gctgagcaat 60
gctacaattc tactgacaat ctggctctgat cgtactcttc gggaccctat gttctacttt 120
ctagccatct tatcagccat agacctagcc ctctcaacat cctcagtgcc tcgtatgttg 180
ggtatcttct ggtttgatgc acataaaatt ggctttggag cctgggtagc ccagatgttt 240
ctgatacaca ctttcacagg aatggagtcc actgtgctgc tggcaatggc ctttgaccgc 300
tatgtggcca tctgtacatc actccactat acctctactc tgacaccccg agtattggca 360
ggcattgggt tgagcattat aatgcgcccc gtccgtctca tgttgcccat tctctaccta 420
acccatcgct tgccttctgc tgaggctcgg attattgccc actcctactg tgagcacatg 480
ggtattgcta agttggcctg tgctagcatt cacatcaatg ctattttatgg gctttttgtg 540
gcttcttatt ttggatgtcg cacttggttg aatctcctat acctacatc tccgagctgt 600
ttccacctc ccatctcaag acgctcgtca caaagcactg agaacgtgtg gctcacatgt 660

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tggggtcatg tgtgttttct ataccacct cctcttctcc ttectacct accgatttcg	720
caaaaaaaaaa tccccgttat gtccacattc ttgttgccaa cctctatgtg gtcattccac	780
ctgccctcaa tcctattatc tatggtgtga gaaccaaaca gattcatgag catgtgggtcc	840
atactttcac ctcaaagtaa ggtctctta	869

<210> 267

<211> 520

<212> DNA

<213> Unknown (H38g116 nucleotide)

<220>

<223> Synthetic construct

<400> 267

acatgctggg ttttgatggg gaacgtgggt aatgcctaca cctgaggact atcaggagcc	60
actttcaaca ccattctgcac atttgccgc ttcttctgtg atgacaatta gatcaaattc	120
tgtcacatcc tgcccctgct gaagctcatt tgaaatactt caggaaacag caagataatt	180
attgtgatct ttgacagctt ttatgattat agctggcact agggtcaccc tgatctctta	240
cctgctaate atcagggtct tgaggatgaa atcatcgagt ggcaaagcca ataattttat	300
ccatccactt gtgcctccca cctaactgct atgaccttcc tttgggatcc ccattctcag	360
acatgtgaag tacctcagat aaatcactga cagaagacaa gttggcatca tgacttgcac	420
catctttatt cctatgctag aacttttgat ccaaagtcta aagaaggata tacaagttgc	480
cttcaaaaag gccataggta acttctgggt ttttgagagg	520

<210> 268

<211> 952

<212> DNA

<213> Unknown (H38g117 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1) ... (952)

<223> n = A,T,C or G

<400> 268

attagcacaa tgtctgtctt caaaagttct gcataaaacc ctgcttctct ccaaacgggc	60
ctctcaggcc ttgaaagcag atatgacttg atttccctgc ccattctctt ggtttatgcc	120
acctcaattg ccgggaacat tagcatcctc ttcattatca gaactgagtc ttccctccac	180
caaccgatgt attactttct gtcaatgctg gcattcactg acctgggcct atctaact	240
accttaccta ccatgttcag tgtcttcttg ttccatgccc gggagatctc cttcaatgct	300
tgtctgggtcc aaatgtactt cattcatggt ttctcgatta ttgagtcagc tgtactcctg	360
gctatggcct ttgactgctt tatagcaatc tgagaaccct tgcgctatgc agccatccta	420
accaatgatg taatcatttg gattgggttg gcaattgctg gaagggcctt ggctctggte	480
tttccagctt ctttctctt gaagaggctt caatatcatg atgtcaatat tctgtcctac	540
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atctatggcc tcatgggtgg catctgttcc atgggacttg attcagtgtc tctcctctc	660
tcctatgtcc tcatcctggg cacagcgttg agtatagcct ccaaggcaga gagagtgaga	720
gccctcaata cttgcatctc ccacatctgt gctgtactca ccttctatac accaatgatt	780
gggctatcta tgatccatcg ctatggacag aatgctcctc aattgtccat gtgctgatgg	840
ccaatgtcta cttgntgggt ccacctctca tgaaccccggt gttctacagt gttagaccag	900
ncagattcgt gacagaatct ttcaaataaa attcagaaac atgaagtgtga ga	952

<210> 269

<211> 944

<212> DNA

<213> Unknown (H38g118 nucleotide)

<220>

<223> Synthetic construct

<400> 269

atggaagagg	aaaatgcaac	attactgaça	gaatttggtc	tcacaggatt	tttatgtcaa	60
caaggatttt	tatgggaaat	acccctgttc	ctggcattct	tggtaataga	tctcatcacc	120
atcatgggga	atcttgggtc	gattttttct	atctggaaag	accctcacct	tcatatttca	180
atgtacttat	tccttgggag	tttagctttt	gtggatactt	ggttatcatc	cacagtgact	240
ccgaagatgc	tgatcaactt	cttagctaag	agtaagatga	tatctctctc	tgaatgcattg	300
gtacaatttt	ttttcccttg	caatcagttg	aaccacagaa	tgttttatct	cggcatcaat	360
ggcatatgat	cgctatgcag	acatatgcaa	acctttactt	tatccagtca	ttatgaccaa	420
tgaactatgc	atctggctat	ttgtcttggt	atttctaggt	ggcctttttc	atgctttaat	480
ccatgaagg	tttttattca	gactaacctt	ctgtaactcc	aacatgatac	aacattttta	540
ctgtgacatt	atcccattgt	taaagatttc	atgtactgat	tcttgattta	attttctaat	600
gtttttttat	ttctcaggtt	caattcaagt	tttaaccatt	gggattggtt	ttgtattctta	660
tatgtttggt	ctcttttaca	tcttaaaaaa	gaagtctaac	aaaggcataa	gggaagcctt	720
ttccacctgt	ggagcccat	acatacctct	ctctttatgt	tatggcctcc	ttctcttcat	780
gtatgtgggc	cctgcagctc	cacaagcaga	taatcaagat	atgatggagt	atctatttta	840
ccctatcatt	gtgcgtttgt	taaaccatat	tactacagcc	tgagaaataa	gcaataatag	900
gttcactcac	aaaaatgtta	aaataaaaata	tttgattgac	atac		944

<210> 270

<211> 939

<212> DNA

<213> Unknown (H38g119 nucleotide)

<220>

<223> Synthetic construct

<400> 270

atgtccatta	tcaacacatc	atatgttgaa	atcaccacct	tcttcttggt	tgggatgcca	60
gggctagaat	atgcacacat	ctggatctct	atccccatct	gcagcatgta	tcttattgct	120
attctaggaa	atggcaccat	tctttttatc	atcaagacag	agccctcctt	gcatgggccc	180
atgtactatt	ttctttccat	gttggctatg	tcagacttgg	gtttgtcttt	atcatctctg	240
cccactgtgt	taagcatctt	cctgttcaat	gccccgaaa	cttcttctag	tgccctgctt	300
gcccaggaat	tcttcattca	tggattctca	gtactggagt	cctcagtcct	cctgatcatg	360
tcatttgata	gattcctagc	catccacaat	cctctgagat	acacctcaat	cctgacaact	420
gtcagagttg	cccaaataag	gatagtattc	tcctttaaga	gcatgctcct	ggttcttccc	480
ttccctttca	ctttaagaag	cttgagatat	tgcaagaaaa	accaattatc	ccattcctac	540
tgtctccacc	aggatgtcat	gaagttggcc	tgctctgaca	acagaattga	tggtatctat	600
ggcttttttg	gagcactctg	ccttatggta	gactttatct	tcattgctgt	gtcttacacc	660
ctgatccctca	agactgtacc	gggaattgca	tccaaaaagg	aggagcttaa	ggctctcaat	720
acttgtgttt	cacacatctg	tgcagtgtac	atcttctacc	tgcccatcat	caacctggcc	780
gttgtccacc	gatttgcggg	gcatgtctct	ccccctatta	atgttctcat	ggcaaatgtt	840
ctcctacttg	tacctccgct	gatgaaacca	attgtttatt	gtgtaaaaac	taaacagatt	900
agagtggag	ttgtagcaaa	atttgtgtcaa	tggaagatt			939

<210> 271

<211> 940

<212> DNA

<213> Unknown (H38g120 nucleotide)

<220>

<223> Synthetic construct

<400> 271

atggaagaga	aaaatgcaac	attgctgaca	gagtttggtc	tcacattatt	tttatatcaa	60
cctcactgga	aaatacccct	gttccctggc	ttcttggtaa	tatatctcat	caccatcttt	120
gggaatcttg	gtctgattgc	tgtcgtatgg	aaagaccctc	accttcata	cccaatatac	180
ttattccttg	agaatttagc	ttttgtggat	gatttggtat	catccacatg	actctgaaga	240
tgctgatcaa	cttcttctac	aagagtaagt	tgatttctct	ctgaatgctg	gatacatttt	300
ttttcccttg	caattgggtg	aaccacagaa	tgttttatct	tggaacaat	ggcatatgat	360
cgctatgtag	ccatatgcaa	acctttactt	tatccagtca	ttatgaccaa	tggaactgtgc	420

atctggctat	taatcttgtc	atttctagggt	ggccttcttc	atgctttaat	tcatgaaggt	480
tttttataga	ttaaccttct	gtaattccaa	cacaatacat	cacttttaat	gtgacattat	540
cccattgtta	aaaattttct	gtactgattc	ttctattaac	tttccaatgg	tttttaattt	600
ctcatgttca	attcaagttt	tcaccattgg	gactgttctt	gtatcttata	catttgtcct	660
ctctacaatc	ttgaaaaaga	agtctgtcaa	aggcataaga	aaagacttct	ccacctgtgg	720
agctcatatc	ttacctgtat	ctttatacta	tgggcccctc	gccttcatgt	atgtgggctc	780
tgcattccaa	cgggctgatg	accaagatat	gatggagtct	ctatittaca	ctgtcacagt	840
tcctttatta	aatcccatga	tctacagcct	gagaaataag	caagtaatag	attcattcac	900
aaaaatgttc	aaaggaaata	atgttttagat	ctcttactca			940

<210> 272

<211> 512

<212> DNA

<213> Unknown (H38g121 nucleotide)

<220>

<223> Synthetic construct

<400> 272

tgctgagtc	aagtttctctg	agtagcagaa	aagtattgat	aaattttatt	tgttgcaactt	60
tttaacaaaa	caaaaagcat	ctgccaacca	cagaacattg	caacacctag	gccctgggct	120
ttccccagc	attcattcac	tagcacctca	tgttttgggg	gcacaagcac	agggctttct	180
taggctgtaa	aatcacctat	atcatctgtc	tgtccactgc	ttcaactcct	tctgcagtat	240
ccctgcaaca	atattacatg	cttatgaaat	gctgcagaca	gggaattcct	gtccttctag	300
gacccctctc	tggctgtggg	cagctttacc	ataagttctt	gtcttcttat	gctgaaattg	360
atttcatttt	cattcttcacg	tattattgct	tctttgctct	ctcgggtgtc	aactgagtct	420
catcgctctc	ccttctaata	ctccttctgt	catctatttt	gtcttttctt	cttcagactg	480
aaaatccctg	gtagtacctg	tagtttcctt	cc			512

<210> 273

<211> 924

<212> DNA

<213> Unknown (H38g122 nucleotide)

<220>

<223> Synthetic construct

<400> 273

atgaatacca	ctctatttca	tccttactct	ttccttcttc	tgggaattcc	tgggctggaa	60
agtatgcac	tctgggttgg	ttttccttct	tttgcctgtg	tctgacagc	tgtccttggg	120
aatatcacca	tcctttttgt	gattcagact	gacagtagtc	tccatcatcc	catgttctac	180
ttcctggcca	ttctgtcatc	tattgaccgg	ggcctgtcta	catccaccat	ccctaaaatg	240
cttggcacct	tctggtttac	cctgagagaa	atctcctttg	aaggatgcct	taccagatg	300
ttcttcatcc	acctgtgcac	tggcatggaa	tcagctgtgc	ttgtggccat	ggcctatgat	360
tgctatgtgg	ccatctgtga	ccctcctttg	tacacgttgg	tgctgacaaa	caagggtggg	420
tcagttatgg	cactggccat	ctttctgaga	cccttagtct	ttgtcatacc	ctttgttcta	480
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gccatctcta	tcctgggtct	tgacatcata	gcaattgtca	tttcctatgt	acagatcctt	660
tgtgctgtat	ttctactctc	ttcacatgat	gcacgactca	aggcattcag	cacctgtggc	720
tctcatgtgt	gtgtcatggt	gactttctat	atgcctgcat	ttttctcatt	catgacccat	780
aggtttggtc	ggaatatacc	tcactttatc	cacattcttc	tggctaattt	ctatgtagtc	840
attccacctg	ctctcaactc	tgtaatattt	gggtgtcagaa	ccaaacagat	tagagcacaa	900
gtgctgaaaa	tgtttttcaa	taaa				924

<210> 274

<211> 927

<212> DNA

<213> Unknown (H38g123 nucleotide)

<220>

<223> Synthetic construct

<400> 274

atggaagagg	aaaatgcaac	attgctgaca	gagtttggtc	tcacaggatt	tttacatcaa	60
cctgactgta	aaataccgct	cttcctggca	ttcttggtta	tatatctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	cccaatgtac	180
ttcttccctg	ggagtttagc	ctttgtggat	gcttcgttat	catccacagt	gactccgaag	240
atgctgatca	acttcttagc	taagagtaag	atgatatctc	tctctgaatg	catgggtacaa	300
tttttttccc	ttgtaaccac	tgtaaccaca	gaatgttttc	tcttggcaac	aatggcatat	360
gatcgctatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caatgaacta	420
tgcattcagc	tattagtctt	gtcatttata	gggtggccttc	ttcatgcttt	aatccatgaa	480
gctttttcat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgttaaagat	ttcctgtact	gattcctcta	ttaactttct	aatgggtttt	600
attttgcgag	gtttctgttca	agttttttacc	attggaaacta	ttcttatatc	ttatacaatt	660
atcctcttta	caatcttaga	aaagaagtct	atcaaaggga	tacgaaaagc	tgtctccacc	720
tgtggggctc	atctcttata	tgtatcttta	tactatggcc	ccctcacctt	caaatactctg	780
ggctctgcat	ctccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atagttcctt	tattaaatcc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900
ttcacaaaaa	tgttcaaaag	caatggt				927

<210> 275

<211> 924

<212> DNA

<213> Unknown (H38g124 nucleotide)

<220>

<223> Synthetic construct

<400> 275

atggcgaata	gaaacaacgt	gacagagttt	attctattgg	ggcttacaga	gaatccaaaa	60
atgcagaaaa	tcataattgt	tgtgttttgt	catctacatc	accaccatga	taggaaatgt	120
gctcattgtg	gtcaccatca	ctgccagccc	atcattgagg	tcccccattg	aatttttcct	180
ggcctatctg	tcctttattg	atgcctgcta	ttcctctgtc	aatgtctcta	agctgatcac	240
agattcactc	tatgaaaaca	agactatctt	actcaatgga	tgtatgactc	aagtctttgg	300
agaacatttt	ttcagaggtg	ttgaggtcat	cctacttact	gtaatggcct	atgactgcta	360
tgtggtcate	tgcaagccct	tgcgtatac	caccatcatg	aagcagcatg	tttgtagcct	420
gctagtggga	gtgtcacggg	tgggaggctt	tcttcatgca	accatacaga	tcctcttcat	480
cttccaatta	cctttctgta	gttctaattg	catagatcac	tttactgtga	tctcaaccct	540
ttgctcaatc	ttgcctgcac	taatacccac	actctaggac	tcttcgttgc	tgccaacagt	600
gggttcatat	gcctgttaaa	ctttctcttg	ctcctggtct	cctatgtggt	catactgtac	660
tccttaagga	cccacagctt	agaggcaagg	cacaaaaggcc	tctccacctg	tgtctcccac	720
aacacagttg	tcatcttatt	ctttataccc	tgcataattg	tgtacatgag	acctccagct	780
actttaccca	ttgataaagc	agttgctgta	ttctacacta	tgataaactcc	tatgtttaa	840
cccttaatct	acaccttgag	gaatgctcag	atgaaaaatg	ccattaggaa	attgtgtagt	900
aggaaagcta	tttcaagtgt	caaa				924

<210> 276

<211> 963

<212> DNA

<213> Unknown (H38g125 nucleotide)

<220>

<223> Synthetic construct

<400> 276

atgttccttc	ccaatgacac	ccagtttcac	ccctcctcct	tcctgttgct	ggggatccca	60
ggactagaaa	cacttcacat	ctggatcggc	tttcccttct	gtgctgtgta	catgatcgca	120
ctcataggga	acttcactat	tctacttggt	atcaagactg	acagcagcct	acaccagccc	180
atgttctact	tcctggccat	gttggccacc	actgatgtgg	gtctctcaac	agctaccatc	240
cctaagatgc	ttggaatctt	ctggatcaac	ctcagaggga	tcactcttga	agcctgcctc	300
accagatgt	tttttatcca	caacttcaca	cttatggagt	cagcagtcct	tgtggcaatg	360

gcttatgaca	gctatgtggc	catctgcaat	ccactccaat	atagcgccat	cctcaccaac	420
aaggttggtt	ctgtgattgg	tcttggtgtg	tttgtgaggg	ctttaatttt	cgtcattccc	480
tctatacttc	ttatattgcg	gttgcccttc	tgtgggaatc	atgtaattcc	ccacacctac	540
tgtgagcaca	tgggtcttgc	tcactctatc	tgtgccagca	tcaaaatcaa	tattatttat	600
ggtttatgtg	ccatttgtaa	tctggtgttt	gacatcacag	tcattgacct	ctcttatgtg	660
catattcttt	gtgctgtttt	ccgtcttctc	actcatgagc	cccgaactca	gtccctcagc	720
acatgtgggt	cacatgtgtg	tgtaatcctt	gccttctata	caccagacct	cttttccttt	780
atgactcatt	gctttggccg	aaatgtgccc	cgctatatcc	atatactcct	agccaatctc	840
tatgtttgtg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tataaatgtg	taaagaaaat	attattgcag	gaacaaggaa	tggaaaagga	agagtaccta	960
ata						963

<210> 277

<211> 894

<212> DNA

<213> Unknown (H38g126 nucleotide)

<220>

<223> Synthetic construct

<400> 277

atgagaaatc	acacaatggt	gactgaattc	atccttcttg	gaatccctga	gacagagggc	60
ctagagacag	cccttttatt	cctgttctcc	tcattttatt	tatgcacct	cttgggaaac	120
gtgcttatcc	ttacagctat	catctcctcc	actcgacttc	acactcctat	gtattttttc	180
ttgggaaacc	tctccatctt	tgacctgggt	ttctcttcaa	cgactgttcc	caagatgttg	240
ttctaccttt	cggggaacag	ccatgctatc	tcgtatgcag	gctgcgtgtc	ccagcttttc	300
ttctaccatt	tcctaggctg	tactgagtgt	ttcctctaca	cagtgatggc	ctgtgaccgc	360
tttggttgcca	tatgtttttc	tttgagatac	acggtcatca	tgaaccacag	ggtgtgcttt	420
atgttgccca	cggggacctg	gatgattggc	tgtgtccatg	ccatgatcct	aactcccttc	480
accttccagt	taccttactg	tggccctaac	aagggtgggt	attacttctg	tgatattcct	540
gcagtgttac	ctctagcctg	taaggacaca	tccttagccc	agagggtagg	ttttacaaat	600
gttggctctt	tgtctctcat	ttgctttttt	ctcctccttg	tttctatac	ttgcattggg	660
atttccatat	caaaaatccg	ctcagcagag	ggcaggcagc	gggccttctc	cacctgcagc	720
gctcacctca	ctgcaatcct	ttgtgcttat	gggccagtca	tcgttatcta	ctacaaccc	780
aatcccagtg	ccttgcttgg	ttccataatt	cagatattga	ataatctggt	aaccccaatg	840
ttgaatccac	taatctatag	ccttaggaat	aaggatgtaa	aatcagatca	gcc	894

<210> 278

<211> 972

<212> DNA

<213> Unknown (H38g127 nucleotide)

<220>

<223> Synthetic construct

<400> 278

atggaggagg	aaaatacaac	attgctgaca	gagtttgttc	tcacaggatt	tttatatcaa	60
ccacagtggg	aaataccctt	gttcttgcca	ttcttggtaa	tatagctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	ccaatgtat	180
ttattccgtg	ggagtttggc	ctttgtggat	gcttggttat	catccacagt	gactccaaag	240
atgctgatca	acttcttagc	taagagtaag	atgatatctc	tctctgaatg	catggtacaa	300
tttttttctt	ttgtaatcag	tgttaaccaca	gaatgtttta	tctcggcata	aatggcatat	360
gacgcgtatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caacggacta	420
tgcattccagc	tattagtctt	gtcattttata	ggtggccttc	ttcatgcttt	aatccatgaa	480
atttttttat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgttaaagat	ttcctgtact	gattccttta	ttactttctt	aatggttttt	600
attttcgcag	attcaattca	agttttttacc	attggaacta	ttcttatata	ttatacactt	660
gtcctcctta	taatcttaaa	aaataagttc	gtcaaaggga	tacaaaaagc	tgtctccacc	720
tgtggagctc	atctcttatc	tgtatcttta	tactatgggc	cccttgctct	catgtatgtg	780
ggctctgcat	ccccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atcgttcctt	tattaaattc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900

ttcacaaaaa tgttcaaaag aaatgttttag atctcataca atctctgttc tctgtttact 960
 aaaattttcc ca 972

<210> 279

<211> 924

<212> DNA

<213> Unknown (H38g128 nucleotide)

<220>

<223> Synthetic construct

<400> 279

atgatgagta	accagacgtt	ggtaaccgag	ttcatcctgc	agggcttttc	ggagcaccca	60
gaataccggg	tgttcttatt	cagctgtttc	ctcttccctc	actctggggc	cctcacaggt	120
aatgtcctca	tcaccttggc	catcacgttc	aaccttgggc	tccacgtctc	tatgtacttt	180
ttcttactca	acttggctac	tatggacatt	atctgcacct	cttccatcat	gccaagggcg	240
ctggccagtc	tgggtgctga	agagagctcc	atctcctacg	ggggctgcat	ggcccagctc	300
tatttccctca	cgtgggctgc	atcctcagag	ctgctgctcc	tcacgggtcat	ggcctatgac	360
cggtagcgag	ccatctgcc	cccgtgcat	tacagcagca	tgatgagcaa	ggtgttctgc	420
agcgggtgg	ccacagccgt	gtggctgctc	tgcgcctca	acacggccat	ccacacgggg	480
ctgatgctgc	gcttggattt	ctgtggcccc	aatgtcatta	tccatttctt	ctgcgaggtc	540
cctccccctgc	tgttctcttc	ctgcagctcc	acctacgtca	acgggtgcat	gattgtcctg	600
gcggatgctt	tctacggcat	agtgaacttc	ctgatgacca	tcgcgtccta	tggcttcctc	660
gtctccagca	tcctgaaggt	gaagactgcc	tgggggaggc	agaaagcctt	ctccacctgc	720
tcttcccacc	tcaccgtggt	gtgcatgtat	tacaccgctg	tcttctacgc	ctacataagc	780
ccggtctctg	gctacagcgc	aggggaagagc	aagttggctg	gcttctgtga	cactgtgctg	840
agtcctaccc	tcaaccccct	catctatact	ttgagaaaca	aggaggtcaa	agcagccctc	900
aggaagcttt	tccctttctt	caga				924

<210> 280

<211> 958

<212> DNA

<213> Unknown (H38g129 nucleotide)

<220>

<223> Synthetic construct

<400> 280

atggatgacg	aaaatgcaac	attgctgaca	gagtttgttc	tcacaggact	tacatatcaa	60
tcagagtggg	aaatacccct	gttcctggca	ttcttggtaa	tatatctcat	caccatcatg	120
gcaaactctg	gtctgattgc	tgtcatctgg	aaagactcac	accttcacat	tccaatgtac	180
ttattccttg	ggagttagc	ctttgtggat	gcttggttat	catcctcagt	gacccttaag	240
atgctgatca	gctttttagc	taagagtatg	attatttctg	tctctgaatg	caagatacaa	300
tttttttctt	ttggaatcag	tggaaccaca	gaatgttttc	tcttggcaac	aatggcatat	360
gacgctatg	tagccatatg	caaaccttta	ctttatccag	tcattatgac	caatggactg	420
tgtatctggc	tattagtctt	gtcatttata	ggtggctttc	ttcatgcctt	aattcatgaa	480
ggtattttat	tcagattaac	cttctgtaat	tccaacataa	tacatcactt	ttactgtgac	540
attatcccat	tgttaaagat	ttcctgtact	gacctttcta	tttaattttt	aatgtttttt	600
attttgtctg	gttcaatata	ggtattcact	attttgactg	ttcttgtctc	ttatacattt	660
gtcctcttta	caatcttaaa	aaaaaaagtc	tgccaaagac	ataaggaaag	ccttttccac	720
ctgtggagcc	catctcttat	ctgtttcttt	atactatggc	ccccttctct	tcagtatgt	780
gcaccttgca	tctccacaag	cagatgatca	agatatgggtg	gagtctctat	tttacctgt	840
cataattcct	ttcttaaatc	ccattatcta	cagcctgaga	aataagcaag	tcatagattc	900
actgacaaaa	acattaaaag	gaaatgttta	gatctcatat	tggaatgtat	tctctatt	958

<210> 281

<211> 933

<212> DNA

<213> Unknown (H38g130 nucleotide)

<220>

<223> Synthetic construct

<400> 281

atggttgaag	aaaatcatac	catgaaaaat	gagtttatcc	tcacaggatt	tacagatcac	60
cctgagctga	agactctgct	gtttgtggtg	ttctttgcca	tctatctgat	caccgtggtg	120
gggaatatta	gtttggtggc	actgatattt	acacaccgtc	ggcttcacac	accaatgtac	180
atcttictgg	gaaatctggc	tcttgtggat	tcttgtctgt	cctgtgctat	tacccccaaa	240
atgttagaga	acttcttttc	tgagggcaaa	aggattttcc	tctatgaatg	tgcagtacag	300
ttttattttc	tttgcactgt	ggaaactgca	gactgctttc	ttctggcagc	agtggcctat	360
gaccgctatg	tggccatctg	caaccactg	cagtaccaca	tcattgatgtc	caagaaactc	420
tgcattcaga	tgaccacagg	cgccttcata	gctggaaatc	tgcattccat	gattcatgta	480
gggcttgtat	ttagggttagt	tttctgtgga	ttgaatcaca	tcaaccactt	ttactgtgat	540
actcttccct	tgtatagact	ctcctgtgtt	gaccctttca	tcaatgaact	ggttctatct	600
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tgtgcatccc	acttttcatc	agtttcatta	ttctatggat	ctattttttt	cctatacatt	780
agaccaaatt	tgcttgaaga	aggaggtaat	gatataccag	ctgctattttt	atttacaata	840
gtagtccct	tactaaatcc	tttcatttat	agtctgagaa	acaaggaagt	aataagtgtc	900
ttaagaaaaa	ttctgctgaa	aataaaatct	caa			933

<210> 282

<211> 979

<212> DNA

<213> Unknown (H38g131 nucleotide)

<220>

<223> Synthetic construct

<400> 282

tatacagacc	cacagaatct	aacagatgtc	tttatattcc	tcctcctaga	actctcagag	60
gatccagcac	tgcagctggt	cgtcactggg	ctgtgcctgt	gtgcctgggc	acgggtgctgt	120
ggaacctgtc	cagcactcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcctcctctg	caacctgtcc	ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaaccctgtg	420
ttctgtggct	tcctggtttt	gttgtctttt	ttttctcagt	cttttagact	cccagctgca	480
aaactgatcg	ccttaaaaaa	cacctgtctc	aaggatgtgg	aaattcctaa	ttttttctgt	540
gacccttctc	aactccccca	tcttgcattg	tgtgacacct	tcaccaataa	cattatcatg	600
tatttccctg	ctgccatatt	tgggtttctt	cccattctcg	ggaccctttt	ctcttactat	660
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acctgtggat	ctcacctgtc	agttgtttgc	tgattttatg	gaacaggcgt	tggagggtac	780
ctcagttcag	atgtgtcgtc	ttccctgaga	aagcgtgcag	tggcctcagt	gatgtacacg	840
gtggtcaccc	ccatgctgaa	tccttgatc	tacagcctga	gaaacaggga	tattaaaggt	900
gtcctgtggc	agccgtgcag	cgcacggca	gcacagtctc	atctcaatat	cttatctggt	960
ccatttcttt	tgcaggatg					979

<210> 283

<211> 987

<212> DNA

<213> Unknown (H38g132 nucleotide)

<220>

<223> Synthetic construct

<400> 283

atggaaccac	agttcaccac	ccagggatca	atgtttgtcc	tgtaggggta	gtcacagacc	60
caagagctcc	agagagtcac	gttcattctg	ttcctgttag	tctatgttac	caccattgtg	120
ggaaacctcc	ttatcatggt	cacagtgaat	tttgactgcc	ggctccacac	ccatgtatct	180
tctgtctcga	aatctagctc	tcataagagt	ctgctattcc	acagtcacct	ctccaaagat	240
gctggtggac	ttcttccatg	agaccaagac	gatctcctac	cagggtgca	tggccagat	300

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cttcttcttc cacccttttg gaggtgggac tgtctttttt ctctcagtc tggcctatga 360
ccgctacata gccatctccc agcccctccg gtatgtcacc atcatgaaca ctcaattgtg 420
tgtgggacct gtagtagccg cctggcggtg ggggctttgt ccactccatt gtccaactgg 480
ctgtgatacg tccacagcct ctatgtggcc ccaatatcct agataacttc tactgtgatg 540
ttccccaagt actgagactt gcctgcactg atacctccct cctggagtgc ctcatgatgt 600
ccaacagtgg gctgctagtt atcatctggt tcctcctcag tctgatgtct tatactgtca 660
tcctgggtgat gctgagggtc cactcgggaa aggcaagcag taaggcagct tccacttgca 720
ccaccacat catcgtggtg tccatgatct tcattccatg tatctatata tatacctggc 780
cctttcaccc cattcatcat ggacaaggct gtgtccatca gctacacagt catgaccccc 840
atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900
ttaggcaagt gcctagtaat ttgcagggag ttaaacttta agtaagttga ctttaaataga 960
caaattgctc tggattttta ttttccc 987

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<210> 284

<211> 387

<212> DNA

<213> Unknown (H38g133 nucleotide)

<220>

<223> Synthetic construct

<400> 284

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atgcaaggag aaaacttcac catttggagc atttttttct tggagggatt ttcccagtac 60
ccagggttag aagtggttct ctctgtcttc agccttgtaa tgtatctgac aacgctcttg 120
ggcaacagca ctcttatttt gatcactatc ctagattcac gccttaaaac ccccatgtac 180
ttattccttg gaaatctctc tttcatggat atttgttaca catctgcctc tgttcctact 240
ttgctggtga acttgcctgc atcccagaaa accattatct tttctgggtg tgctgtacag 300
atgtatctgt cccttgccat gggctccaca gagtgtgtgc tcctggccgt gatggcatat 360
gaccgttatg tggccatttg taacccg 387

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<210> 285

<211> 1005

<212> DNA

<213> Unknown (H38g134 nucleotide)

<220>

<223> Synthetic construct

<400> 285

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tctacagacc cacagaatct aacagatgtc tctatatctc tcctcctaga acctcagagg 60
atccagaacg gcagctggtc ctgtctgggc tgttcctgtc catgtgcctg gtcacgggtg 120
tggggaacct gatcatcacc ctggacgtca gccctgactc ccacctcccc acccccatgt 180
acttcttctc ctccaacctg tccttgccctg acatcggttt caccctccacc acggtcccca 240
agatgattgt ggacatccaa tctcacagca gagtcatctt ctatgcaggc tgcctgactc 300
agatgtctct ctttgccatt tttggaggca tgggaagagag acacgctcct gagtgtgatg 360
gcctatgacc ggtttgtagc catctgtcac cctctatgtc attcagccag catgaacccg 420
tgtttctgtg gctttctagt tttgttgtct ttttttttct tcagtctttt agacacccag 480
ctgcacaact tgattgcctt acaaatgacc tgcttcaagg atgtggacat tcctaatttc 540
ttctgtgacc cttctcaact cccccatctt gcatgttgtg acaccttcac caataacata 600
atcatgtatt tcctgtctgc catatttggt tttcttcaga tctcggggac ccttttctct 660
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aaaagtgtcc tgcggcggcc gcaaggcagc aagggtctaat atcaatatct tcttatctgt 960
tccattcctt ttgtagggtg ggttaaaaaa ggcagcaagg tcaaa 1005

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<210> 286

<211> 958

<212> DNA

<213> Unknown (H38g135 nucleotide)

<220>

<223> Synthetic construct

<400> 286

atgaagaata	aaaggaatgt	gactgaattc	gttttaacag	gtcttacaca	gaaccctaaa	60
atggagaaag	tcatgtttgc	agtatttttg	gttctttaca	tgataacact	ttcaggcaac	120
ctgctccttg	tggttacaat	taccaccagc	caggctctta	gtcccccat	gtacttcttc	180
ctgagccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtcgattccc	ttcatgagaa	gaaaatcatc	tcctttaatg	gggtgatggc	tcaagcctat	300
gaagaacaca	tttttggtgc	tactgagatc	atcctgctga	cagtgatggc	ctgtgacaac	360
tatgtggcca	tctgcaaac	tctgcactac	acaaccatca	tgagccacag	cctgtgcatt	420
ctcctagtgg	tagtggcctg	gataggagga	tttctccatg	caaataattca	gattctattt	480
acagtatggc	tgcccttctg	tgcccccaat	gtcatagacc	acttcatgtg	tgacttgtgc	540
cctttgttaa	aacttgtttg	cctggacact	catacccttg	gtctctttgt	tgctgccaac	600
agtgggttca	tctgcttatt	aaacttcctt	ctctaggtgg	tatectatgt	gatcatcttg	660
agatgtttaa	agaactatat	cttggagggg	aggggtaaag	ccctctccac	ctgtatttct	720
cacatcataa	tagttgtctt	attctttgtg	ccttgtatat	ttgtgtatct	gcaccagtg	780
acaaactctg	cccattgata	aagctgctgc	tgtattttat	actatgggtg	tccaatgtt	840
aaatcctttg	atctacacac	tcagaaatgc	tgaggtaaaa	agtgcaataa	ggaagctttg	900
gagaaaaaaa	gttattttcag	ataatgacta	aataagacca	ttgagcactc	atcataga	958

<210> 287

<211> 937

<212> DNA

<213> Unknown (H38g136 nucleotide)

<220>

<223> Synthetic construct

<400> 287

atggagattg	gaaaccatac	cacagtgaca	gagtttatta	ttttgggggt	aactgaggat	60
cctacacttt	gtgacatctt	ctttgtgata	tttctaggaa	tctacattgt	caccttaata	120
ggcaatatca	gcataataaa	gaagctgttc	ccaacttcac	actcccatgt	acctgttcct	180
cagccacttg	gctttttgtg	acatagggct	tgccacagta	gtcacaccta	taatgcttat	240
gggattccta	agacgtggaa	cagccctccc	tgctactagc	tgtgaagccc	agctctgttc	300
tgtagtcatg	tttgggacgt	ctgaatgctt	cctactggcg	accatggcct	atgatcgcta	360
tgtggccatc	tgctcacccc	tggtgaactc	cacccacttg	ccccccataa	tctgcatact	420
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tttgttgaaa	ctttcctgct	caaatacttc	cattcctgaa	attatccctt	ccatctcttc	600
tggatctatc	attgtgggtca	cagtatttgc	catagccatc	tcctacatct	acatccctcat	660
caccatcctg	aagatgcgct	ccgcgcaggg	gcgccacaag	gccttctcca	cctgtacctc	720
ccacctcgct	gcggttactc	tctactatgg	aacgattacc	ttcatttatg	tgatgcccaa	780
atccagttac	tcaactagcc	agaacagatt	gatatcgctg	tcctacacag	tggtaatccc	840
catactgaac	cccttttatct	atagtctgag	gaacagagat	gtaaaggagg	cactaagaaa	900
ggcaactgtc	agaatatatt	cttaggatca	atttgtga			937

<210> 288

<211> 971

<212> DNA

<213> Unknown (H38g137 nucleotide)

<220>

<223> Synthetic construct

<400> 288

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tcagccgggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggtc	120
acgggtgctga	ggaacctgct	gagcatcccc	gctgtcagct	ctgactcccc	gtccacacc	180
cccacgtact	tcttctcttc	catectgtgc	tggtgtgaca	tcggtttcac	ctcgccacag	240

gtttccaaga	cgattgtgga	catgcagtc	catagcagag	tcattctctca	tgcgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	aggcatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctgttctg	acagcgtcat	caatagcatt	600
ttcatatatt	ttggtagtag	tatgtttggg	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	tcgtccctct	cattctaagg	atttcacgtt	cagatgggaa	gtataaagcc	720
ttctccacct	atggctctca	cctagcagtt	ttttgctgat	ttgatggaac	aggcattggc	780
gtgtacctga	cttcagctgt	ggcaccaccc	ctcaggaatg	gtgtgggtgg	gtcagtgatg	840
taagctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcggagggt	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttctgggtg	t					971

<210> 289

<211> 954

<212> DNA

<213> Unknown (H38g138 nucleotide)

<220>

<223> Synthetic construct

<400> 289

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ctcacctgct	tccccaactt	ccagagttgg	cagcactggc	tctccctgcc	cctcagcctt	120
ctcttctctc	tggccatggg	agctaaccac	accctcctga	tcaccatcca	gctggaggcc	180
tctctgcacc	agccctgtga	ctacctgctc	agcctcctct	ccctgctgga	catcgtgctc	240
tgcctcaccg	tcattcccaa	ggctcctggc	atcttctggg	atgatcttag	gtcgtacagc	300
ttccctgacct	gttccctcca	gatgttcatc	atgaacagtt	tcctcccat	ggagtccctg	360
acgtttatgg	tcattggccta	tgaccgttat	gtggccatct	gccacccact	gcggtaccca	420
tccatcatca	ctaatacaatt	tgtggccaaa	gctagtgtct	tcattgtggg	gcggaatgcg	480
cttcttactg	cacccattcc	tatcctcact	tccctgctcc	attactgtgg	ggaaaatgtc	540
attgagaact	gcattctgtc	caacttgtct	gtgtccaggc	tctcctgtga	taatttcacc	600
cttaacagaa	tctaccaatt	tgtggctggg	tggaccttgc	tgggctcaga	tttattcctc	660
atcttcctct	cttacacctt	cattctaaga	gctgtgctta	gattcaaagc	agagggggcg	720
gcagtgaagg	cctgagcac	atgtggctcc	cacttcaccc	tcattctttt	cttcagcacc	780
atactgctgg	ttgtgggtgt	gacaaacgtg	gccagaaaaga	aggtccccat	ggacatcctg	840
atcctgctga	acgtccttca	tcaccttatt	cctcctgcgt	tgaaccctat	tgtgtatggg	900
gttcggacca	aagagataaa	acagggaatt	cagaagttac	tgcagagagg	gagg	954

<210> 290

<211> 713

<212> DNA

<213> Unknown (H38g139 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(713)

<223> n = A,T,C or G

<400> 290

cccaagggtcc	cggacttttt	tgtgtttggc	ctaagggcc	ttagttttcc	ggccggtttt	60
ctccaaaagt	acattaagaa	ttgtttccaa	gccaggagtt	ttggccattc	aagggtcaggg	120
ccataggatc	gttaaggaac	ccttctgcca	cccccttgaa	atatccctcc	attcatcacg	180
gacccctttg	gagtcgaagg	tgccagggtt	attttgcccc	gnaatgggtg	taatgactct	240
gcccattccc	catcctttca	gcacaactcc	gttattgtgg	aagaaatgtc	attgagaact	300
gcattctgtc	caatatgtct	gtttccagac	tctcctgcga	tgatgtcacc	atcaatcacc	360
tttaccatt	tgctggaggc	tggtactctg	taggatctga	cctcatcctt	atcttctctt	420
cctacacctt	cattctgcga	gctgtgctga	gactcaaggc	agaggggtgc	gtggcaaagg	480

ccctaagcac	atgtggctcc	cacttcatgc	tcatectctt	cttcagcacc	atccttcttg	540
tttttgcct	cacacatgtg	gctaagaaga	aagtctcccc	tgatgtgcca	gtcttgctca	600
atgttctcca	ccatgtcatt	cctgcagccc	ttaaccccat	catttacggg	gtgagaaccc	660
aagaaattaa	gcagggaatg	cagaggttgt	tgaagaaagg	gtgctaacaa	gga	713

<210> 291

<211> 924

<212> DNA

<213> Unknown (H38g140 nucleotide)

<220>

<223> Synthetic construct

<400> 291

atgaattccc	tgaaggacgg	gaatcacacc	gctctgacgg	ggttcatcct	attgggctta	60
acagatgac	caatccttcg	agtcacccct	tccatgatca	tcctatctgg	taatctcagc	120
ataattattc	ttatcagaat	ttcttctcag	ctccatcatc	ctatgtattt	ctttctgagc	180
cacttggctt	ttgctgacat	ggcctattca	tcttctgtca	cacccaacat	gcttgtaaac	240
ttcctgggtg	agagaaatac	agtctcctac	cttggtatgtg	ccatccagct	tgggttcagcg	300
gctttctttg	caacagtcga	atgcgtcctt	ctggctgcca	tggtctatga	ccgctttgtg	360
gcaatttgca	gtccactgct	ttattcaacc	aaaatgtcca	cacaagtcag	tgtccagcta	420
ctcttagtag	tttaccatagc	tggtttttctc	attgctgtct	cctatactac	ttccttctat	480
tttttactct	tctgtggacc	aaatcaagtc	aatcattttt	tctgtgattt	cgctccctta	540
cttgaactct	cctgttctga	tatcagtgtc	tccacagttg	ttctctcatt	ttcttctgga	600
tccatcattg	tggtcactgt	gtgtgtcata	gccgtctgtc	acatctatat	cctcatcacc	660
atcctgaaga	tgcgtccac	tgaggggcac	cacaaggcct	tctccacctg	cacttcccac	720
ctcactgtgg	ttaccctgtt	ctatgggacc	attaccttca	tttatgtgat	gccccatttt	780
agctactcaa	ctgaccagaa	caaggtgggtg	tctgtgttgt	acacagtggt	gattcccatg	840
ttgaaccccc	tgatctacag	cctcaggaac	aaggagatta	agggggctct	gaagagagag	900
cttgtagaa	aaatactttc	tcat				924

<210> 292

<211> 1006

<212> DNA

<213> Unknown (H38g141 nucleotide)

<220>

<223> Synthetic construct

<400> 292

gatacagacc	cacagagtct	aacagatgtc	tctatattcc	tcctcctcga	actctcagag	60
gatccagaac	tgcaaccggg	cgctcgctgg	ctgttcctgt	ccatgtgcct	cgtcagtgtg	120
ctggagaacc	tgtcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	cacggteccc	240
aagatgattg	tgacatcca	gtctcacagc	agagtcatct	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tggaggcatg	gaagagagac	atgtcctga	gtgtgatggc	360
ctatgaccgg	tttgtagcca	tctgtcaccc	tctatatcgc	tcagccatct	tgaaccctgtg	420
tttctgtggc	ttcctagatt	tggtgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	ttccctgct	gccgtatttg	gttttctttc	catctcgggg	acccttttct	660
cttactgtaa	aatgggtttc	tccattctga	gggtttcatc	atcagggtgg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tgttgctga	ttttatggaa	caggcggttg	780
agagtacctc	ggttcagatg	gtcatcttcc	cccgagaaag	ggtgcagtgg	cctcagtgtg	840
gtacacggtg	gtcaccacca	tgctgaaccc	cttcactctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcggcggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	ttttaggggt	gggttaacaa	agacagcaag	gtcaaa		1006

<210> 293

<211> 933

<212> DNA

<213> Unknown (H38g142 nucleotide)

<220>

<223> Synthetic construct

<400> 293

atggggactg	gaaatgacac	caactgtggta	gagtttactc	ttttgggggt	atctgaggat	60
actacagttt	gtgctatttt	atttcttgtg	tttctaggaa	tttatgttgt	caccttaatg	120
ggtaatatca	gcataattgt	attgatcaga	agaagtcac	atcttcatac	acccatgtac	180
attttcctct	gccatttggc	ctttgtagac	attgggtact	cctcatcagt	cacacctgtc	240
atgctcatga	gcttcctaag	gaaagaaacc	tctctccctg	ttgctggttg	tgtggcccag	300
ctctgttctg	tagtgacgtt	tggtagggcc	gagtgtctcc	tgctggctgc	catggcctat	360
gatcgctatg	tggccatctg	ctcaccctg	ctctactcta	cctgcatgtc	ccctggagtc	420
tgcctcatct	tagtgggcat	gtcctacctg	ggcggatgtg	tgaatgcttg	gacattcatt	480
ggctgcttat	taagactgtc	cttctgtggg	ccaaataaag	tcaatcactt	tttctgtgac	540
tattcaccac	ttttgaagct	tgttgttcc	catgatttta	cttttgaaat	aattccagct	600
atctcttctg	gatctatcat	tgtggccact	gtgtgtgtca	tagccatac	ctacatctat	660
atcctcatca	ccatcctgaa	gatgcactcc	accaagggcc	gccacaaggc	cttctccacc	720
tgcacctccc	acctactgc	agtcactctg	ttctatggga	ccattacctt	catttatgtg	780
atgcccaagt	ccagctactc	aactgaccag	aacaaggtgg	tgtctgtgtt	ctacaccgtg	840
gtgattccca	tgttgaaacc	cctgatctac	agcctcagga	acaaggagat	taagggggct	900
ctgaagagag	agcttagaat	aaaaatattt	tct			933

<210> 294

<211> 942

<212> DNA

<213> Unknown (H38g143 nucleotide)

<220>

<223> Synthetic construct

<400> 294

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ccagggtttag	aggaaagcca	gcaactggatt	gcaactgcccc	tgggcatcct	ttacctcctt	120
gcttttagtgg	gcaatgttac	cattctcttc	atcatctgga	tggaccatc	cttgacccaa	180
tctatgtacc	tcttctctgc	catgctagct	gccatcgacc	tggttctggc	ctcctccact	240
gcacccaaag	cccttgcaat	gctcctgggt	catgcccacg	agattgggta	catcgtctgc	300
ctgatccaga	tgttcttcat	ccatgcattc	tcctccatgg	agtcaggggt	acttgtggcc	360
atggctctgg	atcgctatgt	agccatttgt	cacccttgc	accattccac	aatcctgcat	420
ccaggggtca	tagggcgcat	cggaatgggt	gtgctgggtga	ggggattact	actccttata	480
cccttcccca	ttttgttggg	aacacttatc	ttctgccaag	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgtctag	aaaccacagt	caatcgagct	600
tatgggtctga	ctatggcctt	gcttgtgatt	gggctggagt	ttctggccat	tgggttttcc	660
tatgcccaca	tcctccaggc	agtgtggaag	gtaccaggga	gtgaggcccg	acttaaggcg	720
tttagcacat	gtggctctca	tatttgtgtc	atcctgggtc	tctatgtccc	tgggaattttc	780
tccttctctca	ctcaccgctt	tggatcatcat	gtaccccatc	atgtccatgt	tcttctggcc	840
acacgggtatc	tcctcatgcc	acctgcgctc	aatcctcttg	tctatggagt	gaagactcag	900
cagatccgcc	agcgagtgtc	cagagtgttt	acacaaaagg	at		942

<210> 295

<211> 945

<212> DNA

<213> Unknown (H38g144 nucleotide)

<220>

<223> Synthetic construct

<400> 295

atgacaaaag	gcaatcgtag	cacagtgtac	gaatttgtcc	tcatgggatt	cacagaccgt	60
cctgagctgc	agctccccct	ctttgtgggt	ttccttgtca	tttatctcat	caccctgggtg	120
ggaaaccttg	gcatgatcct	gctgatcaga	gcagactcgc	ggctccacac	ccccatgtac	180

tacttctca	gtcacctggc	attcattgat	ctgtgttact	catcttctat	tgggccaag	240
atgctgcaaa	atgtattggt	gaagaaaaaa	accatctcct	tttcaggctg	ttttgtcag	300
ctgtacttct	ccggtgcttt	tgccactaca	gaatgattcc	tcttgccac	aatgccctac	360
gaccgctacg	tggccatctg	caacccccctg	atttacacag	ctattatgac	gcagcgggtc	420
tgcaggaggt	tagtgatagg	ggctctatacc	tatggcttcc	gaaactctgt	gatacagaca	480
gctctgacgt	ttcagctgtc	tttctgcaac	tccgacgtca	tccaccactt	ctactgtgct	540
gacccccctc	tcttggccct	ctctgtctct	gacaccaca	acaaagaaaa	gcagctcatg	600
atcttctctg	cagtaaactc	cactgggtcc	ctccttacca	tcttcactct	ctacatttgc	660
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cgtgcctccc	acctcactgt	cgtcaccatc	ttttatggca	cactatTTTT	catgtacctg	780
cagcaaccaa	aagcggggaa	ttcatggaag	ccaaacaaag	tagtctctgt	gttttatagt	840
cttgaatttc	ccatgcttaa	ccctcttata	tatcgctga	gaaacacaga	agtaaaggat	900
gccctgaaaa	aaatgctaga	gggcaaagag	ttatagtgtg	tgagt		945

<210> 296

<211> 605

<212> DNA

<213> Unknown (H38g145 nucleotide)

<220>

<223> Synthetic construct

<400> 296

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttctc	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttctct	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccctgtg	actacctgct	cagcctcctc	tccaaactgg	acatcggtgt	ctgcctcact	240
gtcatcccca	aggtcctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgcttctctc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcggtt	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtcaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctggccatcc	ccatcctttc	agcacaaactc	ttattgggaa	caatgttttt	aaaaccattc	540
ttggcaaattg	ttttgttcac	aatttctgcg	gagatgcacc	ttaataacct	tacacatttc	600
tgaag						605

<210> 297

<211> 609

<212> DNA

<213> Unknown (H38g146 nucleotide)

<220>

<223> Synthetic construct

<400> 297

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagttca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctage	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	taccctaaa	240
atgattgcag	actttctggt	tgagcacaag	actatttctt	ttgatgcca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtc	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgttgtgc	tgcctctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcc	ttttgtggtc	ctaataaggt	agatagtttt	tttctgtgac	540
cttcctctag	cgctgaagtt	agcctgcata	gacacttatg	ttgtcagcct	actaatagtt	600
gcagatagt						609

<210> 298

<211> 912

<212> DNA

<213> Unknown (H38g147 nucleotide)

<220>

<223> Synthetic construct

<400> 298

atggcactca	gcaattccag	ctggaggcta	ccccagcctt	cttttttctt	ggtaggaatt	60
ccgggtttag	aggaaagcca	gcactggatc	gcactgcccc	tgggcatcct	ttacctcctt	120
gtcttagtgg	gcaatgttac	cattctcttc	atcatctgga	tggaccatc	cttgacacaa	180
tctatgtacc	tcttctgtc	catgctagct	gccatcgacc	tggttgtggc	ctctccact	240
gcaccaaag	cccttgcagt	gtccttggtt	cgtgccccag	agattgggta	cactgtctgc	300
ctgatccaga	tgttcttcac	ccatgcattc	tcctccatgg	agtcaggggt	acttgtggcc	360
atggctctgg	atcgctatgt	agccatttgt	caccccttgc	accattccac	aatcctgcat	420
ccagggtgca	tagggcacat	cggaatgggt	gtgctgggtc	ggggattact	actcctcate	480
cccttctcca	ttctgttgcg	aaaacttata	ttctgccaa	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgctcag	aaaccacagt	caatcgagct	600
tatgggctga	ctgtggcctt	gcttgtgggt	gggctggatg	tcctggccat	tgggtgttcc	660
tatgccaca	ttctccaggc	agtgtgaag	gtaccaggaa	atgaggcccg	acttaaggcc	720
tttagcacat	gtggctctca	tgtttgtgtc	atcctgggtc	tctatatccc	gggaatgttc	780
tccttctcca	ctcaccgctt	tggatcatcat	gtaccccatc	acgtccatgt	tcttctggcc	840
atactgtatc	gccttgtgcc	acctgcactc	aatcctcttg	tctatagggg	gaagaccag	900
aagatccacc	ag					912

<210> 299

<211> 330

<212> DNA

<213> Unknown (H38g148 nucleotide)

<220>

<223> Synthetic construct

<400> 299

agtcacacag	aaccacagaa	tctcacaggt	gtctcagaat	tccttctcct	gggactctca	60
gaggatccag	aactgcagcc	tgtcctcgct	tggctgtcct	tgtccattta	cctgggcaca	120
gtgctgggga	acctgctcat	catcctggct	gtcagctctg	actcccacct	ccacaccccc	180
atatacttct	tcctcttcaa	cctgtccttg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcaatcgcat	agcagagtca	tctcttatgc	gggctgcctg	300
acatagatgt	ctttctttgt	cctttttttt				330

<210> 300

<211> 980

<212> DNA

<213> Unknown (H38g149 nucleotide)

<220>

<223> Synthetic construct

<400> 300

tttttttcca	ataattctgt	tctcttccca	catactttct	tcctggctgg	catcccagga	60
ttgactgcc	cccacatttg	gattttactt	cccttttgct	ttatgttttt	cctgtcattg	120
actgggaatg	gtgtcctgct	ttttctcctc	cggacagaat	gcagccttcg	ccagcccatg	180
tttcttttcc	ttgccatgct	ctcctttgtc	gacttgggtc	tctctctctc	cacactgcct	240
aagatgctgg	ccattttctg	gtttgggtgt	acagccatca	gctcgcattc	ctgtctttcc	300
cagatgttct	tcatccatgc	attctctgcc	atggagtcag	gggtgctagt	ggccatggcc	360
ctggaccgct	ctgtggccat	ctgcaaccca	ctgcgttatg	caaccatcct	tccacctgtt	420
gttgttgcca	agattggagg	cctgggtggg	ttgtgagggg	tgggattgac	catctccttt	480
ccaagcttgg	cccataggct	gcactacat	ggctcacaca	tgattgccta	taccttctgt	540
gagcatatgg	cagtgggtgaa	gcttgccctg	gaggccacca	ctgtggacaa	cctctatgcc	600
tttgtgggtg	caatctttct	tgggtggggg	gatgtggtct	tattgcctat	tcttatgggc	660
tgattgtgag	gactgtaatg	cattttcctt	cacctgagga	acgtgcgaaa	gcaggcagca	720
catgtacagc	ccatgtctgt	gtcatcctct	tcttctatgg	actgggcttt	ctttctgtgg	780
tcatgcagcg	ctttggagca	cccacagctt	ctactgccaa	ggcatcctt	gccaatctct	840
acttgcctct	tccccagca	ctggatccca	ttgtctatgg	catggagacc	aagcagatct	900

aggagcggct attgatgatt ctaagcccca agcagattga gcttacctga gtatagttat 960
caccagctgg acttcagggt 980

<210> 301
<211> 721
<212> DNA
<213> Unknown (H38g150 nucleotide)

<220>
<223> Synthetic construct

<400> 301
cttagacaac ttcacaacct ttttcttctt gttggatttt ttctttcttt tactcctttt 60
aagttatatg cataatctaa attctgtgac taaattttcc agtaaaacag atgaatcaaa 120
gctcaaaagc taatgtaaag tcaaattctt tttctttacc tatgctggat gctgtgagaa 180
actactgctt gctgtagaaa agagagatct tcctttttgt tcattcattt cctccttcac 240
tagtcaactg ctgtttctga ccatgccaaag gtggaacctg gagtaggaag gagagagaga 300
gggtaaggga agtctcattg actgacgcta aaataagatg gcttcacatt ttctggctct 360
ggccaatggt tactatttct tactcatatt aaacctctct gaatgcattt aaccatggga 420
gcaagtcttc tccccgaggt gcgtcccccga gatttctttc agttcccagt ggtcccat 480
aatctctcac agctggacgt tcaactcagta tgtaagacta ccatcttggg tacaatccct 540
ttcaaagcaa ctaaccact ttagtttcca tggccagtcc ttcaaactct catatatctg 600
actagctata agtggagctg taactcccat ttgtctgcaa agaccacggg gccagagttc 660
ggttgcagtc tgacatatcc ctgatgacag gatacacaca ttaaaacctc tgagtggccc 720
c 721

<210> 302
<211> 939
<212> DNA
<213> Unknown (H38g151 nucleotide)

<220>
<223> Synthetic construct

<400> 302
atggcatctc ccaacaatga ctccactgcc ccagtctctg aattcctcct catctgcttc 60
cccaacttcc agagctggca gcactgggtg tctctgcccc tcagccttct ctctcctctg 120
gccatgggag ctaacaccac cctcctgac accatccagc tggaggcctc tctgcaccag 180
ccccgtact acctgctcag cctcctctcc ctgctggaca tcgtgctctg cctcaccgtc 240
atccccagg tcttgccat ctctgggtt gacctcaggt cgatcagctt cccagcctgc 300
ttcctccaga tgttcacat gaacagtttt ttgaccatgg agtctgcac gttcatggtc 360
atggcctatg accgttatgt ggccatctgc catccattga gataccgctc tatcatcact 420
gaccagtttg tggctagggc cgtgggtctt gttatagccc ggaatgcctt tgtttctctt 480
cctgttccca tgctttctgc caggctcaga tactgtgcag gaaacataat caagaactgc 540
atctgcagta acctgtctgt gtccaaactc tcttgtgatg acatcacttt caatcagctc 600
taccagtttg tggcaggctg gactctgttg ggctctgatc ttatccttat tgttatctcc 660
tattctttta tattgaaagt tgtgcttagg atcaaggccg aggggtgctgt ggccaaggcc 720
ttgagcacgt gtggttccca cttcatcctc atcctcttct tcagcacagt cctgctgggt 780
ctggtcatca ctaacctggc caggaagaga attcctccag atgtcccat cctgctcaac 840
atcctgcacc acctcattcc cccagctctg aaccccatg tttatggtgt gagaaccaag 900
gagatcaagc agggaatcca aaacctgctg aagaggttg 939

<210> 303
<211> 405
<212> DNA
<213> Unknown (H38g152 nucleotide)

<220>
<223> Synthetic construct

<221> misc_feature

<222> (1)...(405)

<223> n = A,T,C or G

<400> 303

aaagatttgt	gaaggagaag	taataattaac	tttagaatag	aaagtattat	atTTTTTTTat	60
ataggggttg	gagagangat	gggtttatga	aatttaattgt	taatgttttg	tgaaagtttt	120
taatgataaa	aaactgtgtt	aaggattaag	ggtgagggag	atatggccaa	agctctaggt	180
acttgtgggt	cccacttcat	cctcatcctc	ttcttcacca	cagtcctgct	ggttctggtc	240
atcactaacc	tggccaggaa	gagaattcct	ccagatgtcc	ccatcctgct	caacatcctg	300
caccaccta	ttccccagc	tctgaacccc	attgtttatg	gtgtgagaac	caaggagatc	360
aagcagggaa	tccagaacct	gctgaggagg	ttgtaaaaaa	taaaa		405

<210> 304

<211> 960

<212> DNA

<213> Unknown (H38g153 nucleotide)

<220>

<223> Synthetic construct

<400> 304

atggctccga	ccaacctcac	atctgcccc	gtgttccctc	tcctcggcct	ggtggacgga	60
acagacagac	gcccaccgc	tgctgttcc	gctctgcctt	ggcatctatc	tgctcaacgc	120
cctgagcaac	ctgagcatgg	tggcgctgg	gagatctgac	ggggccctcc	gctcccccat	180
gtattacttc	ttgggtcacc	tgagcctcgt	ggacgtctgc	tttaccaccg	tcacgggtccc	240
caggctgctg	gccggcctgc	tccaccggg	ccaggccata	tccttccagg	cgtgctttgc	300
cgagatgtac	ttcttcgtgg	ctctgggcat	caccgagagc	tacctcccg	cggccatgtc	360
ctacgaccgc	ccgacggcgg	cgtgccggcc	cctgcgtac	ggcgcgctgg	tgacgccatg	420
ggcgctgcgc	ctcgctgggt	cgtgcgtcgt	gggcccgtgac	gcacctgcac	tcgctgctgc	480
acacgctgct	cctctccg	ctctccctacc	cctacccccc	ccccgtgcgc	cccttctttt	540
gcgacatgac	ggtgatgctg	agcttgggca	cctcggacac	gtccgcgcgc	gagacggcca	600
tcttctccga	gggcctggcc	gtgggtgttg	ccccgctgct	cctcgtgttc	cttttccctac	660
gcgcgcaccc	tggtcgcggt	gctcggcttg	ccgcggccgg	cgccgcgcct	tctccacctg	720
cggggccccc	ctagtggcgg	tggcggtggc	ggtggcgctt	ttctttgggt	ctgtcctctc	780
cgtgtatttc	ccgccgtcgt	ctgcctactc	agcccgctgg	gaccgcctgg	ccagcgtgggt	840
ctacgctgtc	atcacgccga	ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	900
caagggcgcc	ctgaaaaggg	ggctcagatg	gagggctgca	ccccaagagg	cgtgagggca	960

<210> 305

<211> 975

<212> DNA

<213> Unknown (H38g154 nucleotide)

<220>

<223> Synthetic construct

<400> 305

atgttccctc	ccaataaac	ccagtttcac	ccctcctcct	tcctgttgct	ggggatccca	60
gggctagaaa	cacttcacat	ctggatcggc	tttccctttt	gtgctgtgta	cataattgca	120
ctcatagggc	gcttcactat	tctacttggt	atcaagactg	acagcagcct	ataccagccc	180
atgttctact	tcctggccat	gttggccacc	attgacttgg	gcctttcaac	agctaccatc	240
cctaagatgc	ttgggatctt	ctggtttagc	ctcagggaga	ttatctgtga	tgccctgcctc	300
atccagatgt	ttttcatcca	caactttact	ggcatggagt	cagcagccct	cgtgggaatg	360
gcttatgacc	actttgtggc	catctgcaac	ccgctacgat	atagcatcat	cctcaccaaa	420
aaggctgttt	ctgtgattgg	tcttgggtgt	ttagttaggt	catttatgtc	tgttattcca	480
tttgtttttc	tcatttttgc	gttgcccttc	tgtggggatc	atgtcattcc	ccacaccaac	540
tgtgagcaca	tgggtcttgc	tcactctgtc	tgttccagta	tcaagatcaa	tataatctat	600
ggcttgggtg	ctatttcaat	cctagtattc	gacatcatag	ccattgccct	ttcttatgtg	660
caaatacttc	acgctgtttt	ccatcttcc	tcctgtaaag	cctgactcaa	gtccctcagc	720
acatgtgggt	cacatgtgtg	tgtaatcctt	gccttctata	caccagccct	cttttccctt	780
gtgactcatc	gctttggcca	aaatgtgccc	cgctatatcc	atatactcct	agccaatctc	840

tatgtttgtgg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tatgtctgtg	tgaagaatat	attcttacaa	aaataagaaa	ttgaaaagaa	atcgcatcta	960
ataatataa	gaagg					975

<210> 306

<211> 957

<212> DNA

<213> Unknown (H38g155 nucleotide)

<220>

<223> Synthetic construct

<400> 306

atgtctcctc	ttaatgacac	aaaaatggaa	gtccttagat	tcctccttat	cgggatcact	60
ggactggaga	aaagtcgcac	ctggatatcc	attcctttct	tatctgtgta	ccttctttct	120
tggatgggta	attttaccgt	cctctttttt	atcaagacag	agcaaagcct	ccatgaacct	180
atgtattatt	tgttttccat	gctctccatc	tctgacctag	ggctgtctct	gtcttcctta	240
cccatcactt	tgggactatt	cctatttgat	gtccatgaaa	ttcatgcagc	tccatgcttt	300
gcctaggaat	tttttatcca	tctgtttaca	gtcagtgaag	cctctgtact	gtctgtaatg	360
gcatttgact	ggatgtggc	aatccacagt	cctttgagat	acagcactat	cttaactagt	420
cccagagcca	tcaaaacagg	ggttcttctg	acttccaaga	atgttctttt	gacccctcca	480
ctgccctttc	tcttgcaaag	gctgagatat	tgtcatcaaa	acctgctctc	ccactcctat	540
tgtctccacc	aggatgtcat	gaagctgatg	tgttctgaca	acacagtcaa	tgttgtctac	600
ggactctgtg	caggactttc	tactatgctg	gacttggtgt	tgattacctt	ctcctaaatt	660
atgattttaa	gggctgtact	gggaattgct	acccccagac	agcagttcaa	ggccctcaac	720
acgtgcactc	ctcacatctg	tgctgtgctt	atcttctatg	tgcccacgct	gagtgctgcc	780
atgctccacc	agtttgccag	ggatgtgtct	cctatgatcc	acgtcctcat	ggctgatatt	840
tttctgctgg	tgccaccctt	gttgaatccc	atcgtgtact	gtgtgaagac	ccaccaaatc	900
cgagaaaagg	ttgtggggaa	actttgtcca	aaagtaagtt	gatcaaagga	atgagaa	957

<210> 307

<211> 939

<212> DNA

<213> Unknown (H38g156 nucleotide)

<220>

<223> Synthetic construct

<400> 307

atgtccatta	tcaacacatc	atatgttgaa	atcaccacct	tcttcttggt	tgggatgcc	60
gggctagaat	atgcacacat	ctggatctct	atccccatct	gcagcatgta	tcttattgct	120
attctaggaa	atggcaccat	tctttttatc	atcaagacag	agccctcctt	gcatgagccc	180
atgtactatt	ttctttccat	gttggtctatg	tcagacttgg	gtttgtcttt	atcatctctg	240
cccactgtgt	taagcatctt	cctgttcaat	gtcctgaaa	tttcatccaa	tgccctgctt	300
gcccaggaat	tcttcattca	tggattctca	gtactggagt	cctcagtcct	cctgatcatg	360
tcatttgata	gattcctagc	catccacaac	cctctgagat	acacctcaat	cctgacaact	420
gtcagagttg	cccaaataag	gatagtattc	tcctttaaga	gcatgctcct	ggttcttccc	480
ttccctttca	ctttaagaaa	cttgagatat	tgcaagaaaa	accaattatc	ccattcctac	540
tgtctccacc	aggatgtcat	gaagttggcc	tgttctgaca	acagaattga	tgttatctat	600
ggcttttttg	gagcactctg	ccttatggta	gactttatc	tcattgctgt	gtcttacacc	660
ctgatcctca	agactgtacc	gggaattgca	tccaaaaagg	agcagcttaa	ggctctcaat	720
acttggtgtt	cacacatctg	tgcagtgatc	atcttctacc	tgcccatcat	caacctggcc	780
gttgccacc	gctttgccc	gcatgtctct	cccctcatta	atgttctcat	ggcaaatgtt	840
ctcctacttg	tacctccact	gacgaacca	attgtttatt	gtgtaaaaac	taaacagatt	900
agagtgaag	ttgtagcaaa	attgtgtcaa	cggaagatt			939

<210> 308

<211> 925

<212> DNA

<213> Unknown (H38g157 nucleotide)

<220>

<223> Synthetic construct

<400> 308

atgggtgaata	gaaacaatgt	gacagagttt	attctactgg	gctttataga	gaatccaaaa	60
atgcagaaaa	tcatatttgt	tgtgttttgt	catctacatc	cccacccatga	taggaaatgt	120
gctcattgtg	gtcaccgtca	ctgccagccc	atcatgagg	tcccccatgt	acttttacct	180
ggcctatctg	tcctttattg	atgcctgcta	ttcctccgtc	aatgccccta	agctgatcac	240
agattcactc	tatgaaaaca	agactatctt	actcaatgga	tgtatgactc	aagtctttgg	300
agaacatttt	ttcggagggtg	ttgagggtcat	cctacttact	gtaatggcct	atgaccgcta	360
cgtggtcac	tgcaagccct	tgcaactatac	caccatcatg	aagcagcatg	tttgtagcct	420
gctagtggga	gtgtcatggg	taggagggtt	tcttcatgca	accgtacaga	tcctcttcat	480
cttccaatta	cctttctgtg	gtcctaattg	catagatcac	tttatgtggg	atctcaaccc	540
tttgctcaat	cttgctgca	ctaataccca	cactctagga	ctcttcgttg	ctgccaacag	600
tgggttcata	tgccctgttaa	actttctctt	gtcctctggc	tcctatatgg	tcatactgta	660
ctccttaagg	acccacagct	tagaggcaag	gtgcaaagcc	ctctccacct	gtgtctccca	720
catcacagtt	gtcatcttat	tctttataacc	ctgcatatgt	gtgtacatga	gacctccagc	780
tactttaccc	attgataaag	cagttgctgt	attctacact	atgatagctc	ctatgttaaa	840
ccccttaatc	tacaccttga	ggaatgctca	gatgaaaaat	gccattagga	aattgtgtag	900
taggaaagct	atttcaagtg	tcaaa				925

<210> 309

<211> 963

<212> DNA

<213> Unknown (H38g158 nucleotide)

<220>

<223> Synthetic construct

<400> 309

atggcataacc	atggcaacag	gggcactttt	cacccagcca	cattttttct	cattggaatc	60
ccagggtctgg	aagacgtcca	tatgtgaatc	tccttgcact	tctgctctgt	ttaccttttg	120
gcttttctgg	gaaatgctac	cattctgcta	gtcatcaagg	cagaacagac	cctccgggag	180
cccattgttct	actttctggc	catcctttcc	acaattgatt	tggccctttc	tacaacctct	240
gtgcctcgta	cgctgggtat	cttctgggtt	gatgctcatg	agattaactt	tggagcatgt	300
gtggcccaga	tgtttctgat	ccatgccttc	actggcatgg	aggctgaggt	ctgggtggcca	360
tggcctttga	ccgttacgtg	gccatctgca	atccacttca	ctacacaaac	atcttgacat	420
ccgggtgtct	ggtgggcac	actatgtgca	ttgtaattcg	tccagttctg	tttactactcc	480
cgataatcta	tctcatctac	cgtttaccat	tttggtcagg	gtcatataaa	tagccccattc	540
ctactatgag	cacatgggca	ttgcaaaatt	gtcctgtgga	aacatccgtg	tcaatgctat	600
ctatgggctc	tttgtgggtc	cctctatctc	ctgaacctgg	tccttattgt	tatctcatat	660
gtgtacattc	tctgtgctgt	cttctgcctc	gcatcacatg	atgctcggct	aaaagcccta	720
agcaaacatg	ggctctcatg	ttggggtcac	ctgtgttttc	tatatcccgt	cggacttctc	780
tttctactc	attgatttgg	acacaacatt	ccacattaca	tgcacattct	tgttgcctact	840
ctctatttgg	ttatcccacc	ctctctcaac	cccatcattt	gtgggggtgag	gaccaaattgg	900
aaacgagagc	gagtgtctta	tgtacttact	aaaaaataag	attctgacca	tgttctttta	960
cta						963

<210> 310

<211> 483

<212> DNA

<213> Unknown (H38g159 nucleotide)

<220>

<223> Synthetic construct

<400> 310

ggcacagttt	agatcctctc	cccagttctga	cttctctttc	atgatcccaa	tgtcatagct	60
cattcatgtg	tgacttaaac	actttgttga	aactcctctg	catgggtact	actaatacac	120
ttgggtttctt	tgttgcctgcc	aatgggtgggt	tcaactacct	attaaacatc	attttcttga	180
tgggtttctta	agtggccatc	ctatgtactt	tgaaaactca	cagcttggag	gaaagatgct	240

aaagccctct	ctacctgcat	ctctcacacc	accgtgggtca	tcttatcttt	gggttctgta	300
tatctgtgta	tctgtgcccc	gtgacccttc	cccaatcaat	aaagcagtgg	ctgtgtttta	360
taccatgata	aatcctatgt	taaaaccctt	agtctaacc	tcagaaatgc	agaggtgaaa	420
agtgccttga	gaaagctctg	ggcctaaaaga	tgaactgaag	agagaaataa	tccaaacata	480
aga						483

<210> 311

<211> 933

<212> DNA

<213> Unknown (H38g160 nucleotide)

<220>

<223> Synthetic construct

<400> 311

atgtttttatc	acaacaagag	catattttcac	ccagtcacat	ttttcctcat	tggaaatccca	60
gggtctggaag	acttccacat	gtggatctcc	gggcctttct	gctctgttta	ccttgtggct	120
ttgctgggca	atgccaccat	tctgctagtc	atcaaggtag	aacagactct	ccgggagccc	180
atgttctact	tcctggccat	tctttccact	attgatttgg	ccctttctgc	aacctctgtg	240
cctcgcatgc	tgggtatctt	ctggtttgat	gctcacgaga	ttaactatgg	agcttgtgtg	300
gcccagatgt	ttctgatcca	tgccttcact	ggcatggagg	ctgaggtctt	actggctatg	360
gcttttgacc	gttatgtggc	catctgtgct	ccactacatt	acgcaacat	cttgacatcc	420
ctagtgttgg	tgggcattag	catgtgcatt	gtaattcgtc	ccgttttact	tacacttccc	480
atgggtctatc	ttatctaccg	cctacccttt	tgtcaggctc	acataatagc	ccattcctac	540
tgtgagcaca	tgggcattgc	aaaattgtcc	tgtggaaaca	ttcgtatcaa	tggatatctat	600
gggttttttg	tagtttcttt	ctttgttctg	aacctgggtc	tcattggcat	ctcgtatggt	660
tacattctcc	gtgctgtctt	ccgcctccca	tcacatgatg	ctcagctaaa	agccctaagc	720
acgtgtggcg	ctcatgttgg	agtcactctg	gttttctata	tccttccagt	cttctctttc	780
cttactcacc	gattttggaca	ccaaatacca	ggttacattc	acattcttgt	tgccaatctc	840
tatttgatta	tcccaccctc	tctcaacccc	atcatttatg	gggtgaggac	caaacagatt	900
cgagagcgag	tgctctatgt	ttttactaaa	aaa			933

<210> 312

<211> 946

<212> DNA

<213> Unknown (H38g161 nucleotide)

<220>

<223> Synthetic construct

<400> 312

atggagaata	ggaataacgt	gacagagttt	gttttactag	ggcttacaga	gaatccaaag	60
atgcagaaaa	tcatatttgt	tgtgtttttt	tgatcatctat	atcatcactg	tgggtgggaaa	120
tgcgctcatt	gtggtcacca	tactgcccag	cccatcactg	gggtccccc	tgtacctttt	180
cctggcctat	ctctccttta	tagatgcctg	ctattcttct	gtcaataccc	ctaagctgat	240
cacagattca	ctctatggaa	agaacaccat	cctattcaat	ggatgcatga	ctcaagtctt	300
tggagaacat	ttcttcggag	gtgcagaggg	tatcctactt	actgtgatgg	cctatgaccg	360
ctatgtggcc	atctgcaagc	ccttgcaacta	tatgactatc	atgaaccagt	gtgtgtatgc	420
cctgctaagt	ggagtgggtg	ggatgggagg	ctttcttcat	gcaaccatac	agatcctctt	480
catcttccaa	ttacctttct	gtggtcctaa	tgtcatagat	cactttatgt	gtgatctgaa	540
ccctttgctc	aacctcgcc	gcactgacac	ccatagtctg	ggactcttca	ttgctgccaa	600
cagtggattc	atctgcttgt	taaactttgt	cctcctgctg	gtctcctatg	tggtcactct	660
gcgctcccta	aggactcaca	gcttggaggc	aaggcaca	gccctctcca	cctgtgtctc	720
ccacatcaca	gttgtcatct	tattctttgt	gccctgcata	tttgtgtaca	tgagacctgc	780
agctacttta	cctattgata	aagcagttgc	tatattctac	actatgataa	ctcctatggt	840
aaacccttta	atctatacct	tgaggaatgc	ccagatgaaa	aatgccatca	ggaaattgtg	900
tagtagaaaag	gacattttcag	gtaacaaata	aatgtaacta	gagctc		946

<210> 313

<211> 966

<212> DNA

<213> Unknown (H38g162 nucleotide)

<220>

<223> Synthetic construct

<400> 313

tcaaatactg	ggatgtccat	tctcaatacc	tctgaaatgg	aaatctctat	tcttacttg	60
gttgggatcc	caggtttggg	gcatgccaat	atttggatct	ctatcccat	atgtctcatg	120
tacactgttg	ctatcctagg	gaattgtacc	attctgtttt	tcataaaaac	agagccttct	180
ttgcatgagc	ccatgtacta	ttttctctcc	atgttggttc	tctctgacct	gggactatcc	240
ctctcctctc	tccctaccat	gttaaggatt	ttcctgttca	atgctccagg	aatttcccct	300
gatgcctgta	ttgctcaaga	gtttttcatc	catggattct	cagctatgga	gtcatctgta	360
cttcttataa	tgctcttga	tcgctttatt	gccatctgca	acccctgag	atacacttcc	420
atcctcacca	gtgccagagt	cattcaaatt	gggttgctt	tttctctcaa	aaatgttttg	480
ttgatcctcc	catttccttt	cactctaaaa	catctaaaat	attgtaagaa	gaacctcctg	540
tcccaatcct	actgcctcca	tcaagatgtc	atgaaactgg	cctgcactga	caacaaggtc	600
aacatcatct	atggcttatt	tgtggctctc	acaggcatcc	tagacttgac	atttattttc	660
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atagctgatg	ctttctgtct	ggtgcctcca	ttgatgaacc	ccattgtata	ctgtgtgaag	900
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<210> 314

<211> 961

<212> DNA

<213> Unknown (H38g163 nucleotide)

<220>

<223> Synthetic construct

<400> 314

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atgctgggga	actgtctatc	atcctggccg	tcacctgac	tccacctcc	acatcccat	180
gtacttcttc	ctctccaacc	tggtccttgg	ccatgacatt	gcgtttcacc	ttaggccacg	240
gtccccaaga	tgattgtaga	catgcaatca	catagcagag	tcattctcca	tgcaggctgt	300
ctgacacaga	tacctttctt	tgctcttttt	gtatgtatag	atgacatgct	cctgactgtg	360
atggcctatg	actgatttgt	ggccatctgt	cacccctgc	actaccagct	catcatgaat	420
cctcacctct	gctgtcttct	tagtggtgat	gtcttttct	tagcctgttg	gattcctagc	480
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taaaattgtg	ccctccattc	taagaattcc	attgtcagat	gggaagtata	aagccttctc	720
cacctgtggc	tctcacctgg	caattgtttg	cttattttat	ggaacaggca	ttggcatgta	780
cctgacttca	gctgtgtcac	cagccccag	gaatgggtgtg	gtggcatcag	tgttgtacgc	840
tatgtcacc	ccatgctgaa	ccccttcac	tgcagcctga	gaaacagggg	gcattcaaag	900
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<210> 315

<211> 960

<212> DNA

<213> Unknown (H38g164 nucleotide)

<220>

<223> Synthetic construct

<400> 315

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tctcgacttc acactcccat gtaatttttt ctctccagtt tgtccattct agatctgtgt 240
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<210> 316

<211> 947

<212> DNA

<213> Unknown (H38g165 nucleotide)

<220>

<223> Synthetic construct

<400> 316

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caaacgtgtc cataatgggg gccatcaagc tcagccacaa ccttcacact cctatgtact 180
ttttcctctg tggcctgtcc ttttcagaaa cttgtaccac tgtggtagta atccctcgca 240
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ggcccaagaa cagcaactcc ttcgatgaag acatgctgac ggccatgata tatacaatac 840
tgatgcctct gcttaacccc atcgtgtaca gtctgagaaa caaagaaatg cagatagccc 900
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<210> 317

<211> 955

<212> DNA

<213> Unknown (H38g166 nucleotide)

<220>

<223> Synthetic construct

<400> 317

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ctactgggaa acggctctct tctgtttatc atcaagacag agccagcct ccatgagcca 180
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cccaaacttc tcagtctctt ctggttccat gatggagaga ttgcttttga aacctgcctc 300
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tgtaattggg agagtggggc tagctattgt tctcaggggc atagcacttc tcagtccctc 480
ctctttccta ctacgtggc ttccctactg cagaacccat atcatttctc acacctactg 540
tgagtccatg gccctcatca ggattgcctg tgctgagaca aaattccgca gagcctacag 600

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cctcattgtt	gccttcctta	ctgggggtggt	agactttata	ttgatcattt	attcttatgt	660
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cacctgtggc	tcccatgtct	gtgtcatctt	agtatcctat	actccagcct	tcttctcggt	780
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ctatcttctt	gtcccaccca	tgggtgaacc	cattatctat	ggggtaaaga	ccaaaaggat	900
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<210> 318

<211> 921

<212> DNA

<213> Unknown (H38g167 nucleotide)

<220>

<223> Synthetic construct

<400> 318

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tggcaagtgc	tcttcttcat	catctttctt	gtgggtctaca	tcatcaccat	ggtggggcaat	120
atcggcatga	tgggtgtta	caaggtcagt	cctcagctta	acaaccccat	gtactttttc	180
ctcagtcact	tgtcatttgt	tgtatgtgtg	ttttcttcca	atgtcaccce	taaaatgttg	240
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ttcttcattg	ctcttgtcca	tgtggaaatt	tttattcttg	ctgcgatggc	ctttgataga	360
tacatggcaa	ttgggaatcc	tctgctttat	ggcagtaaaa	tgtcaagggg	tgtctgtatt	420
cgactgatta	ctttccctta	catttatggg	tttctgacga	gtctggcagc	aacattatgg	480
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cctctcatca	aaatggcctg	tgccggggacc	tttgtaaaa	aatatacaat	gatcatactt	600
gccggcatta	acttcacata	ttccctgact	gtaattatca	tctcttactt	attcactctc	660
attgccattc	tgcgaatgcg	ctcagcagaa	ggaaggcaga	aggccttttc	cacagtggg	720
tcccactctga	cagctgtcat	tatattctat	ggtagcttga	tcttcattga	tctcagacgt	780
cccacagagg	agtctgtgga	gcagggggaag	atgggtggctg	tgttctatac	cacagtgatc	840
cccattgtga	atcccatgat	ctacagctctg	aggaacaagg	atgtgaaaaa	ggccatgatg	900
aaagtgatca	gcagatcatg	t				921

<210> 319

<211> 966

<212> DNA

<213> Unknown (H38g168 nucleotide)

<220>

<223> Synthetic construct

<400> 319

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ttgaggtaca	ccgctaaaca	ttctagcctc	ttcttctctc	tcttctctct	catctacagc	120
atcactgtgg	ctgggaatct	cctcatcctc	ctaactgtgg	gctctgactc	tcacctcagc	180
ttacccatgt	accatttctt	ggggcacctc	tccttctctg	atgcctgttt	gtctacagtg	240
acagtgccca	aggctcatgg	aggcctgctg	actctgggat	ggaagggtgat	ctccttttag	300
ggctgtgccg	tacagcttta	ttgcttccac	tttctggcca	gcactgagtg	cttctctgtac	360
acagtcatgg	cctatgaccg	ctatctggct	atctgtcaac	ccctgcacta	cccagtggcc	420
atgaacagaa	ggatgtgtgc	agaaatggct	ggaatcacct	gggccatagg	tgccacgcac	480
gctgcaatcc	acacctccct	caccttccgc	ctgctctact	gtgggccttg	ccacattgcc	540
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gagctagtca	tgcttgccag	cattggcctc	gtggctgcag	gctgcctcat	cctcatcggt	660
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tacacaatcg	taactccaat	gctcaaccca	ttcattttaca	ctttgcggaa	caaggagggtg	900
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ccccca						966

<210> 320

<211> 967
 <212> DNA
 <213> Unknown (H38g169 nucleotide)

<220>
 <223> Synthetic construct

<400> 320
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 aatatcgga tgatgttggt aatcaagggt agtcctcagc ttaacagccc catgtacttt 180
 ttctcagtc acttgtcatt tgttgatgtg tgggtttctt ccaatgtcac ccctaaaatg 240
 ttggaaaatc tggtatcaga taaaaaaaaa acaattttct tatgctggct gtttagcaca 300
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 tgatagatac acagtgattg gaaatccttt gctttatggc agcaaaatgt caagggatgt 420
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 agtgatcccc atgttgaatc ccatgatcta cagtctgagg aacaaggatg tgaaaaaggc 900
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 tgtcttc 967

<210> 321
 <211> 933
 <212> DNA
 <213> Unknown (H38g170 nucleotide)

<220>
 <223> Synthetic construct

<400> 321
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 ctggagcccc tcctcttttg aatcttctgt gtgggtttac tgctcactgt gctggggaac 120
 ctctcatccc tgctggtgat cagggtggat tctcacctcc acaccccat gtactacttc 180
 ctaccaaac tgctcttcat tgacatgtgg ttctccactg tcacgggtgc caaaatgctg 240
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 tattttttcc acttcttggg gagcaccgag tgttctctct acacagtcac gtcctatgat 360
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 gccctcctgg ccaccggcac ttggctcagt ggctctctgc actctgctgt ccagaccata 480
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 gacattggga tagtggcctc aggtgtcttt gtcctgatag tgctgtccta tgtgtccatc 660
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 cttctcaacc ctgttgtgta caccctgaga aacaaggagg tgaagaaagc tgtgttgaag 900
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<210> 322
 <211> 953
 <212> DNA
 <213> Unknown (H38g171 nucleotide)

<220>
 <223> Synthetic construct

<400> 322

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tgggaaatgt	tttctctctc	aattttacaa	cttccttaga	tgtacactgt	ggccctctca	120
gggacatcta	ttctgatttt	cttgatttag	acagatttct	gagttcacac	atcattgtac	180
tctttctgag	ttctcattga	tatagccatt	tctgttggtta	aaattgggtat	tgagggttttc	240
tctggaaaga	taaactttctc	acatactggt	tgtggaactc	agattttctt	ctttctgact	300
gctggcattt	tcaaatatgt	ccttctcact	tatatggctt	atgaccataa	cgtggctatc	360
lytgcctgag	tgaccaacct	tcatgagtga	tcaggctctc	tagcaatggg	cagtagagtc	420
ttggattgga	ggaaaacttt	cttctttggc	tcataccatt	tatatattttc	atattattcag	480
ctataaagca	aaggagatta	gccacttatg	gcccaagctc	ttttaaagct	cctctgtggg	540
gatccccat	atacaaaatg	atgttttttt	cacaataatt	acattcttgt	tcaccctgct	600
tcctcttact	ctgaccttat	cctccaagct	tattgtgttc	actatcctac	acatgaactc	660
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tgctgtggcc	aggccacttc	gtctacatga	cttccagctc	cttctgaact	gtaaacaaat	780
accagaccat	gtctgcttga	cagcataatt	atatccacgt	tgaaccctct	gatagacatt	840
ctgaagaatg	cagaagtggc	aggagcttgg	agcaagtctt	tgtaaaagaa	agcgctaaaa	900
agtcaacacc	ttattatcgt	agctgtgaaa	ataaataaac	aacagagcag	agt	953

<210> 323

<211> 960

<212> DNA

<213> Unknown (H38g172 nucleotide)

<220>

<223> Synthetic construct

<400> 323

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ctccacaccc	ccatgtattt	ctttcttgct	agtttgcctt	gcttggattt	gtattactcc	240
actaatgtga	ctcccaagat	gttgggtgaac	ttcttctcag	acaagaaagc	catttcctat	300
gctgcttgtt	tagtccagtg	ctattttttc	attgctgtgg	tgattactga	atattatatg	360
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aagatgtcca	aagggtctctg	tattcgccctg	attgctgtgc	catatgtcta	tgggtttctt	480
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gctgttttct	acacttttgt	aagccctatg	ttgaacccca	tcatctatag	tttgaggaac	900
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<210> 324

<211> 705

<212> DNA

<213> Unknown (H38g173 nucleotide)

<220>

<223> Synthetic construct

<400> 324

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gtcttctctg	tgggttatgt	gcttactgtg	ctggggaacc	tctctatcct	gctgggtgac	180
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cacttcccag	gtagtgaaaa	cactccccc	gaagtgaacc	aaatgctagt	ggcccgggg	480
gcacacgggc	tcccactcat	catcctggca	gatctgagtg	ggtaactaag	agttgatagt	540

tcttagtggg	caattcaaaa	ttagtaatat	aatttagtta	tccaagtga	atttattaca	600
tgtataggtc	tcagcattaa	acattattcc	aaacaacttg	cacagttata	attcctttcac	660
agattatcta	agacattttt	aaattcacag	ctagattttt	attta		705

<210> 325

<211> 921

<212> DNA

<213> Unknown (H38g174 nucleotide)

<220>

<223> Synthetic construct

<400> 325

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gcaattccaa	ctatttcttt	ctctggatgt	gtgggtccagc	tctatttatt	tgtgggcttg	300
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aaccocctta	actacacact	cattgtcagc	tgagccacct	gcatgcagct	ggttctagcc	420
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cttgtctata	cactgagaaa	taaagaagta	aagatggctc	tgagaaaggt	tctgggtaga	900
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<210> 326

<211> 470

<212> DNA

<213> Unknown (H38g175 nucleotide)

<220>

<223> Synthetic construct

<400> 326

atttgccaca	atagaaaagt	catccctgca	tctatgtgaa	atatgtttta	tttctcttga	60
aagttgccta	agacaatttt	ctgcatgtac	tgttcact	agctaaaact	gctccccact	120
cttattcctc	taggaaatc	ctagttattt	ttcaagcccc	agttagatta	ttgtcctttg	180
atgcttacc	tgattcctga	aacaattagt	tattttgttt	gtatttttat	tattgaacta	240
atcatattta	actttaattt	tcagtctcct	taccatgaaa	atcaaccagc	tctttcaagg	300
caagcactgt	gatcagttgt	cttcaattcc	ccagcaaagc	aacttgcatg	catggagtgt	360
tcagtgtgt	ttgtgcacaa	atgtaaccat	attacaatgg	ttaaatcatt	tagcatcctg	420
aaagcatcac	agagtcaaag	tagctaactt	gtgtgaacct	tttaattcaat		470

<210> 327

<211> 959

<212> DNA

<213> Unknown (H38g176 nucleotide)

<220>

<223> Synthetic construct

<400> 327

gggaccaagt	caatcaagct	aacttctctg	tcagagttcc	tgcttcttga	gttctccagc	60
cttgaagaaa	tccagcagat	cctttttctg	tctgcttgtg	gctatatctg	attgttctga	120
gtggaaatat	caccactgtc	actgtcatcc	gctggatca	aagcctccac	atacctgtat	180
acttattcct	agggatcctc	tccatttctg	ggacatgcta	tacctttgtc	attctgccca	240

agatgctcat	agatctgttg	tctttgctca	gaacaatctc	atttattaac	tgccactcca	300
gtgttcttct	ttctgggttt	tgctgtcact	aatttcatgt	tcctgggcat	gacagtttat	360
gattcctatg	ttgccatctg	ccatccactt	cactaccctg	tccttacgag	ctggcagata	420
tgtaaacaac	tggcagcaac	gtgtgctgtg	attgtttttt	tttgtttgtt	tgttttcact	480
gataggctcc	ttcttagatt	ttcagctgct	tttctgtggc	ccaaacaaga	tcaaccacta	540
cttctgtgac	atctcactgc	ttatcagct	tgccgtgact	gataacctaca	tcaggagct	600
agtcattctt	attgggtgga	ttctagcact	tacggttcct	ctgattttat	ttgcatctcc	660
tatggcttca	ttgttcacac	catcctgagg	atcccatatg	tgaaagcaag	caaaaagcca	720
tctctacttg	tgccctccat	cttattatgg	tcgttgctca	ttatggctgt	gcctcctttg	780
tcaacctgtg	accatcagcc	aaataatcat	ccagcaaata	accatctagc	aagaacaggc	840
tggtgacagt	gaccttacac	agttgtgact	ccgttggtga	atccatggta	tatagcttca	900
agaataagaa	cgttcagatg	gccatttgga	aagtgatttg	ccaaggagga	tttctctct	959

<210> 328

<211> 952

<212> DNA

<213> Unknown (H38g177 nucleotide)

<220>

<223> Synthetic construct

<400> 328

atgagaagaa	actgtacatt	ggtgactgag	ttcattctcc	tgggactggc	caatcacccg	60
gaattacaga	ttttcctctt	cacgctgttt	ctcaccattt	acatgggtcac	ggtggcagga	120
aatcttggca	tgattgccct	catccaggcc	aacgcccccg	ctccacacgc	ccatgtactt	180
tttctgagc	aacttatcct	ttgtggatct	gtgcttctct	tccaatgtga	ctccaaggat	240
gctggagatt	ttcctttcag	agaagaaaag	catttcctat	cctgcccgtc	ttgtgcagtg	300
ttaccttttt	atcaccttgg	tccacgttga	gctctacatc	ctggctgtga	tggcctttga	360
ccggtcacatg	gccatctgca	accctctgct	ttatggcagc	agaatgtcca	agagcgtgtg	420
ctctttcctc	atcacagtgc	tttatgtgta	tggagcactc	actggcctga	tggagactat	480
gtggacctac	aacctagcct	tctgtggccc	cagtgaatt	aatcacttct	actgtgtgga	540
cccaccactg	attaagctgg	cttgttctga	cacctacaac	aaggagggtg	caatgtttgt	600
tgtggctggg	ttcaacttca	cttatcctct	ccttatcatc	ctcatttctc	atctctacat	660
atttcctgcc	accctaagga	tctgtcttac	agaaggcagg	cacaaagctt	tttctacctg	720
tggtcccat	ctgacagccg	ttactatttt	ctattcagct	cttttcttca	tgtatctcag	780
acgtccatca	gaagagtcca	tggagcaggg	gaaaatggta	gctgtatttt	ataccactgt	840
aatcccatg	ttgaatccca	tgatctacag	cttgagggaac	aaagatgtga	aagaggcatt	900
atgcaaagaa	ctgttcaaaa	gaaaattggt	ttctaaataa	acattactac	tg	952

<210> 329

<211> 949

<212> DNA

<213> Unknown (H38g178 nucleotide)

<220>

<223> Synthetic construct

<400> 329

acagatgtct	gagaattcct	cctcctggga	ctctcagagg	atccagaact	gcagccggtc	60
ctcgctttgc	tgccctgtgc	cctgtccatg	tatctgggtca	cggtgctgag	gaacctgtct	120
agcatcctgg	ctgtcagctc	tgactccccc	ctccacaccc	ccatgtactt	cttctctctc	180
aacctgtgct	ggcctgacat	cggtttcacc	tgggccatgg	ttcccaagat	gattgtggac	240
acgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	tgacacagat	gtctttctctg	300
ctccttgttg	catgtataga	aggcatgtct	ctgactgtga	tggcctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctacccaatc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
gttttgggtg	cctttttcct	tagcctgttg	gattcccagc	tgacacagttg	gattgtgtta	480
caattaacca	tcatacaaga	tgtggaaatc	tctaatttgg	tctgtgaccc	ctctcaactt	540
ctcaaatctg	cctgttctga	cagcgtcacc	aataacatat	tcatatattt	cgatagtact	600
atgtttgggt	ttcttcccat	ttcagggtac	tttttgcctt	actataaaat	tgtcccctcc	660
attctaagga	tttcatcgct	agatgggaag	tataaagcct	tctccacctg	tggtctctcat	720
ctagcagttg	tttgcctgggt	ttatggaaca	ggcattggct	tgtacctgac	ttcagctggg	780

tcaccacetc	ccaggaatgg	tgtgggtggct	tcagtgatgt	acgctgtggg	caccccatgc	840
tgaacctttt	catctgcagc	ctgagaaaca	gggacataca	aagtgccttg	cggaggctgc	900
gcaycagagc	agtcgaatat	catgatctgt	tccatccttt	ttcttgtgt		949

<210> 330

<211> 942

<212> DNA

<213> Unknown (H38g179 nucleotide)

<220>

<223> Synthetic construct

<400> 330

atgcgaggtt	tcaacaaaac	cactgtgggt	acacagttca	tcctgggtgg	tttctccagc	60
ctggggggagc	tccagctgct	gctttttgtc	atctttcttc	tcctatactt	gacaatcctg	120
gtggccaatg	tgaccatcat	ggccgttatt	cgcttcagct	ggactctcca	cactcccatg	180
tatggctttc	tattcatcct	ttcattttct	gagtcctgct	acacttttgt	catcatccct	240
cagctgctgg	tccacctgct	ctcagacacc	aagaccatct	ccttcatggc	ctgtgccacc	300
cagctgttct	ttttccttgg	ctttgcttgc	accaactgcc	tcctcattgc	tgtgatggga	360
tatgatcgct	atgtagcaat	ttgtcaccc	ctgaggtaca	cactcatcat	aaacaaaagg	420
ctgggggttg	agttgatttc	tctctcagga	gccacaggtt	tctttattgc	tttgggtggc	480
accaacctca	tttgtgacat	gcgtttttgt	ggccccaaca	gggttaacca	ctatttctgt	540
gacatggcac	ctgttatcaa	gttagcctgc	actgacaccc	atgtgaaaga	gctggcttta	600
tttagcctca	gcacccctgg	aattatgggt	ccttttctgt	taattctcat	atcctatggc	660
ttcatagtta	acaccatcct	gaagatcccc	tcagctgagg	gcaagaaggc	ctttgtcacc	720
tgtgcctcac	atctcactgt	ggctcttgtc	cactatggct	gtgcctctat	catctatctg	780
cggcccaagt	ccaagtctgc	ctcagacaag	gatcagttgg	tggcagtgac	ctacacagtg	840
gttactccct	tacttaatcc	tcttgtctac	agtctgagga	acaaagaggt	aaaaactgca	900
ttgaaaagag	ttcttgggaat	gcctgtggca	accaagatga	gc		942

<210> 331

<211> 942

<212> DNA

<213> Unknown (H38g180 nucleotide)

<220>

<223> Synthetic construct

<400> 331

atgatgggac	aaaatcaaac	cagcatctca	gacttcctgc	tcctgggcct	gccccatccaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	cacctcctg	120
gggaacctcc	tcacatttgt	cctcattcga	ctggactccc	atctccacac	gcctatgtat	180
ttgtttctca	gcaacttgtc	cttctctgac	ctctgcttct	cttccgtgac	cattcccaag	240
ttgttacaga	acatgcagaa	ccaggaccca	tccatcccc	atgcggactg	cctgacccaa	300
atgtacttct	tcctgttatt	tggagacctg	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tggccatctg	cttccccctg	cactacaccg	ccatcatgag	ccccatgctc	420
tgtctcgccc	tgggtggcgt	gtcctgggtg	ctgaccacct	tcctatgcat	gttacacact	480
ttactcatgg	ccaggttgtg	tttttgtgca	gacaatgtga	tcctccactt	tttctgtgat	540
atgtctgctc	tgtgaagct	ggccttctct	gacactcgag	ttaatgaatg	ggatgatatt	600
atcatgggag	ggctcattct	tgtcatccca	ttcctactca	tccttgggtc	ctatgcaaga	660
attgtctcct	ccatcctcaa	ggctccttct	tctaagggtg	tctgcaaggc	cttctctact	720
tgtggctccc	acctgtctgt	gggtgtcactg	ttctatggaa	ccgttatttg	tctctactta	780
tgtcatcag	ctaatagttc	tactctaaag	gacactgtca	tggctatgat	gtacactgtg	840
gtgaccccca	tgtgaaccc	cttcatctac	agcctgagga	acagagacat	gaaggagacc	900
ctgagcagag	tcattcatca	gaagaaaact	ttcttctctc	tc		942

<210> 332

<211> 822

<212> DNA

<213> Unknown (H38g181 nucleotide)

<220>

<223> Synthetic construct

<400> 332

accataataa	atgtcaatat	tagtcctgag	tttgtccttg	tgggattttc	cagtgatgca	60
gagatccaga	tcatgctctt	tgtgctaate	ctgggtgattc	atctcctgac	tttgacgggg	120
aagctgggga	tgatcctgga	gatcagggct	gattctcacc	ttcaaagacc	catgtacttc	180
ttcctttgac	atctgtcctt	tctggatctc	agctactcct	agttactgtg	cccaggatgc	240
tacaaaattt	cctctcagaa	gaaaagcatc	tcaatgtggg	gctgcctcac	caagtttctt	300
tttcactctc	tctgggggaa	cggaagcctg	tctgttctct	gccatggcct	atgatcacta	360
tgctaccatc	cgccaccctg	tggctctatac	catgggtcatg	aacagatctc	tctgtatggg	420
gattttgaga	attgcttggg	cagcgggatt	tctgatttcc	ttgatggaca	gtcttttcac	480
ccacaagtta	catttctgtg	ggcctgacat	catccttatt	tcagggtgtaa	gctgctcca	540
ttcttccctc	tgtcctacat	tgatcccact	gtcaatgaga	ttcttctagc	tgtgtcacag	600
gcattctggg	ggctactgac	actttcccta	atcttcttct	cttactctag	aatcacatct	660
gtcatactga	gcactctgctc	ctctgagggc	caaggcaaaag	ccttctccgc	atgcccttct	720
catctcgctg	tggttctctc	attctatggg	acagcttttt	tcagataccc	aggctctact	780
tcagggttcg	tggtggggca	agtgggtctct	gttcagtata	gt		822

<210> 333

<211> 935

<212> DNA

<213> Unknown (H38g182 nucleotide)

<220>

<223> Synthetic construct

<400> 333

atgagaagga	acttcacggt	ggtgactgag	ttcattctcc	tgggactgac	gaatcaccag	60
gaattacaga	ttctcctctt	catgctgttt	ctggccattt	acatgggtcac	agtggcaggg	120
aatcttagca	tgattgccct	catccaggcc	aatgcccggc	tccacacgcc	catgtacttt	180
ttcctgagcc	acttatcctt	cctggatctg	tgcttctctt	ccaatgtgac	cccaaagatg	240
ctggagattt	tccttttcaga	gaagaaaagc	atttcctatc	ctgcctgtct	tgttcagtgt	300
tacctttata	tcactcttgg	acacgttgag	atctacatcc	tggctgtgat	ggcctttgac	360
tagtacatgg	ccatctgaaa	ccctctgctt	tatggcagca	aaatgtccaa	aagtgtgtgt	420
tccttcctca	tcacgggtgcc	ttatgtgtat	ggagcgctca	ctggcctgat	ggagaccatg	480
tggacctaca	acctagcctt	ctgtggcccc	aacgaaatta	atcacttcta	ctgtgcagac	540
ccaccactga	ttaagctggc	ttgttctgac	acctacaaca	aggagtgtgc	aatgtttggt	600
gtggctgggt	ggaatctttc	gttttctctc	ttcatcatat	ttatttcccta	cttttacatt	660
tttctgcta	tcttaaggat	tcgctctaca	gagggcaggg	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	tactattttc	tatgcaactc	tgttcttcat	gtgtctcaga	780
ctcccatcag	aagagtccat	ggagcaagga	caaatggtag	ctgtacttta	taccactgtg	840
atcccatagt	taatcccatg	atctacagtc	tgaggaaaca	ggatgtgaaa	aaggctttat	900
ccaaagaact	gttcaaaaaga	aaattgtttc	ctaaa			935

<210> 334

<211> 945

<212> DNA

<213> Unknown (H38g183 nucleotide)

<220>

<223> Synthetic construct

<400> 334

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgctcc	tcctctttgc	ctatctgggc	120
acaattgggg	gcaacctcag	catcctggca	gccgtcttgg	tggagcccaa	actccacgcc	180
cccatgtact	tcttctctgg	gaacctatca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgca	tgttgggtcg	tctcttgtcc	cacaagtcca	caatttcccta	tgacgcctgc	300
ctctcccagc	tcttcttctt	ccaccttctg	gctgggatgg	actgcttctt	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagccctcca	cctacagcac	cgcgatgagt	420

cagacagtcc	agaggatggt	ggtggctgcg	tcctgggctt	gtgccttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgctcca	gcacccaact	caatgagctg	600
ctgctctttg	tagcagcagc	cttcatggct	gtggcaccct	tggctctcat	cagtgtgtcc	660
tatgcccattg	tggtagctgc	tgtgctgcaa	atccgctctg	ctgagggcag	aaagaaggcc	720
ttctccacat	gtggctccca	cctcactgtg	gtgggcatct	tctatgggac	aggtgtcttc	780
agctacatga	ggctgggttc	agtgggaatct	tcagacaagg	ataagggggt	tggggttttc	840
atgactgtga	tcaaccccat	gctgaaccca	cttatctaca	gcctcagaaa	tactgatgtt	900
cagggcgctc	tgtgtcagct	acttgtgggg	gagcgatcac	tgacc		945

<210> 335

<211> 950

<212> DNA

<213> Unknown (H38g184 nucleotide)

<220>

<223> Synthetic construct

<400> 335

atgctaagga	atggcagcat	agtgaaggaa	tttatcctcg	tgggctttca	gcagagctcc	60
acttccacac	gagcattgct	ctttgcccct	ttcttgcccc	tctacagcct	caccatggcc	120
atgaatggcc	tcattcatctt	tatcacctcc	tggacagacc	ccaagctcaa	cagcccatg	180
tactttcttc	tgggcctctg	tctctcctgg	atgtctgctt	catcaccact	accatcccac	240
agatgttgat	ccacctcgtg	gtcagggacc	acattgtctc	ctttgtatgt	tgcattgacc	300
agacgtactt	tgtctctctg	gttgggtgtg	cagagtgcac	cctcttggct	ttcatggcct	360
atgaccgtta	tgttgctatc	tgtaccacac	ttaactatgt	cccgatcata	agccagaagg	420
tctgtgtcag	gcttgtggga	actgcctggt	tctttgggct	gatcaatggc	atctttctcg	480
agtatatattc	attccgagag	cccttccgca	gagacaacca	catagaaagc	ttcttctgtg	540
aggcccccat	agtgattggc	ctctcttgtg	gggaccctca	gtttagtctg	tgggcaatct	600
ttgcccgatgc	catcgtggta	attctcagcc	ccatggtgct	cactgtcact	tcctatgtgc	660
acatcctggc	caccatcctc	agcaaagcct	cctcctcagg	tggggggaag	actttctcta	720
cttgtgcctc	tcacctgact	gtggtcatct	ttctctacac	ttcagctatg	ttctcttaca	780
tgaaccccca	cagcacacat	gggcctgaca	aagacaaacc	ttctccctc	ctgtacacca	840
tcattacccc	catgtgcaac	cccatcattt	atagtttccg	caacaaggaa	attaaggagg	900
ccatggtgag	ggcacttgga	agaaccaggc	tggcccagcc	acagtctgtc		950

<210> 336

<211> 972

<212> DNA

<213> Unknown (H38g185 nucleotide)

<220>

<223> Synthetic construct

<400> 336

atgttttact	tctttccccc	tttgagatc	ttggcagaaa	acctcaccat	ggtcaccgaa	60
ttcctgttgc	tgggtttttc	cagccttggt	gaaattcagc	tggccctctt	tgtagttttt	120
ctttttctgt	atctagtcat	tcttagtggc	aatgtcacca	ttatcagtgt	catccacctg	180
gataaaaagcc	tccacacacc	aatgtacttc	ttccttggca	ttctctcaac	atctgagacc	240
ttctacacct	ttgtcattct	acccaagatg	ctcatcaatc	tactttctgt	ggccaggaca	300
atctccttca	actgttgtgc	tcttcaaagt	ttcttcttcc	ttgggttttgc	cattaccaac	360
tgccctgctat	tgggtgtgat	gggttatgat	cgctatgctg	ccattttgtca	ccctctgcat	420
taccccactc	ttatgagctg	gcaggtgtgt	ggaaaactgg	cagctgcctg	tgcaattgggt	480
ggcttcttgg	cctctcttac	agtagtaa	ttagttttca	gcctcccttt	ttgtagcgcc	540
aacaaaagtca	atcattactt	ctgtgacatc	tcagcagctc	ttcttctggc	ttgtaccaac	600
acagatgtta	acgaatttgt	gatattcatt	tgtggagttc	ttgtacttgt	ggttcccttt	660
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tatggctgtg	cttccttcat	ctacctgagg	cctacagcaa	actatgtgtc	caacaaagac	840
aggctgggtga	cgggtgacata	cacgattgtc	actccattac	taaaccccat	ggttttatagc	900
ctcagaaaca	aggatgtcca	acttgcctatc	agaaaagtgt	tgggcaagaa	aggttctcta	960

aaactatata at

972

<210> 337

<211> 982

<212> DNA

<213> Unknown (H38g186 nucleotide)

<220>

<223> Synthetic construct

<400> 337

aagcttcaat	taaacaattt	tactgaagtc	accatgttta	tattaataag	cttcacagaa	60
gaatttgatg	tgcaagtctt	cctattttta	ttatttttag	caatctatct	attcactcta	120
ataggcaatt	tagggctggt	tgtaccgatc	attggggatt	tctggcttca	cagcccaatg	180
tactattttc	ttgggtgttt	atcattcttg	gatgtctgct	attctacagt	tgctactcca	240
aaaatgttgg	tcaatttcct	ggcaaaaaat	aaatctatct	catttcttgg	atgtgcaaca	300
cagatgtttc	ttgcttgtag	ttttggaacc	acagaatgct	ttctcttggc	tgcaatggct	360
tatgatcgct	atgtagccat	ctacaaccct	ctcctgtatt	cagtgcagcat	gtcaccacga	420
gtctatgtgc	cactcatcac	tgcttcctat	gttgctagca	ttttacatgc	tactatacat	480
acagtggcta	catttagcct	gtccttctgt	ggatccaatg	aaattaggca	tgtcttttgt	540
aataatgcct	cctctgcttg	ctatttcttg	ttctgacact	cacgtaatcc	agcttctatt	600
cttctacttt	gtgggctcta	ttgagatagt	cactatcctg	attgtcctga	tctcctatgg	660
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tacatgtgga	gctcacctaa	ctggagtgc	aatttatcat	gggacaatcc	tcttcatgta	780
tgtgagacca	agttccagct	acacttcgga	caatgacatg	atagtgtcaa	tattttatac	840
cattgtgatt	cccatgctga	atcccatcat	ctacagtttg	cggaacaaag	atgtaaagga	900
ggcaatcaaa	agattgcttg	tgagaaattg	gttcataaat	aagttatagt	tttaaaattg	960
agtaaagttg	caaataatat	tg				982

<210> 338

<211> 962

<212> DNA

<213> Unknown (H38g187 nucleotide)

<220>

<223> Synthetic construct

<400> 338

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgatttggac	tttccaagcc	60
tccttgggag	atgcatcttt	ttcttttttg	gttcttctct	gtgttctaca	tggaattat	120
cctggaaaat	ctcttcattg	tgttcacagt	aattattgac	tctcatTTaa	attccccagg	180
tactgcctac	tggaacaacat	ttatcttctt	gatctgggtc	ttctcttaca	gttctgactt	240
tttactaac	tgagcatca	tttcttttcc	aagatgcac	atacagatat	tttctatttg	300
tgctatgcgt	aaaaattgag	atgggtgctg	tcataaccat	ggcatagagc	aggtacactg	360
ccaatctgta	agcctcccca	ttacctgacc	acaatgaacc	ccaaaatgtg	tgtttccttt	420
gttggaggca	tcctggatag	tcaggataat	ccatgctgta	tctcagtttg	tttttgccat	480
aaacttgcc	ttttgtggcc	ctaataagat	aggtagtttt	cactgtgatt	ttccttatgt	540
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gcttatatcc	atagctacct	gtttcttatt	aataatatcc	tatattttca	tttcggtaac	660
cgtctagaat	ccttcttcag	gagacttate	taaagcattt	gtgtcatggt	agatcacatc	720
acagtaggga	ttttgttttt	tatgccatgt	atatttctgt	atgtgtagcc	tttgccctaaa	780
acaacacatg	attaatat	gttcattggt	ccttttgcta	tcaccctgt	ctaggatcta	840
cacattaaga	aacaaagaca	tgaacgtctc	catggaaaga	ctgggaaaat	ggattgcagg	900
ttctagcagg	atgtcataat	aaatgggtgca	tatccagagt	gcaagatgat	tcagtctcac	960
ca						962

<210> 339

<211> 972

<212> DNA

<213> Unknown (H38g188 nucleotide)

<220>

<223> Synthetic construct

<400> 339

atgaccacca	taattctgga	agtagataat	catcacagtga	caacacgttt	cattctttctg	60
gggtttccaa	cacgaccagc	cttcagctt	ctctttttct	ccattttcct	ggcaacctat	120
ctgctgacac	tgctggagaa	tcttcttata	atcttagcta	tccacagtga	tgggcagctg	180
cataagccca	tgtactttct	cttgagccac	ctctccttcc	tggagatgtg	gtatgtcaca	240
gtcatcagcc	ccaagatgct	tgttgacttc	ctcagtcatg	acaagagtat	ttccttcaat	300
ggctgcatga	ctcaacttta	cttttttgtg	acctttgtct	gcactgagta	catccttctt	360
gctatcatgg	cctttgaccg	ctatgtagcc	atttgtaate	cactacgcta	cccagtcate	420
atgaccaacc	agctctgtgg	cacactggct	ggaggatgct	ggttctgtgg	actcatgact	480
gccatgatta	agatggtttt	tatagcacia	cttcactact	gtggcatgcc	tcagatcaat	540
cactactttt	gtgatatact	tccactcctt	aacgtctcct	gtgaggatgc	ctcacaggct	600
gagatgggtg	acttcttctt	ggcctcatg	gtcattgcta	ttcctcttgg	tggtgtgggtg	660
gcacccatag	ctgctatact	tgccaccatc	ctcaggatcc	cttctgctca	gggccgcaa	720
aaggcattct	ccacctgtgc	ctcccacctg	accgtcgtaa	ttctcttcta	ttccatgaca	780
cttttcacct	atgcccgctc	caaactcatg	tatgcctaca	attccaacaa	agtgggtatct	840
gttctctaca	ctgtcattgt	tccactcctc	aaccccatca	tttactgtct	gaggaaccat	900
gaagtaagg	cagccctcag	aaagaccata	cattgcagag	gaagtgggccc	ccagggaat	960
ggggctttca	gt					972

<210> 340

<211> 969

<212> DNA

<213> Unknown (H38g189 nucleotide)

<220>

<223> Synthetic construct

<400> 340

atgatgggac	aaaatcaaac	cagcatctca	gacttccctgc	tcctgggccc	gcccattccaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	cacctcctg	120
gggaacctcc	tcattattgt	cctcattcga	ctggactccc	atctccacac	gcctgtgtat	180
ttgtttctca	gcaacttgtc	cttctctgac	ctctgctttt	cctcagtcac	aatgcccata	240
ttgctgcaga	acatgcagaa	ccaagaccca	tccatccctt	atgcagactg	cctgacccaa	300
atgtactttt	tcttgtatct	ttcggatcta	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tggccatctg	cttccccatg	cactacaccg	ccatctgctt	cctcctgcac	420
tacaccgcca	tcatgagccc	catgctctgt	ctctccgtgg	tggcgctgtc	ctgggtgctg	480
accaccttcc	atgccatgtt	acacacttta	ctcatggcca	ggttgtgttt	ttgtgcagac	540
aatgtgatcc	cccacttttt	ctgtgatatg	cttgccttgc	tgaagctggc	ctgctctgac	600
actcgagtta	atgaatgggt	gatatttatc	atgggagggc	tcattcttgt	catccattc	660
ctactcatcc	ttgggtccta	tgcaagaatt	gtctcctcca	tcctcaaggc	cccttcttct	720
aagggtatct	gcaaggcctt	ctctacttgt	ggtcccccac	tctctgtggc	gtcactgttc	780
tatgggaccg	ttattgggtc	ctacttatgc	ccatcagcta	atagttctac	tctaaaggac	840
actgtcatgg	ctatgatgta	cactgtgggt	acccctatgc	tgaccgccct	catctacagc	900
ctgaggaaca	gagacatgaa	gggagccctg	gaaaggggtca	tttgtaaaag	gaaaaatccc	960
ttccttcta						969

<210> 341

<211> 933

<212> DNA

<213> Unknown (H38g190 nucleotide)

<220>

<223> Synthetic construct

<400> 341

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gaagaggtcc	agatggccct	ctttatacta	tttctcctga	tatacctaata	tactatgctg	120
ggcaatgtgg	ggatgatatt	gataatccgc	ctggacccct	agcttcacac	tcccatgtat	180

tttttcccta	ctcacttgtc	atattattgac	ctcagttact	caactgtcat	cacacctaaa	240
accttagcga	acttactgac	ttccaactat	atttccttca	tgggctgctt	tgcccagatg	300
ttcttttttg	tcttcttggg	agctgctgaa	tgttttcttc	tctcatcaat	ggcctatgat	360
cgctacgtag	ctatctgcag	tcctctacgt	taccagtta	ttatgtccaa	aaggctgtgt	420
tgcgctcttg	tcactgggcc	ctatgtgatt	agctttatca	actcctttgt	caatgtgggt	480
tggatgagca	gactgcattt	ctgogactca	aatgtagtcc	gtcacttttt	ctgcgacacg	540
tctccaattt	tagctctgtc	ctgcatggac	acatacgaca	ttgaaatcat	gatacacatt	600
ttagctgggt	ccaccctgat	ggtgtccctt	atcacaaat	ctgcatacta	tgtgtccatt	660
ctctctacca	tcctgaaaat	taattccact	tcaggaaagc	agaaagcttt	gtctacttgt	720
gcctctcatc	tcttgggagt	caccatcttt	tatggaacta	tgatttttac	ttatttaaaa	780
ccaagaaagt	cttattcttt	gggaagggat	caagtggctt	ctgtttttta	tactattgtg	840
attcccatgc	tgaatccact	catttatagt	cttagaaaca	aagaagttaa	aaatgctctc	900
attagagtca	tgcagagaag	acaggactcc	agg			933

<210> 342

<211> 915

<212> DNA

<213> Unknown (H38g191 nucleotide)

<220>

<223> Synthetic construct

<400> 342

atggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttcccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcggtgttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcaactc	cccatgtact	tcctgctagc	caacctctca	180
ctcattgata	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcactctctt	caagggctgc	cttgttcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aagccccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
acatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cgtttgccgt	gcacttactc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atgggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaagtac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccc	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 343

<211> 936

<212> DNA

<213> Unknown (H38g192 nucleotide)

<220>

<223> Synthetic construct

<400> 343

atggagcggg	tcaatgagac	tgtggtgaga	gagggtcatct	tcctcgggctt	ctcatccctg	60
gccaggctgc	agcagctgct	ctttgttatc	ttcctgctcc	tctacctgtt	cactctgggc	120
accaatgcaa	tcatactttc	caccattgtc	ctggacaggg	cccttcatat	ccccatgtac	180
ttcttccctg	ccatccctctc	ttgctctgag	atttgctaca	ccttcatcat	tgtacccaag	240
atgctggttg	acctgctgtc	ccagaagaag	accatttctt	tcctgggctg	tgccatccaa	300
atgttttctt	tcctcttctt	tggctgctct	cactcctttc	tgtgtggcag	catgggttat	360
gatcgttaca	tagccatctg	taacccactg	cgctactcag	tgctaagtgg	acatgggggtg	420
tgtatgggac	tagtggtgtc	tgcctgtgcc	tgtggcttca	ctgttgacac	gatcatcaca	480
tccttgggat	ttcacctgcc	tttttatccc	tccaatcaac	tacatcactt	cttctgtgac	540
attgtcctga	tcctcaagct	ggcatctcac	cataaccact	ttagtccagt	tgtcatcttc	600
atgctctgtg	cattgggtcct	ggctatcccc	ttattgttga	tcttgggtgc	ctatgttccac	660
atcctctctg	ccatacttca	gtttccttcc	acactgggta	ggtgcaaagc	tttttctacc	720

tgtgtatctc	acctcattat	tgtcactgtc	cactatggct	gtgcctcctt	tatctactta	780
aggcctcagt	ccaactactc	ctcaagccag	gatgctctaa	tatcagtatc	ctacactatt	840
ataactccat	tgttcaaccc	aatgatttat	agcttgagaa	ataaagaggt	caaattcagt	900
ctttgtaaaa	ttgtgagaag	aacaatttcc	ctgttg			936

<210> 344

<211> 732

<212> DNA

<213> Unknown (H38g193 nucleotide)

<220>

<223> Synthetic construct

<400> 344

atgatgattt	cctcagatga	agaaaatgat	acaaatatga	tggaaatttat	tctggtagga	60
ctgtccagac	agcctgcac	tcagctactc	ttcttttagg	caatattggt	catctactct	120
gtcaccctgg	ttggtaatat	tctcatcatt	gttattatcc	agattgatc	ccatcttcaa	180
acccccatgt	acttctttct	catacaagta	tccttcttag	atatctgctc	cacacccacg	240
gttctggtag	actgctagaa	ggactttcca	agtgtatcct	atagtggctg	cttattctaa	300
atgactatct	ttctttactt	aggggtgacg	gagtggtgtt	tttttttggt	ctgttttgag	360
tgttttctta	ttgctgttat	ggcctatgac	aggtttgttg	ccatctcaaa	acccttggtg	420
taccatttca	ttatcaatag	caatgtttgc	atctggatgg	tggcaggagt	ttgggcccac	480
cctggctgca	ccaatccaat	tctgtggcca	caatgtagtc	aacattttac	atgtgagctc	540
caagtaattt	tcaaactcac	ttgctctcct	gtactagtca	aagagatcca	gtgattcatg	600
attccagggt	gtacattata	ggcattgtat	cagcatgaag	tgtgctccta	cagttaagct	660
cgccagcaaa	cccatcccag	gagctgagag	gcatacaatt	agggcataag	gtgaggtatt	720
atcggggtag	ac					732

<210> 345

<211> 919

<212> DNA

<213> Unknown (H38g194 nucleotide)

<220>

<223> Synthetic construct

<400> 345

acagctggca	gcaatttcac	tgaggtgact	gtcttcatcc	tctctggata	tgcaaatcac	60
cctgaattac	aagtcagttt	tttcttgatg	tttctcttca	tttatctatt	cactattttg	120
ggaaacctgg	gactgatcat	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
ttttctctca	gcaatttagc	attcattgac	atattttact	cctcttccgt	aacacctaa	240
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atgtactttt	ctgttggatt	ggtgtgtact	gagtgtttcc	tgctgggatc	aatggcctat	360
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gataagtggg	tttgttctgt	gattccagca	tcaatctttt	ttttctgtga	caccacagct	540
cttttagcac	tgtcctgtgt	agatgcattc	agcacagaaa	tggtgagctt	tgccctagct	600
ggattcactc	ttcttggctc	tatccttata	atcacagtca	cttatatcgc	catcacctca	660
gccatcctga	agaaccagtg	ggcagcagga	tggcagaagg	ccttctccac	ctgcgcattc	720
cacctcatgg	gttaactata	ttctatgggt	ccctgatttt	cacctatttg	caactggata	780
aaacatcatc	cctgatccac	gcacagttgg	catttgattt	ctatatgact	gtcattccca	840
tgctgaatcc	actcatctag	agtctgagga	acaaagatgt	aaaaaatgct	ctttgagagt	900
catacataga	aaacttttt					919

<210> 346

<211> 753

<212> DNA

<213> Unknown (H38g195 nucleotide)

<220>

<223> Synthetic construct

<400> 346

atggcraatt	cttctctgt	cactgagttc	ttagtgctgg	gcttctctag	ccttggggaa	60
ttgcagcttg	tctcttttg	agtctttctc	tgctcttatt	tgattatctt	gagtggaaac	120
atcatcaca	tctcagtcac	tcatttggat	cacagcctcc	acacacccat	gtacttcttt	180
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tatgctgcc	tctgtcagcc	tttgcaatac	gctgttctca	tgagctggag	agtatgtgga	420
caactgatag	caacttgtat	tattagtggc	ttcctaatat	ctctgggtgg	aacaactttt	480
gtcttttagc	tccttttctg	tggtccaac	aaggccaacc	actacttttg	tgatatttca	540
ccagttatcc	gtctgcctg	tgctgacagc	tacatcagtg	aactgggtcat	cttcatcttc	600
ggggtcttgg	tgcttggtgt	gcccttgata	tttatctgca	tttctatgg	cttcattgtc	660
cgcaccatcc	tgaagatccc	atcagctgaa	ggcaaacaaa	aagccttctc	cacctgtgct	720
tcccatctca	ttgtagtcac	tgtccattat	ggt			753

<210> 347

<211> 941

<212> DNA

<213> Unknown (H38g196 nucleotide)

<220>

<223> Synthetic construct

<400> 347

atgggtgggc	taaaaagaga	caatgcctct	gagatgactg	aactcaccct	tggtggattt	60
gcccaacacc	ctgaaatcca	gactgccttc	ttcttggaac	tactgttttt	ctactagtca	120
cagcgtttga	gaacatcctt	atcgttgctg	tagtgagatg	agattctcga	cttcatactc	180
ctatgggatt	tttttttctt	cagtacctta	tcctcccttg	aaatgtgtta	ctccatcagc	240
tgggagctat	aagtcttggc	tcaatgcac	aaggacttcc	ccaccatctc	ctataacagc	300
tgttctgttc	agatgatcac	acacctcttt	ctggggatga	cagtgtctcc	tccttgctgg	360
catggcttac	aacaggtttg	ttgaaatctc	ttatctcctc	cattacacta	ttattatgag	420
caatcgggtc	tgtatacagt	tggtcttggg	aatctggacc	catgccttct	tagtagcagt	480
cacactaatc	attgcaattc	ctgctagtta	ttatggacac	aatgtcatca	accattttac	540
cttgagatcc	aggccctgct	gaagctcgtc	tgctcagaca	cccttgtcag	cctgattcag	600
ggtctgggta	tcagtgtgtt	cacactgccc	ctgcccttca	cattcatcct	catctcctaa	660
ttttgcattt	ttgttgtgct	gtggaggcta	ggcgtgaagc	tttctccacc	tgtggatctc	720
atctgactgg	agtcaccata	ttttatgggg	cagccatctg	catgtacttg	aaacctcagt	780
caaaggggaa	ccaggaagag	gataaagtgt	tctcaaaact	ttatggagca	gttactccca	840
tgttaaatcc	cccaatttac	attcagagaa	ataaggatat	aaaagggtgca	cttagaaaagt	900
tagccaaagg	aaatgaaaaa	tcctaacagt	tctcttttaa	c		941

<210> 348

<211> 957

<212> DNA

<213> Unknown (H38g197 nucleotide)

<220>

<223> Synthetic construct

<400> 348

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atggggatta	cagacaaccc	tgggctgcag	gtccactgtt	ttggactctt	cctcatcata	120
tatctgggtc	cagtgatagg	caatctgggc	atgggttatct	tgacctactt	ggactccaag	180
ctacacaccc	ccatgtactt	tttcttaga	catttgtcaa	tcactgatct	tggttactcc	240
actgtcattg	ccccgaagat	gttagtaaac	ttcatagtgc	acaaaaacac	aatttcttac	300
aattggtag	ccactcagct	agcattcttt	gagattttca	tcactctctga	gctctttatt	360
ctatcagcaa	tggtctatga	tcgctacgta	gccatctgta	aacctcttct	gtacgtgatc	420
atcatggcag	agaaagtact	ttgggtgctg	gtaattgttc	cctatctcta	tagcacgttt	480
gtgtcactat	ttctcacaat	taagttattt	aaactgtcct	tctgtggctc	aaacataatc	540
agctattttt	actgtgactg	tatccctctg	atgtccatac	tctgttctga	cacaaatgaa	600

ttagaattaa taatTTTTgat cttctcaggc tgtaatttgc tcttctccct ctcaattggt	660
ctcatatcct acatgtttat tctagtggcc attctcagaa tgaactcaag gaaagggagg	720
tacaaagcct tctccacctg tagctctcat ctgacagtgg tgatcatgtt ctatgggaca	780
ttgttattta ttactttgca acccaagtcc agtcatactt tggctattga taaaatggcc	840
tcagtgtttt ataccctgtt gattcctatg ctgaatccgt tgatctacag cctaaggaac	900
aaagaagtaa aagatgtctt aaagagaact ttaaccaatc gattcaaaat tcccatt	957

<210> 349

<211> 471

<212> DNA

<213> Unknown (H38g198 nucleotide)

<220>

<223> Synthetic construct

<400> 349

tttttaaaaa tgagattaaa ggaattaatg taagatagaa ccataatgga ttattggagg	60
gaaggtaggc acatttaggg gatgttcttg gcctttccgt ttggctgacc tatcccaaaa	120
cttttctctt gggctctctat cagagacatg gcagtaacct ggatggacca taggcacgag	180
tcctgtagcc cattctccc gaagctgcag cctttttcat cctgccatgt atctgagtta	240
tgcacgtgcc ttgacacctt cactaaatca tatataactt gaatccgggg actcaagggt	300
ttcaaccatc tttgttttct tctccattac tgtcactgtg ctagagccca agtctcctga	360
aatgcgccct ggagccttgc tcaaagatgt caaccaca tgctgatcag gtagctattt	420
tgctgaagc tggtagttca tgacaggctc tgacatgtgc tgagcttgct c	471

<210> 350

<211> 951

<212> DNA

<213> Unknown (H38g199 nucleotide)

<220>

<223> Synthetic construct

<400> 350

atgggccaaa agaattctaac agtgcttact gaattaattc tgatggaaat cacaaggcgg	60
cttgagctgc agctctccct tttttgggtc ttctcatca tctgcacatt cacagtgggtg	120
agcaaagagt gcataatcat tttgaacaat gtggacttgg gtctacacaa catttgtgta	180
ttttttaaat cagggtacctg aattttatta atcttggtaa ttctatgggtc atttatccca	240
agatactggg aaactttgtt gtggctcaaa atgccattcc ctgttatgca tgtaccatgc	300
agatggcctt cttcattatg ttcatatct gtgaactttt cgtctcatca gccatggcct	360
atgaccacta tgtggacatc catagccttc tgccataaaa tgttatgtct caggaaacttt	420
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aaagattttt atattggcct tctatggctc caatgtcata agttatttct actgttaaga	540
tgtttctttg ttagccatgg tggactcaaa tgcattgagg atagaaatgt tgatcacact	600
attttcagta cttaatttga tattctttct tctggtagtc ctaatgtcct ccatgctgat	660
tctattaact gtttgttgaa tgcattctgc agagagcagt aaaaaacttt cttcacgtat	720
gtttcttgtc tgatagtggg ggttgtgttc tgtgggtttc tatactttat gtacttgcag	780
ctcaaattca gttccttttt ttttgataat aataaaatga cctccatgtt ttctctttta	840
gtgattacca tgctttacca tttggctctg agtgtaaaga acaaaggagg taaaaaaat	900
gccttctata gtttttttat gaagcagtga aaactttgta atttaatggg c	951

<210> 351

<211> 906

<212> DNA

<213> Unknown (H38g200 nucleotide)

<220>

<223> Synthetic construct

<400> 351

atgacgaact tgaatgcac acaggccaac caccgtaact tcattctgac aggtatccca	60
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ggaacgccag acaagaaccc atggttgccc tttcccctgg gatttctcta cacactcaca 120
ctcctgggaa atggtaccat cctagctgtc atcaagggtg agccaagtct ccatgagccc 180
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gcctccatga tccacagatt ttggggagcat ttatcaccag tagtgacat ggtcatggct 840
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906

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<210> 352

<211> 971

<212> DNA

<213> Unknown (H38g201 nucleotide)

<220>

<223> Synthetic construct

<400> 352

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971

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<210> 353

<211> 431

<212> DNA

<213> Unknown (H38g202 nucleotide)

<220>

<223> Synthetic construct

<400> 353

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tgcatttttg tattagagat tcctctagt ggaaaataac agtttattac ttatagttct 240
atattttgtg acagatcgtt ttagaacaag taaaacacat ttgagaatga agtctcagtt 300
tagaatttgt aatattttga tacttctaca agggggacct tgcccttaaa cagaactttg 360
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atcagcattt c
431

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<210> 354
 <211> 938
 <212> DNA
 <213> Unknown (H38g203 nucleotide)

<220>
 <223> Synthetic construct

<400> 354
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 atttataatt tactatttaa cttatcactt aaattgaatc cagatattca aaacactggc 180
 cattctttct actatgatgt ttttgtaatg ttttattcca ccttgactgt gatagtcccg 240
 tttgtaatac caagaggatc agatcatttt ttgttctaga aagataaaaa agttcctgaa 300
 agagtggaaa aatacacttt tgaacccgaa acaaagtctc attttctaag attttggcat 360
 aaaatatacc gtgtaccttt tgctcttaaa acacttcgtt gttataacat tcaattttta 420
 ggtacttatg agtggcaggc tatgggacta gttagttctt gtctagaatc tcctctataa 480
 ccctcaagaa ataatatgta ttttaaaaaa atcttaccat tttttcagtg tacaatatac 540
 aatttcttac attgatccat ttattaactc attagtgttt ttgtggtttt cactgctttt 600
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 ctctctgtct ctttgttcta tagcagtgtc ttcttcatgt atgggtgcc cagggtctggc 780
 ccagattaac agtggaatga aatgtatttt ccgttctaca tgattataat tcctctgcag 840
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 agaaatattt ttggagaaca ctttcataat tctttcca 938

<210> 355
 <211> 759
 <212> DNA
 <213> Unknown (H38g204 nucleotide)

<220>
 <223> Synthetic construct

<400> 355
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 atccaactat tttctttcca tttcctgggc tgtactgagt gcttccttta cacactcatg 180
 gcttatgacc gtttccctgc catttgtaag cccttacact atgctaccat catgaccac 240
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 acctttgcag acattggctt cctggccctc acctgcttca tgctcatcct cacttctat 480
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 tccacttgtg ctgcccacct cactgttgtc attgtttact atgtgccctg caccttcatt 600
 tacctgcggc cttgttcaca ggagcccctg gatggggtgg tagctgtctt ttacactgtc 660
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 ttacagaggc tagggggcca caaggaagtg cagcctcac 759

<210> 356
 <211> 933
 <212> DNA
 <213> Unknown (H38g205 nucleotide)

<220>
 <223> Synthetic construct

<400> 356
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 ggcaacacca tcatcatcgc tctctcctgg ctgacacctc ggctgcacac acctatgtac 180

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ctcttcatct	acctagccct	gggctccaca	gagtgtgtgc	tcctgggtgg	gatggccttt	360
gaccgctatg	ctgctgtctg	tcgtccactc	cactacatgg	ccatcatgca	cccccatctc	420
tgccagaccc	tggctatcgc	ctcctggggg	gcgggtttcg	traactctct	gatccagaca	480
ggtctcgcaa	tggccatgcc	tctctgtggc	catcgactga	ctcacttctt	ctgtgagatg	540
cctgtatttc	tgaagttagc	ttgtgcggac	acagaaagaa	cagaggccaa	gatgtttgtg	600
gcccagagtc	tagtcgtggc	tggtcctgca	gcacttattc	taggctccta	tgtgcacatt	660
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gggtcccacc	tcctagtagt	tttccttttt	tatggctcag	ccatctacac	atatctccaa	780
tccatccaca	attattctga	gcgtgaggga	aaatttggtg	ccctttttta	tactataatt	840
accccatctc	tcaatcctct	catttatata	ctaagaaaca	aggacgtgaa	gggggctctg	900
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<210> 357

<211> 934

<212> DNA

<213> Unknown (H38g206 nucleotide)

<220>

<223> Synthetic construct

<400> 357

atgaagataa	agaatcacac	tccagtaact	gaggtcccc	tgatgggaat	ccctcataca	60
aaggggatgg	aaaatgtgct	ttttgtctta	tttttggcct	tctacctctt	caccttgctg	120
gggaacctac	tcattcttct	ggcgcctctc	actttctcca	acctccacac	ccccatgtat	180
ttcttctctg	gaaacctgtc	tgtgtttgac	atatttttcc	cttcagttag	ttccccaaa	240
atgatgctct	gcttagtggg	acaaagctgc	accatctctt	tccagggttg	tgctcccag	300
ctcttctttc	accatttctt	gggttgccac	gagtgtttcc	tgtacactgt	gatggcctat	360
gaccgatctg	cagccatctg	ccaccctttg	ccatacacgg	tcacatgaa	acgcagggtg	420
tgtgccctcc	tgacgctagg	cacctggacg	gggagctgtc	tgcatgcac	tgtcctcaca	480
ctcctcatct	ttaagttatc	ctactgtggc	cccaatgaag	tggacaattt	ttttctgtga	540
tattccgggtg	gtgctgcccc	tgccctgcgc	agacacctct	ctagcacgga	cagttagttt	600
catcaacgta	ggtgttggtg	cgctcatgtg	ttttcttctt	atcctcacct	cttatgcttg	660
cattgtttatc	tctatactga	aaatcagttc	ctcagaaggt	aggcgagag	ccttctcaac	720
ctgcagtgcc	catctgacgt	ccatcctgct	cttctatgga	ccaatagtcc	tcatttatct	780
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ccttccctcg	aatcctttga	tatatacttt	gagaaacaaa	ggtgtaaagc	tggcactgag	900
aaaggtgctc	attcaaggag	tacataattg	tgga			934

<210> 358

<211> 892

<212> DNA

<213> Unknown (H38g207 nucleotide)

<220>

<223> Synthetic construct

<400> 358

gtgcgtgggt	ccaagcagct	gcggaatggg	accctagtgt	cccagtttct	tctgaaaggc	60
ctgagggaca	gcaaggcttg	gaggcccttg	ctgttcacca	cctttctgct	aatctacata	120
gtggttggtg	tggggagcca	catgttcaca	gtggactacc	gacgccacac	tcccatgtac	180
ttcttcttgg	gcggccactc	gctgatggat	gcgcctgtga	tctccaacat	ggtgactcag	240
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atatgctttc	tccacttctt	ggcaccctag	gagtccttcc	tctcacagc	cgtggcctat	360
gattctatgc	agctatctgc	cagccattgc	actactttgt	cctcgtgggc	cgactgaccc	420
acacgggcct	cacttccatc	tctgcctg	tggccttggc	caacgcattc	acctacagca	480
tcttcacagc	tctacccaag	ttctgcaggc	cttgccctcat	caccacttcc	ttctgcgacc	540
tccgtcactg	ctcagactct	cttgcttcag	cacacgtacc	aatgaacttg	ccctgttctt	600
cagttttctg	gtggctcttg	cacactgcgt	cctggtcgtg	gtctcctatg	gacacgttgc	660
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cccacctcgc	tatgatecgt	cttttctacg	tcacttcagt	cccctgctac	atccttccca	780
actctgcata	ctctggett	ggcgactggg	tgcctctcgt	gctatgtgtg	gtcctcactc	840
acatgctaaa	ccccatcttc	cccagcatgc	tgggatgaca	ggcatgagcc	ac	892

<210> 359

<211> 936

<212> DNA

<213> Unknown (H38g208 nucleotide)

<220>

<223> Synthetic construct

<400> 359

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gcagagcttc	agctgcccct	cttctgcctc	ttcttaggaa	tttacacagt	tactgtggtg	120
ggaaacctca	gcatgatctc	aattattagg	ctgaatcgtc	aacttcatac	ccccatgtac	180
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atgctatcag	ggtttttatg	cagagataga	tccatctcct	attctggatg	catgattcag	300
ctgttttttt	tctgtgtttg	tggtattttct	gaatgctaca	tgctggcagc	catggcctgc	360
gacgcgtacg	tggccatctg	cagcccactg	ctctacaggg	tcacatgtgc	ccctagggtc	420
tggtctctgc	tgggtggctgc	tgtcttctca	gtagggtttca	ctgatgctgt	gatccatgga	480
ggttgtatac	tcaggttgtc	tttctgtgga	tcaaacatca	ttaaacatta	tttctgtgac	540
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tgtagctccc	acctgacagc	tggtcttatg	ttttatgggt	ctctgatgtc	catgtatctc	780
aaacctgctt	ctagcagttc	actcaccag	gagaaagtat	cctcagtatt	ttataccact	840
gtgattctca	tggtgaatcc	cttgatatat	agctcgagga	acaatgaagt	aagaaatgct	900
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<210> 360

<211> 753

<212> DNA

<213> Unknown (H38g209 nucleotide)

<220>

<223> Synthetic construct

<400> 360

atgtactatt	tcctcagcca	cctggccttt	ggtgaccttt	gttactcctc	tgctattaca	60
ccgaagatga	tggtgaattt	tggtgtggaa	cgcaacacca	ttcctttcca	tgcttgtgca	120
acccaactgg	gttgttttct	caccttcagt	atcactgagt	gtttccttct	agcctccatg	180
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cacaccgtta	tcactttccg	tctgacttac	tgtggcccaa	acttaattaa	ccatttctat	360
tgtgatgacc	tccccttctt	agctctgtcc	tgctcagaca	cacacatgaa	ggaaattctg	420
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atctttatta	ttgccgctat	cctaaggatc	cgctctactc	aggggcaaca	caaagccatt	540
tccacctgtg	gtcccatat	ggtgactgtc	actattttct	atggcacact	gatctttatg	600
tacctacagc	ccaaatcaaa	tcactccttg	gacacagaca	agatggcttc	tgtattttac	660
acagtgggtga	tcccatgtt	aaacccccta	atctatagtc	taaggaacaa	agaagtgaag	720
gatgcctcaa	agaaagcctt	ggataaaggt	tgt			753

<210> 361

<211> 933

<212> DNA

<213> Unknown (H38g210 nucleotide)

<220>

<223> Synthetic construct

<400> 361

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ctcctcatcc	tgctgggtgat	caggggtggat	tctcacctcc	acacccccat	gtactacitc	180
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tattttttcc	acttcctggg	gagcaccgag	tgtttccctc	acacagtcac	gtcctatgat	360
cgctacctgg	ccatcagtta	cccgtcagg	tacaccaaca	tgatgactgg	gcgctcgtgt	420
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ccgcccattc	tgaaactggc	ctgtgcagac	acctcagcca	acgagatggg	catctttgtg	600
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<210> 362

<211> 827

<212> DNA

<213> Unknown (H38g211 nucleotide)

<220>

<223> Synthetic construct

<400> 362

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gcttctctct	gagcgtattc	tccttcctag	acatctgcag	ttcctccatg	tgacccccag	180
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gtgtgcccag	ctggtgggtg	ttacctctgc	tgtgggggtg	ctcatttcag	ctctagacag	420
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ttccacccaa	ccctgaaatg	gcctcagcct	ataacaaaat	cctcttcacc	gttgtgatcc	780
ccatgctgaa	cctcctggtc	taaggcctga	gaaataaaga	tgtcaaa		827

<210> 363

<211> 937

<212> DNA

<213> Unknown (H38g212 nucleotide)

<220>

<223> Synthetic construct

<400> 363

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aatgcagagc	ttcaagtcac	tctctttggg	atattccttg	tagtatactt	agctagcttt	120
atgggtaatt	tcgggtttgat	tatgctaatt	caaatacagc	ctcagcttca	tacacccatg	180
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caggtatgct	gcttcatacc	atttgtagtt	tgtgaattat	atttgtcttc	aatcatggca	360
tatgatcggt	atggtgccat	ctgtaaccct	ttactttatg	tcattctcat	tcctagaaaa	420
ctgtattaaa	ctgattgcta	gcacgtatgt	gtatggattc	actgtgggac	ttgtacagac	480
agtggcgaca	tcctacttgt	ctttttgtga	ttccaacgtg	atcaaccact	tctaccatga	540
tgatgttcca	ttagtggctc	tggcctgttc	tgacactcat	gtcaaagagc	tgatgttgtt	600

aatcattgct	gggttcaata	ctctctgctc	tctagtaatt	gtgctgattt	cttatggttt	660
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gcagcccaag	tcaagccatt	ccctgaatat	ggataaagtt	gcttctgtgt	ttaatgtggt	840
agtgatccct	acattaaacc	cactgatcta	tagtttaaga	aatcaggagg	taaaaaatgc	900
actaaagaga	attatagaaa	agttatgttt	ggctgtc			937

<210> 364

<211> 697

<212> DNA

<213> Unknown (H38g213 nucleotide)

<220>

<223> Synthetic construct

<400> 364

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tgctcaccct	tcgagatata	ctactattct	gactcccaaa	accattgtca	aaattgctgt	180
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ggtgatgaca	gacgtgatcc	tcattgctgt	ctcctacacc	ctcatcctct	gtgctgtctt	420
ttgcctcccc	tcccaagatg	ccggtcagaa	ggccctttgc	tcctgtgggt	cccatgtctg	480
tggtatccct	atattctata	taccagcatt	cttctccatt	cttgcccatt	gctttgggca	540
taatgtccct	cataccttcc	atattatgtt	tgccaacctt	tatgtaatca	ttccacctgc	600
tctcaactct	attgtctaca	gaataaagac	caagcaaate	cagaacagaa	tccttttgct	660
ctttcccaag	gggtcccgat	gataggtgcc	tgagctc			697

<210> 365

<211> 930

<212> DNA

<213> Unknown (H38g214 nucleotide)

<220>

<223> Synthetic construct

<400> 365

atgtccaacg	ccagcctact	gacagcgttc	atcctcatgg	gccttcccca	tgccccagcg	60
ctggacgccc	ccctcttttg	agtcttctct	gtggtttacg	tgctcactgt	gctggggaac	120
ctcctcatcc	tgctggtgat	cagggtggat	tctcacctcc	acaccacat	gtactacttc	180
ctcaccaacc	tgctgttcat	tgacatgtgg	ttctccactg	tcacgggtgcc	caaattgctg	240
atgacttttg	tggtcccaag	tggcagggtc	atctccttcc	acagctgcat	ggctcagctc	300
tatttctttc	acttccctag	gggcaccgag	tgtttccctc	acagggtcat	gtcctgtgat	360
cgctacctgg	ccatcagtta	cccgtcagg	tacaccagca	tgatgactgg	gcgctcgtgt	420
actcttctgg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccaggccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aactggatcc	agcactattt	gtgtgatgca	540
ccgccccatc	tgaaactggc	ctgtgcagac	acctcagcca	tagagactgt	catttttgtg	600
actgttgga	tagtggtctc	gggtgtcttt	gtcctgatag	tgctgtccta	tgtgtccatc	660
gtctgttcca	tcctgcggat	ccgcacctca	gaggggaagc	acagagcctt	tcagacctgt	720
gcctcccact	gtatcgtggt	cctttgtctc	tttggccctg	gtcttttcat	ttacctgagg	780
ccagggtcca	ggaaagctgt	ggatggagtt	gtggccgttt	tctacactgt	gctgacgccc	840
cttctcaacc	ctgttgtgta	caccctgagg	aacaaggagg	tgaagaaagc	tctgttgaag	900
ctgaaagaca	aagtagcaca	ttctcagagc				930

<210> 366

<211> 933

<212> DNA

<213> Unknown (H38g215 nucleotide)

<220>

<223> Synthetic construct

<400> 366

atgagaagaa	actgcacggt	ggtgactgag	ttcattctcc	tgggactgac	cagtcgccgg	60
gaattacaaa	ttctcctctt	cacgctgttt	ctggccattt	acatggtcac	ggtggcaggg	120
aaccttgga	tgattgtcct	catccaggcc	aacgcctggc	tccacatgcc	catgtacttt	180
ttcctgagcc	acttatcctt	cgtggatctg	tgcttctctt	ccaatgtgac	tccaaagatg	240
ctggagattt	tcctttcaga	gaagaaaagc	atttctctatc	ctgcctgtct	tgtgcagtgt	300
taccttttta	tcgccttggg	ccatgttgag	atctacatcc	tggctgtgat	ggcctttgac	360
cggtagatgg	ccatctgcaa	ccctctgctt	tatggcagca	gaatgtccaa	gagtgtgtgc	420
tccttcctca	tcacggtgcc	ttatgtgtat	ggagcgctca	ctggcctgat	ggagaccatg	480
tggacctaca	acctagcctt	ctgtggcccc	aatgaaatta	atcacttcta	ctgtgcggac	540
ccaccactga	ttaagctggc	ttgttctgac	acctacaaca	aggagtgtgc	aatgtttatt	600
gtggctgggt	ggaacctttc	tttttctctc	ttcatcatat	gtatttccaa	cctttacatt	660
ttccctgcta	ttttaagat	tcgctctaca	gagggcaggc	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	cactatatct	tatgcaacct	ttttcttcat	gtatctcaga	780
ccccctcaa	aggaatctgt	tgaacagggt	aaaatggtag	ctgtatttta	taccacagta	840
atccctatgc	tgaaccttat	aatttatagc	cttagaaata	aaaatgtaaa	agaagcatta	900
atcaaagagc	tgtcaatgaa	gatatacttt	tct			933

<210> 367

<211> 945

<212> DNA

<213> Unknown (H38g216 nucleotide)

<220>

<223> Synthetic construct

<400> 367

atgctgctat	ccaacattac	tcagtttagc	cccatattct	atctcaccag	ctttcctgga	60
ttggaaggca	tcaaactctg	gatttttcac	ccctttttct	ttatgtacat	ggttgccatc	120
tcaggcaatt	gtttcattct	gatcattatt	aagaccaacc	ctcgtctgca	cacacccatg	180
tactatctac	tatccttget	ggccctcact	gacctggggc	tgtgtgtgtc	cacgttgccc	240
accactatgg	ggatcttctg	gtttaactcc	cagagtatct	actttggagc	gtgtcaaate	300
cagatgttct	gcateccact	tttttctctc	atggagtctt	cagtgtctct	catgatgtcc	360
tttgaccgct	ttgtggccat	ctgccaccct	ctgaggtatt	cggtcattat	cactggccag	420
caagtgggtca	gagcaggcct	aattgtcatc	ttccggggac	ctgtggccac	tatccctatt	480
gtcctcctcc	tgaaggcttt	tcctactgtt	ggatctgttg	tcctctccca	ctcattttgc	540
ctgcaccagg	aagtgtatca	gctggcctgc	acagatacca	ccttcaataa	tctgtatgga	600
ctgatgggtg	tagttttcac	tgtgatgctg	gacctgggtc	tcacgcgact	gtcctatgga	660
ctcactctgc	acacagtagc	aggcctggcc	tcccaagagg	agcagcgccg	tgcctttcag	720
acatgcaccg	ctcatctctg	tgtgtgtgta	gtattctttg	tgcccatgat	ggggctgtcc	780
ctgggtgcacc	gttttgggaa	gcatgcccc	ctgctatttc	atcttcttat	ggccaatgtc	840
tacctttttg	tgctcccat	gcttaaccca	atcatataca	gcattaagac	caaggagatc	900
caccgtgcca	ttatcaaaact	cctaggtctt	aaaaaggcca	gtaaa		945

<210> 368

<211> 969

<212> DNA

<213> Unknown (H38g217 nucleotide)

<220>

<223> Synthetic construct

<400> 368

atgaaccctg	aaaactggac	tcaggtaaca	agctttgtcc	ttctgggttt	ccccagtagc	60
cacctcatat	agttcctggg	gttcctgggg	ttaatgggtg	cctacattgt	aacagccaca	120
ggcaagctgc	taattattgt	gctcagctgg	atagaccaac	gcctgcacat	acagatgtac	180
ttcttctctg	ggaatttctc	cttcctggag	ctgttctgtg	taactgttgt	ggttcccaag	240
atgcttgtcg	tcactctcac	gggggatcac	accatctcat	ttgtcagctg	catcatccag	300
tcctacctct	actttctttt	aggcaccact	gactttcttc	tcttggccgt	catgtctctg	360

gatcgttacc	tggcaatctg	ccgaccactc	cgctatgaga	ccctgatgaa	tggccatgtc	420
tgttcccaac	tagtgctggc	ctcctggcta	gctggattcc	tctgggtcct	ttgccccact	480
gtcctcatgg	ccagcctgcc	tttctgtggc	cccaatggta	ttgaccactt	ctttcgtgac	540
agttggccct	tgctcaggct	ttcttgtggg	gacaccacc	tgctgaaact	ggtggcttcc	600
atgctctcta	cgttgggtgt	actgggctca	ctggctctga	cctcagtttc	ctatgcctgc	660
attcttgcca	ctgttctcag	ggccccaca	gctgctgagc	gaaggaaaagc	gttttccact	720
tgcgcctcgc	atcttacagt	ggtggtcac	atctatggca	gttccatctt	tctctacatt	780
cgtatgtcag	aggctcagtc	caaactgctc	aacaaagggtg	cctccgtcct	gagctgcac	840
atcacacccc	tcttgaaccc	attcatcttc	actctccgca	atgacaagg	gcagcaagca	900
ctgagagaag	ccttgggggtg	gccagggtc	actgctgtga	tgaaactgag	ggtcacaagt	960
caaaggaaa						969

<210> 369

<211> 1016

<212> DNA

<213> Unknown (H38g218 nucleotide)

<220>

<223> Synthetic construct

<400> 369

atgatgggag	aagcaaggaa	caggacagta	gtccaggaat	ttatcctgga	gggatttccct	60
gctgtccagc	atctggggaa	tgctcttttc	ctgggtgcacc	tgctggcata	cctggcctcc	120
atcatggcaa	acatgctcat	aatcaccatc	acctgggctg	accatcacct	ccagacacct	180
atgtatttct	tcctcaacag	tttttccttc	tgtgaatgct	gttttatcac	cacagttatt	240
cctaaacttc	tggtcatctt	tctttcaggc	aggcaaataa	tcccctttac	tacttgtctc	300
atgcagtcct	tttcattttt	atttcttggg	tcaacagttt	tcttctttat	ggctgtgatg	360
tccttggatt	gatacctggc	catttgcaag	cctctgcatt	actccacct	catgagcctg	420
aggactagct	tcacactggg	cactgtctgc	tttgtcgtgg	gcttactctt	catcactggg	480
ctcatgggtga	aggtttccca	gttatctttc	tgtggacccc	atgtcatccc	tcacttcttc	540
cgtgacctcg	gccctctgat	ccaactctcc	tgttctgaca	ccagatctac	tgaaacggtg	600
gcctttgtcc	ttgtttcatt	cgttcttttt	acatccctca	ttataaccat	cattgcatat	660
ggcaacatag	tagtcacaa	tgtacgactc	ccatcagcca	aggagcggca	gaaagctttc	720
tcacactgct	cctctcacct	cattgtcttc	tctctgggtg	atggcagctg	tgtcttcata	780
tatgtgaagc	cgaagcaaat	ggacaggctg	gactccaaca	gaatggctgc	tcttgtgaac	840
acagtgggtga	ccccactgct	gaaccgatac	atttacactc	tgcggaacaa	gcagggtccac	900
caggctctga	gggatgctca	gtccagaatg	aaattgtaaa	aacagaatca	caacctccca	960
gtgaaggaat	gcaccttctc	cttgatctaa	tccaatcttt	ctcctgtttc	tggaaat	1016

<210> 370

<211> 927

<212> DNA

<213> Unknown (H38g219 nucleotide)

<220>

<223> Synthetic construct

<400> 370

atggccagta	caagtaatgt	gactgagttg	attttctactg	gcctttttcca	ggatccagct	60
gtgcagagtg	tatgctttgt	ggtgtttctc	cccgtgtacc	ttgccacggt	ggtgggcaat	120
ggcctcatcg	ttctgacggg	cagtatcagc	aagagtctgg	attctcccat	gtactttctc	180
cttagctgcc	tgctcttggg	ggagatcagt	tattctctca	ctatcgcccc	taaattcatc	240
atagacttac	ttgccaagat	taaaaccatc	tctctggaag	gctgtctgac	tcagatatcc	300
ttcttccact	tctttggggg	tgctgagatc	cttttgattg	tggtgatggc	ctatgattgc	360
tacgtggcca	tttgcaagcc	tcttcattat	atgaacatta	tcagtcgtca	actgtgtcac	420
cttctgggtg	ctgttctctg	gctggggggc	ttttgtcact	ccataattca	gattctcgtt	480
atcatccaat	tgcccttctg	tggtcccaat	gtgattgacc	actatttctg	tgacctccag	540
cctttattca	agcttgccctg	cactgacacc	ttcatggagg	gggttattgt	gttggccaac	600
agtggtattat	tctctgtctt	ctccttcttc	atcttgggtg	cctcttatat	tgtcattctg	660
gtcaacttga	ggaaccattc	tgcagagggg	aggcacaag	ccctctccac	ctgtgcttct	720
cacatcacag	tggtcatctt	gttttttggg	cctgctatct	tcctctacat	gcgaccttct	780

tccactttca	ctgaagataa	acttgtggct	gtattctaca	cggtcatcac	ccccatgctg	840
aaccccatca	tttacacact	caggaatgca	gagggtgaaa	tcgccataag	aagattgtgg	900
gcaaaaagg	agaatccagg	gagggag				927

<210> 371

<211> 965

<212> DNA

<213> Unknown (H38g220 nucleotide)

<220>

<223> Synthetic construct

<400> 371

atggcaaaag	gcaatcattc	atcagtgact	gagttcatcc	tcctaggggct	cacagataat	60
caggaacttc	aagtcattct	ctttgggtga	ttcctactga	tttacttagt	tactgtgttg	120
ggtaatcttg	gtttgattgt	gctaattccat	atcagtcctc	agcttcacac	acctatgtat	180
tttttctca	gccatctggc	ttttgtggat	ttttacggta	cctctgctat	cactccaaac	240
acccttgta	actctttgca	tgaaattaaa	agcatgtcat	tttatgcatg	tgccactcaa	300
gtgtgctgct	tcattacact	ttcagtcctg	gaattattgt	tgctctcatg	gcatatgatc	360
ggtatgttgc	catctgcaac	cctttactct	atgtagttct	catgcctagg	agactctgca	420
ttcaaattgg	cactggctta	tatatattat	gtttcaccat	gggactcata	caagcagtgg	480
ccacattcca	catgtcgttt	tgtgactcta	atgtggtcaa	ccagttctac	tgtgatgatg	540
ttcctctgat	tgctctggct	tgttctgata	cacaagtcaa	ggaattgatg	ttgttcatca	600
ttgctgcgtt	caatgttttt	tgttctctta	tcattgttct	catctcctat	gtattcatcg	660
tctttgctat	ctaaggatcc	actctgccgt	aggaagacag	aaagcctttt	ctacctgtgc	720
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taagtcaagc	cactcactag	ataaagacaa	atttgccctca	gtattctatg	cagtggtgat	840
tcccatgcta	aaccatttga	tctatagctt	gaggaatcaa	gaggtaaaaa	aatgctatga	900
aaaaaattat	tgaaaaaatg	tgttcttagta	atcaacagta	aaatttggtg	gtactaaaaag	960
aaata						965

<210> 372

<211> 951

<212> DNA

<213> Unknown (H38g221 nucleotide)

<220>

<223> Synthetic construct

<400> 372

atgtcccagg	tgactaacac	cacacaagaa	ggcatctact	tcatectcac	ggacatccct	60
ggatttgagg	cctcccacat	ctggatctcc	atccccgtct	gctgtctcta	caccatctcc	120
atcatgggca	ataccaccat	cctcactgtc	attcgacacg	agccatctgt	ccaccagcgc	180
atgtatctgt	ttctctccat	gctggccctg	acggacctgg	gtctcaccct	caccacccta	240
cccacagtca	tgcagcttct	ctggttcaac	gttcgtagaa	tcagctctga	ggcctgtttt	300
gctcagtttt	tcttcttcca	tggattctcc	tttatggagt	cttctgtcct	cctggctatg	360
tccgttgact	gctatgtggc	catctgctgt	cccctccatt	atgcctccat	cctcaccaat	420
gaagtcattg	gtagaactgg	gttagccatc	atttgctgct	gtgttctggc	ggttcttccc	480
tcccttttct	tactcaagcg	actgcctttc	tgccactccc	accttctctc	tcgctcctat	540
tgccctccacc	aggatatgat	ccgcctggtc	tgtgctgaca	tcaggctcaa	cagctggtat	600
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acacttatct	tgaaaaatat	cttgggcaca	gccacctggg	ctgagcgact	ccgtgccctc	720
aataactgcc	tgtcccacat	tctagctgtc	ctggctcctc	acattcccat	ggttggtgta	780
tctatgactc	atcgctttgc	caagcatgcc	tctccactgg	tccatgttat	catggccaat	840
atctacctgc	tggcaccctc	ggtgatgaac	cccacatttt	acagtgtaaa	gaacaagcag	900
atccaatggg	gaatgttaaa	tttcctttcc	ctcaaaaata	tgcattcaag	a	951

<210> 373

<211> 945

<212> DNA

<213> Unknown (H38g222 nucleotide)

<220>

<223> Synthetic construct

<400> 373

atgaatccag	caaatcattc	ccagggtggca	ggattttgttc	tactgggggct	ctctcagggtt	60
tgggagcttc	ggtttgtttt	cttcactgtt	ttctctgctg	tgtattttat	gactgtagtg	120
ggaaaccttc	ttattgtggt	catagtgacc	tccgaccac	acctgcacac	aacctatgtat	180
tttctcttgg	gcaatctttc	tttcctggac	ttttgtact	cttccatcac	agcacctagg	240
atgctggttg	acttgccttc	aggcaaccct	accatttcct	ttggtggatg	cctgactcaa	300
ctcttcttct	tccacttcat	tggaggcatc	aagatcttcc	tgctgactgt	catggcgtat	360
gaccgctaca	ttgccatttc	ccagcccctg	cactacacgc	tcattatgaa	tcagactgtc	420
tgtgcactcc	ttatggcagc	ctcctgggtg	gggggcttca	tccactccat	agtacagatt	480
gcattgacta	tccagctgcc	attctgtggg	cctgacaagc	tggacaactt	ttattgtgat	540
gtgcctcagc	tgatcaaatt	ggcctgcaca	gatacctttg	tcttagagct	tttaatggtg	600
tctaacaatg	gcctggtgac	cctgatgtgt	tttctgggtg	ttctgggatc	gtacacagca	660
ctgctagtca	tgctccgaag	ccactcacgg	gagggccgca	gcaaggccct	gtctacctgt	720
gcctctcaca	ttgctgtggt	gaccttaate	tttgtgcctt	gcactctacgt	ctatacaagg	780
ccttttcgga	cattccccat	ggacaaggcc	gtctctgtgc	tatacacaat	tgtcaccccc	840
atgctgaatc	ctgccatcta	taccctgaga	aacaaggaag	tgatcatggc	catgaagaag	900
ctgtggagga	ggaaaaagga	ccctattggt	cccctggagc	acaga		945

<210> 374

<211> 960

<212> DNA

<213> Unknown (H38g223 nucleotide)

<220>

<223> Synthetic construct

<400> 374

atgtcatttc	taaatggcac	cagcctaact	ccagcttcat	tcatacctaaa	tggcatccct	60
ggtttggaag	atgtgcattt	gtggatctcc	ttcccactgt	gtaccatgta	cagcattgct	120
attacagggg	acttcggcct	tatgtacctc	atctactgtg	atgaggcctt	acacagacct	180
atgtatgtct	tccttgcctt	tctttccttc	acagatgtgc	tcattgtgcac	cagcaccctt	240
cccaacactc	tcttcatatt	gtggtttaat	ctcaaggaga	ttgattttaa	agcctgcctc	300
gcccagatgt	tctttgtgca	caccttcaca	gggatggagt	ctgggggtgt	catgtctcatg	360
gccttggacc	actgtgtggc	catctgcttc	cctctgcgtt	atgccaccat	cctcactaat	420
tcagtcattg	ctaaagctgg	gttcctcact	tttcttaggg	gtgtgatgct	tgttatccct	480
tccactttcc	tcaccaagcg	ccttcataac	tgcaagggca	acgtcatacc	ccacacctac	540
tgtgaccaca	tgtctgtggc	caagatatct	tgtggtaatg	tcagggttaa	cgccatctat	600
ggtttgatag	ttgccctgct	gattgggggc	tttgatatcc	tgtgcattac	aatctcctac	660
actatgattc	ttcaagcagt	tgtgagtcta	tcatacagcag	atgctcgaca	gaaggccttc	720
agcacctgca	ctgcccactt	ctgtgccata	gtcctcacct	atgttccagc	cttctttacc	780
ttctttacac	accatttttg	gggacacacc	attcctctac	acatacatat	tattatggct	840
aatctctacc	tactaatgcc	tcccacaatg	aacctatttg	tgtatggggg	gaaaaccagg	900
cagggtacgag	aaagtgtcat	taggttcttt	cttaagggaa	aggacaattc	tcataacttt	960

<210> 375

<211> 915

<212> DNA

<213> Unknown (H38g224 nucleotide)

<220>

<223> Synthetic construct

<400> 375

atgggttgcta	caaacaatgt	gactgaaata	attttcgtgg	gattttccca	gaattggagt	60
gagcagaggg	tcattttctgt	gatgtttctc	ctcatgtaca	cagctgttgt	gctggggcaat	120
ggcctcattg	tggtgaccat	cctggccagc	aaagtgtcta	cctcccccat	gtattttctt	180
ctcagctact	tatcctttgt	ggagatctgc	tactgttctg	tcattggcccc	caagcttate	240

tttgactcct	ttatcaagag	gaaagtcatt	tctctcaagg	gctgcctcac	acagatgttt	300
tccctccatt	tctttggtgg	cactgaggcc	tttctcctga	tggatgatggc	ctatgaccgc	360
tatgtggcca	tctgcaagcc	cttgcaactac	atggccatca	tgaaccagcg	aatgtgtggt	420
ctcctcgtga	ggatagcatg	gggcgggggc	ctgctgcatt	ctgttgggca	aaccttctctg	480
attttccagc	tcccgttctg	tggccccaac	atcatggacc	actacttctg	tgatgtccac	540
ccagtgtctg	agctggcctg	cgcagacacc	ttcttcatta	gcctgctgat	catcaccaat	600
ggcggctcca	tctccgtant	cagttttctt	gtgctgatgg	cttctctacct	gatcatcctg	660
cacttctctga	gaagccacaa	cttggagggg	cagcacaagg	ccctctccac	ctgtgcctct	720
catgtcacag	ttgtcgacct	gttcttcata	ccttgctcct	tggctctatat	taggccctgt	780
gtcacccctcc	ctgcagacaa	gatagttgct	gtattttata	cagtgggtcac	acctctctta	840
aacctgtgta	tttactcctt	caggaatgct	gaagtgaaaa	atgccatgag	gagattttatt	900
gggggaaaag	taatt					915

<210> 376

<211> 939

<212> DNA

<213> Unknown (H38g225 nucleotide)

<220>

<223> Synthetic construct

<400> 376

atggctcctg	aaaatttcac	cagggtcact	gagttttattc	ttacaggtgt	ctctagctgt	60
ccagagctcc	agattcccct	cttcttggtc	tttctgggtc	tctatgggct	gaccatggca	120
gggaacctgg	gcatcatcac	cctcaccagt	gttgactctc	gacttcaaac	ccccatgtac	180
tttttctctg	aacatctggc	tctcattaat	cttggttaact	ctactgtcat	tgccccataa	240
atgctgatta	acttttttagt	aaagaagaaa	actacctcat	tctatgaatg	tgccacccaa	300
ctgggagggg	tcttggttctt	tattgtatcg	gaggtaatca	tgctggcttt	gatggcctgt	360
gaccgctatg	tggctatttg	taaccctctg	ctgtacatgg	tgggtgggtg	tcggcggctc	420
tgctctctgc	tgggtctccct	cacatacctc	tatggctttt	ctacagctat	tgtggtttca	480
tcttatgtat	tctctgtgtc	ttattgctct	tctaataata	tcaatcattt	ttactgtgat	540
aatgttccct	tgtaggcatt	atcttgctct	gatacttact	taccagaaac	agttgtcttt	600
atatctgcag	caacaaatgt	ggttggttcc	ttgattatag	ttctagtatc	ttatttcaat	660
attgttttgt	ctatttttaa	aatatgttca	tcagaaggaa	ggaaaaaagc	cttttctacc	720
tgtgcttcac	atatgatggc	agtcacaatt	ttttatggga	cattgctatt	catgtatgtg	780
cagccccgaa	gtaaccatct	actggatact	gatgataaga	tggcttctgt	gttttacacg	840
ttggtaattc	ctatgctgaa	tcccttgatc	tacagcctga	ggaataagga	tgtgaagact	900
gctctacaga	gattcatgac	aaatctgtgc	tattccttt			939

<210> 377

<211> 979

<212> DNA

<213> Unknown (H38g226 nucleotide)

<220>

<223> Synthetic construct

<400> 377

atgaaaattt	ctaataactc	tttgggggtt	ttacctacga	cattcatttt	ggttggcatc	60
ccagggtcgg	agtcagagca	cctctggata	tccgtcccct	tctctctgat	atacatcatc	120
attttccttg	ggaatggcat	cattcttcac	gtcatcagaa	cagatattgc	cctacatcaa	180
cccatgtacc	tcttctctgc	catgttggca	ctggccgagg	ttcgtgtctc	tgcatccacc	240
ctgcctacag	tgtaggcat	attccttttt	ggaaatactg	aaattagtct	tgaagcttat	300
ctttttccag	atgttctcca	tccattcttt	atccatgatg	gagtcagctg	tgctgctggc	360
catgtctttg	gaccgcttta	tagccatcta	cagcccactg	agctatacac	ctatcctgac	420
actgcccagg	gtctttggca	caggagctat	tatcgtactg	aaaagcatta	tgctcatggc	480
tccgttgccc	attctcttat	ggcgtctgcc	cttctgtggc	cacaatgccc	tctcacatc	540
ctattgtctg	caccccaatc	ttatctatct	atcttgtggg	aacatttctg	ttacaatat	600
ctatgggatt	ttcattgtta	cctctacttt	tgggctggat	tcgttgctga	ttgtgatctc	660
ctatgggctc	atactccaca	ccgtgttggg	tattgccact	ggagaagggc	ggaagaaggc	720
actcaacacg	tgtggctcac	acgtctgtgc	tgtgcttgct	tactatgtgc	ctatgattgg	780

cttgtctata	gtgcaccgcc	ttggacatcg	tgtgtcccct	ctgctgcaag	ccatgatggc	840
caatgcctac	ctcttcttcc	cacctgttgt	caatcctatt	gtctacagca	ttaagaccaa	900
ggagatcca	ggtgccattg	tccgaatgct	attagagaaa	agacgcagag	tgtagccaaa	960
aaccatagta	ggaagaaat					979

<210> 378

<211> 933

<212> DNA

<213> Unknown (H38g227 nucleotide)

<220>

<223> Synthetic construct

<400> 378

atgtccaaga	ccagcctcgt	gacagcgttc	atcctcacgg	gccttcccca	tgccccaggg	60
ctggagcccc	cactcttttg	aatcttcctg	gtgggtttacg	tgctcactgt	gctgggggaa	120
ctcctcatcc	tgctgggtgat	cagggtggat	tctcacctcc	acacccccat	gtactacttc	180
ctcaccaacc	tgctcttcat	tgacatgtgg	ttctccactg	tcacgggtgcc	caaaatgctg	240
atgaccttgg	agtccccaa	cggcagggtc	atctccttcc	acagctgcgt	ggctcagctc	300
tattttttcc	acttctggg	gagcaccgag	tgtttctctc	acacagtcac	gtcctatgat	360
cgctacttgg	ccatcagtta	cccgtcagg	tacaccagca	tgatgagtgg	gagcagatgt	420
gcctcctcgg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccagaccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aaccagatcc	agcactatct	gtgtgatgca	540
ccgcccattc	tgaaactggc	ctgtgcagac	acctcagcca	acgagatggg	catctttgtg	600
gacattgggc	tagtggcctc	gggctgcttt	ctcctgatag	tgctgtctta	tgtgtccatc	660
gtctgttcca	tcctgcggt	ccacacctca	gaggggaggc	acagagcctt	tcagacctgt	720
gcctcccact	gcctcgtgg	cctttgcttt	tttgttccct	gtgttttcat	ttacctgaga	780
ccaggctcca	gggagctcgt	ggatggagtt	gtggccattt	tctacactgt	gctgacaccc	840
cttctcaacc	ctgttgtgta	cacctgaga	aacaaggagg	tgaagaaagc	tgtgttgaaa	900
ctgagagaca	aagtagcaca	ttctcaggga	gaa			933

<210> 379

<211> 936

<212> DNA

<213> Unknown (H38g228 nucleotide)

<220>

<223> Synthetic construct

<400> 379

atgccttcta	tcaatgacac	ccacttctat	cccccttct	tcctcctgct	aggaatacca	60
ggactggaca	ctttacatat	ctggatttct	ttccattct	gtattgtgta	cctgattgcc	120
attgtgggga	atatgaccat	tctctttgtg	atcaaaactg	aacatagtct	acaccagccc	180
atgttctact	tcctggccat	gttgtctatg	attgatctgg	gtctgtccac	atccactatc	240
ccaaaaatgc	taggaatctt	ctggttcaac	ctccaagaga	tcagctttgg	gggatgcctt	300
cttcagatgt	tctttattca	catgtttaca	ggcatggaga	ctgttctggt	gggtggctatg	360
gcttatgacc	gctttgttgc	catctgcaac	cctctccagt	acaccatgat	cctcaccaat	420
aaaaccatca	gtatcctagc	ttctgtggtt	gttggaagaa	atttagttct	tgtaacccca	480
tttgtgtttc	tcattctgcy	tctgccattc	tgtgggcata	acatcgtaac	tcacacatac	540
tgtgagcaca	ggggtctggc	cgggttggcc	tgtgcaccca	ttaagatcaa	cataatctat	600
ggggtcatgg	tgatttctta	tattattgtg	gatgtgatct	taattgcctc	ttcctatgtg	660
cttatcctta	gagctgtttt	tcgccttccc	tctcaagatg	tccgactaaa	ggccttcaat	720
acctgtgggt	ctcatgtctg	tggtatgctg	tgcttttaca	caccagcatt	tttttctttt	780
atgacacatc	gttttgccca	aaacattccc	cactatatcc	atattctttt	ggctaacctg	840
tatgtgggtg	tcccacctgc	ccttaaccct	gtcatttatg	gagtcaggac	caagcagatc	900
cgagagcaaa	ttgtgaaaat	atttgtacag	aaagaa			936

<210> 380

<211> 909

<212> DNA

<213> Unknown (H38g229 nucleotide)

<220>

<223> Synthetic construct

<400> 380

atgactgaat	tcatttttct	ggtactttct	cccaaccagg	aggtgcagag	ggtttgcttt	60
gtgatatttc	tggtcttgta	cacagcaatt	gtgctggga	atttcctcat	tgtgctcact	120
gtcatgacca	gcagaagcct	tggttcccc	atgtacttct	tcctcagcta	cctctccttc	180
atggagatct	gctactcctc	cgctacagcc	cccaaactca	tctcagatct	gctggctgaa	240
aggaaagtca	tatcttggtg	gggctgcatg	gcacagcttt	tcttcttgca	cttctttggt	300
ggcactgaga	ttttcctgct	cactgtgatg	gcctatgacc	actatgtggc	catctgcaag	360
cccctcagct	acaccaccat	catgaactgg	cagggtgtgta	ctgtccttgt	aggaatagca	420
tgggtgggag	gcttcatgca	ttcctttgca	caaatccttc	tcattctcca	cctgctcttc	480
tgtggcccca	atgtgatcaa	tcactatttc	tgtgacctag	ttcccccttc	caaacttgcc	540
tgctctgaca	ccttcctcat	tggtctgctg	attggtgcca	atggaggcac	cctgtctgtg	600
atcagttttg	gggtcctctt	agcatcctat	atggtcattt	tgctccatct	gagaacctgg	660
agctctgaag	ggtggtgcaa	agccctctcc	acctgtgggt	cccatttcgc	tgtgggtatc	720
ttgttctttg	ggccctgcgt	cttcaactct	ctgaggcctt	ctaccactct	gccccatagac	780
aagatgggtg	ctgtgttcta	cacagtgata	accgcgatcc	tgaacctgt	catctactct	840
ctgagaaatg	ctgaaatgag	gaaggccatg	aagaggctgt	ggattaggac	attgagacta	900
aatgagaaa						909

<210> 381

<211> 947

<212> DNA

<213> Unknown (H38g230 nucleotide)

<220>

<223> Synthetic construct

<400> 381

cttatagcta	caggaaactg	gacaagaata	agtgagttaa	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctgggcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatctttc	ctggagattg	gcttcaacct	agtcattgtg	240
cccaaaatgc	tggggaccct	gcttgcccag	gacacaacca	tctccttctt	tggtctgtgc	300
actcagatgt	atttcttctt	cttctttgga	gtggctgaat	gcttccctca	ggctaccatg	360
gcatatgacc	gctatgtggc	catctgcagt	cccttgcact	acccagtcac	catgaaccaa	420
aggactcgtg	ccaaactggc	tgctgcctcc	tggttcccag	gctttcctgt	agctactgtg	480
cagaccacat	ggctcttcag	ttttccattc	tgtggcacca	acaaggtgaa	ccacttcttc	540
tgtgacagcc	cacctgtgct	gaggctgggt	tgtgcagaca	cagcactggt	tgagatctac	600
gccatcgtcg	gaaccattct	ggtggtcatt	atccccctgt	tgctgatctt	gtgttcctat	660
actcgcattg	ctgctgccat	cctcaagatc	ccatcagcta	aagggaagaa	taaagccttt	720
tctacatgtt	cctcacacct	ccttggtgtc	tctcttttct	atatatcatt	aagcctcacc	780
tacttccggc	ctaaatcaaa	taattcacct	gagggcacga	agctgctatc	attgtcctac	840
actgttatga	ctcccatgtt	gaaccccat	atctacagcc	tgagaaataa	cgagggtgaag	900
aatgcctca	gcaggacggt	ctctaaggcc	ctagccctca	gaaactg		947

<210> 382

<211> 927

<212> DNA

<213> Unknown (H38g231 nucleotide)

<220>

<223> Synthetic construct

<400> 382

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ctacaggttc	tcctttttgt	ggtgttccta	gcggtttaca	tgatcactct	gttgggaaat	120
attggatga	tcattttgat	tagcatcagt	cctcagcttc	agagtcctcc	gtactttttc	180
ctgagtcac	tgtcttttgc	ggacgtgtgc	ttctcctcca	acgttacccc	caaaatgctg	240

gaaaacttat	tatcagagac	aaaaaccatt	tcctatgtgg	gatgcttggt	gcagtgtctac	300
tttttcattg	ccgttggtcca	cgtggaggte	tatatcctgg	ctgtgatggc	ctttgacagg	360
tacatggccg	gctgcaaccc	tcctgcttat	ggcagtaaaa	tgtctaggac	tgtgtgtgtt	420
cggtcatctt	ctgtgcctta	tgtctatgga	ttctctgtca	gcctaataatg	cacactatgg	480
acttatgggt	tatacttctg	tggaaacttt	gaaatcaatc	acttctattg	tgcagatccc	540
cctctcatcc	agattgacctg	tgggagagt	cacatcaaag	aaatcacaaat	gattgttatt	600
gctggaatta	acttcacata	ttccctctcg	gtggtcctca	tctcctacac	tctcattgta	660
gtagctgtgc	tacgcatgcg	ctctgccgat	ggcaggagga	aggcggtctc	cacctgtggg	720
tcctacttga	cggctgtttc	tatgttttat	gggaccccca	tcttcattgta	tctcaggaga	780
cccactgagg	aatccgtaga	gcaggggcaa	atggtggctg	tgttttacac	cacagtaatt	840
cctatgttga	atcccatgat	ctacagtctg	agaaataagg	atgtaaaaga	agcagtcaac	900
aaagcaatca	ccaagacata	tgtgagg				927

<210> 383

<211> 960

<212> DNA

<213> Unknown (H38g232 nucleotide)

<220>

<223> Synthetic construct

<400> 383

atgcttcata	ccaacaatac	acagtttcac	ccttccacct	tcctcgtagt	gggggtccca	60
gggctggaag	atgtgcatgt	atggattggc	ttcccttctt	ttgcgggtgta	tctaacagcc	120
cttctagggg	acatcattat	cctgtttgtg	atacagactg	aacagagcct	ccaccaaccc	180
atgttttact	tcctagccat	gttggccggc	actgatctgg	gcttgtctac	agcaaccatc	240
cccaagatgc	tgggaatttt	ctggtttaat	cttggagaga	ttgcatttgg	tgccctgcac	300
acacagatgt	ataccattca	tatatgcact	ggcctggagt	ctgtgggtact	gacagtcacg	360
ggcatagatc	gctatattgc	catctgcaac	cccctgagat	atagcatgat	ccttaccac	420
aaggtaatat	ccattctggg	catagtcac	attgtcagga	ctttgggtatt	tgtgactcca	480
ttcacatttc	tcaccctgag	attgcctttc	tgtgggtgtc	ggattatccc	tcatacctat	540
tgtgaacaca	tgggcttggc	aaagtttagt	tgtgccagta	ttaatgttat	atatggattg	600
attgccttct	cagtgggata	cattgacatt	tctgtgattg	gattttccta	tgtccagatc	660
ctccgagctg	tcttccatct	cccagcctgg	gatgcccggc	ttaaggcact	cagcacatgt	720
ggctctcacg	tctgtgttat	gttggctttc	tacctgccag	ccctcttttc	cttcattgaca	780
caccgctttg	gccacaacat	ccctcattac	atccacattc	ttctggccaa	tctgtatgtg	840
gtttttcccc	ctgctcttaa	ctctgttatc	tatgggggtc	aaacaaaaca	gatacgagag	900
caggtactta	ggataactca	ccctaaaagc	ttttggcatt	ttgaccccaa	gaggatcttc	960

<210> 384

<211> 936

<212> DNA

<213> Unknown (H38g233 nucleotide)

<220>

<223> Synthetic construct

<400> 384

atggaacaac	acaatctaac	aacggtgaat	gaattcattc	ttacgggaat	cacagatatc	60
gctgagctgc	aggcaccatt	atttgcatgt	ttcctcatga	tctatgtgat	ctcagtgatg	120
ggcaatttgg	gcatgattgt	cctcaccaag	ttggactcca	ggttgcaaac	ccctatgtac	180
ttttttctca	gacatctggc	tttcatggat	cttgggttatt	caacaactgt	gggacccaaa	240
atgttagtaa	attttgttgt	ggataagaat	ataatttctt	attatttttg	tgcaacacag	300
ctagctttct	ttcttgtgtt	cattggtagt	gaacttttta	ttctctcagc	catgtcctac	360
gacctctatg	tggccatctg	taacctctg	ctatacacag	taatcatgtc	acgaagggtg	420
tgtcaggtgc	tggtagcaat	cccttacctc	tattgcacat	tcattttctc	tctagtcacc	480
ataaagattt	ttactttatc	cttctgtggc	tacaacgtca	ttagtcattt	ctactgtgac	540
agtctccctt	tgttaccctt	gctttgttca	aatacacatg	aaattgaatt	gataattctg	600
atctttgcag	ctattgattt	gatttcatct	cttctgatag	ttcttttatc	ttacgtctc	660
atccttgtag	ccattctcag	gatgaattct	gctggcagac	aaaaggcttt	ttctacctgt	720
ggagccacc	tgacagtgg	catagtgttc	tatgggactt	tgcttttcat	gtacgtgcag	780

cccaagtcca gtcattcctt tgacactgat aaagtggctt ccatatttta caccctgggt	840
atccccatgt tgaatccctt gatctatagt ttacgaaaca aagatgtaaa atatgcccta	900
cgaaggacat ggaataaactt atgtaaatatt tttgtt	936

<210> 385

<211> 945

<212> DNA

<213> Unknown (H38g234 nucleotide)

<220>

<223> Synthetic construct

<400> 385

atgatgtggg aaaactggac aattgtcagt gaatttgctt tcgtgagctt ctcagccctg	60
tccactgagc ttcaggctct actgtttctc cttttcttga ccatttactt ggttacttta	120
atgggcaatg tctcatcat cctggtcact atagctgact ctgcactaca aagtcctatg	180
tactttctcc tcagaaactt gtccttcctg gagatagggt tcaacttggg cattgtgccc	240
aagatgctgg ggaccctgat cattcaagac acaaccatct ccttccttgg atgtgccact	300
cagatgtatt tcttctctct ttttggggct gctgagtgct gcctcctggc caccatggca	360
tatgaccgct acgtggccat ctgtgacccc ttgcactacc cagtcatcat gggccacata	420
tctgtgccc agctggcagc tgccctcttg ttctcagggt tttcagtggc cactgtgcaa	480
accacatgga ttttcagtgt cctttttgtt ggccccaaca ggggtaacca cttcttctgt	540
gacagccctc ctgttattgc actgggtctgt gctgacacct ctgtgtttga actggaggct	600
ctgacagcca ctgtcccat cattctcttt cctttcttgc tgatcctggg atcctatgtc	660
cgcacctct cactatctt caggatgccg tcagctgagg ggaaacatca ggcattctcc	720
acctgttccg cccacctctt ggttgctct ctctctata gcaactgccat cctcacgtat	780
ttccgacccc aatccagtgc ctcttctgag agcaagaagc tgctgtcact ctcttcaca	840
gtggtgactc ccatgttgaa ccccatcatc tacagctcaa ggaataaaga agtgaaggct	900
gcactgaagc ggcttatcca caggaccctg ggctctcaga aacta	945

<210> 386

<211> 931

<212> DNA

<213> Unknown (H38g235 nucleotide)

<220>

<223> Synthetic construct

<400> 386

atggccaaaa ccaataattc agaagttact gaattcatcc tcttgggact cacagacaat	60
ccagagctcc aagccctttt ttagggggat ctttctagt atcaatttaa gtagtgcat	120
gggtagcctt ggggttaatta tgctaattca tatcagtcct cagcttcaca cagctatgta	180
ttttttctc agccacgtag cttttgttta tttttgctac acctcctcta tcaccctaa	240
cagcctagtg aacctcctcc aagaaactaa aagaatatcc ttacctactt gtgcctctca	300
gttgcatgtc tttatcatgt ttgtggtttg tgacatgtat gtgctctcag ccatggcata	360
tgacaggatg gtggccatct gcaacccttt actctatagt atcatcatga acagaagggt	420
ctgtattcaa atgggtggtaa gtacatattt gtatggcttt tctgtgagac tcctacaggc	480
aattcttaca ttccacttgt ctttctgaga ttcaaatata ataaataatt cctattgtga	540
tgatgttccc ctagcatgtc taccctatca taaaaaccat taaaaagatg taaaaagaact	600
gatattgttc acacttgctg gtttcaatac acttttctcc cttcttatca tctcatctc	660
ctacatatca gtactgtctg ccattctgag aattaattca gctgaaagta gacaaaaggc	720
atthttctact tgtgactccc acctgacttc tatcatcata ttttatggta taattacctt	780
catgtatatg cagtgaataa caaataattc tctggatata gacaaaatag cttctgtttt	840
ctgtattgtg aaaattcctt caatatatag cctgaggaac cacgaagtca aagatgcttt	900
gaagatgatt atggaaaatc tatgtcttac t	931

<210> 387

<211> 552

<212> DNA

<213> Unknown (H38g236 nucleotide)

<220>

<223> Synthetic construct

<400> 387

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acactttctg	taaataataa	caaattttct	taaataataa	ataataattt	ctaggtataa	120
tttaatttac	atagtgaac	aagccattct	taggtataat	ccttagttct	gtcttcgaaa	180
gtctgcatcc	tgtagcagc	tggcgtagtt	ggtagggatac	ttagcagaag	gattgtatgt	240
gtgtcctact	gtttcactgt	cctcctccag	gtccaatgcc	atcaatcact	ttttctgtaa	300
taaatcccta	gggcttggtc	tttcatgcta	caacatttat	atcagcacag	cagtccctgc	360
ctttgctggg	tttgagtgtc	gcattcattg	ccatatttgg	tcacatgttt	ctcctggaca	420
tatatcctgg	ttgctatcaa	gaggatgtcc	tcagtgggga	gaaaagaatt	gtctatttgt	480
gtctcccacc	tgaaaactag	caccattttt	catacagccc	tcttttatgt	gtacttacag	540
cctgattttt	tt					552

<210> 388

<211> 963

<212> DNA

<213> Unknown (H38g237 nucleotide)

<220>

<223> Synthetic construct

<400> 388

atgtctgggg	acaacagctc	cagcctgacc	ccaggattct	ttatcttgaa	tggcgttcct	60
gggctggaag	ccacacacat	ctggatctcc	ctgccattct	gctttatgta	catcattgct	120
gtcgtgggga	actgtgggct	catctgcctc	atcagccatg	aggaggccct	gcaccggccc	180
atgtactact	tcctggccct	gctctccttc	actgatgtca	ccttggtcac	caccatggta	240
cctaataatgc	tgtgcatatt	ctggttcaac	ctcaaggaga	ttgactttaa	cgctgcctg	300
gccagatgt	tttttgcca	tatgctgaca	gggatggagt	ctgggggtgt	catgtctatg	360
gcctgggacc	gctatgtggc	catctgctac	cccttacgct	atgccaccat	ccttaccaac	420
cctgtcatcg	ccaaggctgg	tcttgccacc	ttcttgagga	atgtgatgct	catcatccca	480
ttcactctcc	tcaccaagcg	cctgccttat	tgccggggga	acttcatccc	ccacacctac	540
tgtgaccata	tgctgtggc	caaggatatc	tgtggcaatt	tcaagggtcaa	tgctatttat	600
ggctctgatg	ttgctctcct	gattgggtgt	tttgatatct	gctgtatctc	tgtatcttac	660
actatgattt	tgcaggctgt	tatgagcctg	tcacagcag	atgctcgtca	caaagccttc	720
agcacctgca	catctcacat	gtgttccatt	gtgatcacct	atgttgctgc	ttttttcact	780
tttttcactc	atcgttttgt	aggacacaat	atcccaaacc	acatacacat	catcggtggc	840
aacctttatc	tgctactgcc	tcctaccatg	aacccaattg	tttatggagt	caagaccaag	900
cagattccagg	aagggtgta	ttaaattttta	cttgagagaca	aggttagttt	tacctatgac	960
aaa						963

<210> 389

<211> 400

<212> DNA

<213> Unknown (H38g238 nucleotide)

<220>

<223> Synthetic construct

<400> 389

tgtttctgtg	gctttgctgt	tctcaccagt	tgccgtttct	gtctaacccc	ggagaggtaa	60
ataacaccct	gagaatggcc	ctaggtcac	acagggtttcc	cagttagcca	atcaagaaga	120
attacaaatg	gccacactat	cagccagagc	tgctgcctca	ctggagttcc	aaaacggaga	180
ggatctgtc	ccctgcacc	tcagggttgg	aaatgctgag	aaatgctaag	ccactggggg	240
ttcaattata	cctaatttaa	aacgagcaaa	gtagacttgc	cccccaagg	gttccacaaa	300
aaacttaaag	cctggcagct	cagccctgag	ttcatactgc	ttaaaagaca	ccggggggag	360
aggtaagtga	tcagggtgaga	gaagtctggt	ccccagagag			400

<210> 390

<211> 954

<212> DNA

<213> Unknown (H38g239 nucleotide)

<220>

<223> Synthetic construct

<400> 390

atgaagccaa	caatacaaat	ggcttcagga	aatctcacat	gggtgacgga	gttcattctt	60
gtgggagtct	cagatgatcc	ggagctccag	attccccctc	tcctgggtctt	cctgggtgctc	120
tatttgctga	ccgtggcagg	gaacctgggc	atcatcaccc	tcaccagtgt	tgaccctcaa	180
cttcaaaccc	ccatgtactt	tttctctga	cacttggtga	ttattaatct	ttgcaattct	240
actgtcggtg	cccctaaaat	gctgggttaac	ttcctgggtta	ccaagaaaac	catatcatac	300
tatggatgtg	cagcccaact	gggtggattc	ttggttttca	ttgtggctga	gattttcacg	360
ctggctgcaa	tggcctatga	ccgctatgtg	gctatttggg	gccctctgct	ctacgccgta	420
gtgggtgtctc	caaagggtgtg	tcgtctgctg	gtgtccctca	cataccttca	gagtcttctc	480
acagcactga	ctgtctcttc	ctgtgtgttc	tctgtgtcat	actgttcttc	caacattatc	540
aaccattttt	actgtgatga	tgtccctttg	ctagcattgt	cctgttctga	tacctacatt	600
ccagaaacag	cagtctttat	cttttcaggg	accaacttgc	ttttctccat	gatcgttggt	660
ctgatatact	acttcaacat	tgttattacc	attttgagga	tacgttcttc	agaaggacga	720
caaaaagcct	tttccacctg	tgttctctac	atgatagctg	tggttgtgtt	ctatgggact	780
ctccttttca	tgtatttgca	accaaggagt	aatcattcat	tagatactga	caaaatgggt	840
tcgggtcttct	acacctgggt	gataccagtg	ctgaaccctc	taatctacag	cctcaggaac	900
aagaacgtga	aggatgcact	aaagagggtc	ctagataacc	catgccgata	actc	954

<210> 391

<211> 945

<212> DNA

<213> Unknown (H38g240 nucleotide)

<220>

<223> Synthetic construct

<400> 391

atgttgctcc	caaaccacac	catagtgcac	gaattcattc	tcttaggact	gacagacgac	60
ccagtgcctag	agaagatcct	gtttgggggtg	ttcctgggca	tctacctaat	cacactggca	120
ggcaacctgt	gcatgatcct	gctgatcagg	accaattccc	aactgcaaac	acccatgtat	180
ttcttctctg	gtcacctctc	ctttgtagac	atttgctatt	cttccaatgt	tactccaaat	240
atgctgcaca	atttctctc	agaacagaag	accatctcct	acgctggatg	cttcacacag	300
tgtcttctct	tcacgcctc	agtgatcact	gagttttact	tccttgcttc	aatggcattg	360
gatecgtatg	tagccatttg	cagcccctta	cattacagtt	ccaggatgtc	caagaacatt	420
tgcactctct	tggtcactgt	gccttacatg	tatggcttcc	ttaatgggct	ctctcagaca	480
ctgctgacct	ttcacttatc	cttctgtggc	tcccttgaaa	tcaatcattt	ctactgcgtc	540
gatcctcctc	ttatcatgct	ggcctgctct	gacacccgtg	tcaaaaagat	ggcaatgttt	600
gtagttgcag	gctttactct	ctcaagctct	ctcttcatca	ttcttctgtc	ctatcttttc	660
atttttgcag	cgatcttcag	gatccgttct	gctgaaggca	ggcacaagc	cttttctacg	720
tgtgcttccc	acctgacaat	agtcactttg	ttttatggaa	ccctcttctg	catgtacgta	780
aggcctccat	cagagaagtc	tgtagaggag	tccaaaataa	ttgcagtctt	ttatactttt	840
ttgagcccaa	tgctgaaccc	attgatctat	agcctacgga	acagagatgt	aatccttgcc	900
atacaacaaa	tgattagggg	aaaatccttt	tgtaaaattg	cagtt		945

<210> 392

<211> 939

<212> DNA

<213> Unknown (H38g241 nucleotide)

<220>

<223> Synthetic construct

<400> 392

atgcctatag	ctaacgacac	ccagttccat	actttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ctggattgga	ttcccttttt	tctctgtgta	tcttattgca	120

ctcctgggaa	atgctgctat	cttctttgtg	atccaaactg	agcagagtct	ccatgagccc	180
atgtactact	gcctggccat	gttggattcc	attgacctga	gcttgtctac	ggccaccatt	240
cccaaaatgc	tgggcatctt	ctggttcaat	atcaaggaaa	tatcttttgg	aggcttccct	300
tctcagatgt	tcttcateca	tttcttcaat	gtcatggaga	gcacgtattt	ggtggccatg	360
gcctttgacc	gctacattgc	catttgcaaa	cctctttggg	acaccatgat	cctcaccagc	420
aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcttgtacat	ggtcattcca	480
ctgggtgttc	tcctcttaag	gttgcccttc	tgtggacatc	gtatcatccc	tcatacttac	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattatgttt	600
ggtcttggca	gtattttctt	cttgttattg	gatgtgctcc	ttattattct	ctcccatatc	660
aggatcctct	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtggct	ctcacattgg	tgttatctta	gccttttcta	caccagcatt	tttctctttc	780
tttacacact	gctttggcca	tgatattccc	caatatatcc	acattttctt	ggctaatact	840
tatgtggttg	ttcctccac	cctcaatcct	gtaatctatg	gggtcagaac	caaacatatt	900
aggagacag	tgctgaggat	tttcttcaag	acagatcac			939

<210> 393

<211> 984

<212> DNA

<213> Unknown (H38g242 nucleotide)

<220>

<223> Synthetic construct

<400> 393

atgcatactt	tcaagtttgt	tctagatttc	aacatgaaga	atgtcactga	agttacctta	60
tttgtactga	agggcttcac	agacaatctt	gaactgcaga	ctatcttctt	cttcctgttt	120
ctagcaatct	acctcttcac	tctcatggga	aatttaggac	tgattttagt	ggtcattagg	180
gattcccagc	tccacaaacc	catgtactat	tttctgagta	tgttgtcttc	tgtggatgcc	240
tgctattcct	cagttattac	cccaaataatg	ttagttagatt	ttacgacaaa	gaataaagtc	300
atttcattcc	ttggatgtgt	agcacagggtg	tttcttgctt	gtagttttgg	aaccacagaa	360
tgctttctct	tggctgcaat	ggcttatgat	cgctatgtag	ccatctacaa	ccctctcttg	420
tattcagtga	gcattgtcacc	cagagtctac	atgccactca	tcaatgcttc	ctatgttgct	480
ggcattttac	atgctactat	acatacagtg	gctacattta	gcctatcctt	ctgtggagcc	540
aatgaaatta	ggcgtgtcct	ttgtgatatc	cctcctctcc	ttgctatttc	ttattctgac	600
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tatgggacaa	tctcttctcat	gtatgtgaga	ccaagttcca	gctatgcttc	ggaccatgac	840
atgatagtgt	caatatattta	caccattgtg	attcccttgc	tgaatcccgt	catctacagt	900
ttgaggaaca	aagatgtaaa	agactcaatg	aaaaaaatgt	ttgggaaaaa	tcaggttatc	960
aataaagtat	attttcatat	taaa				984

<210> 394

<211> 984

<212> DNA

<213> Unknown (H38g243 nucleotide)

<220>

<223> Synthetic construct

<400> 394

atgaatggag	ccaacagctc	cagcctgaca	ccaagatatt	tcattctcag	tggcgttcct	60
gggctggaag	ctgcacacat	ctggatctcc	ctgcctttct	gcttcatgta	catcattgtt	120
gtttttgggga	actgtggact	tatatacctc	attagccatg	aggaggccct	gcaccaaccc	180
acctactact	tcttagactt	gctgtctctt	acagatgtta	ctggatgcac	ctcatttgtt	240
cccaatatgt	tatgtatttt	ttggtttggc	ctcaaggaaa	ttgactttaa	tgccctgcct	300
gtgcagatgt	ttttcatcca	catgctgaca	ggcatggagt	ctggggcgct	catgcttatg	360
gctctagacc	gctatgtggc	catttgctac	cctctacact	attccaccat	cttcaccaac	420
actgtaatta	ccaaagtggg	gcttgtcacc	ttcattcaaa	gtgtgttgct	tatgattcca	480
tttgccttcc	tgatcaagtg	tcttccctat	tgcaggggca	acctcatcca	ccacacctat	540
tttaacatat	gtctgtggcc	aaattatcct	gtggtaatgt	ccagattaat	gccatctatg	600

gtctcatagc	tgccatattg	attggggggg	ttgacatggt	ctgtatctcc	atgtcttaca	660
ccatgattat	ccgtgctgta	gtgaatttgt	catctgcaga	tgctgccaca	aagccttcag	720
tacctgtaca	gcacatatat	gtgctatttt	catcacttat	gtcccagcct	ttttcaactt	780
cttcactcac	cgctttgggg	gacacaccat	acctcatcat	gttcacattt	ttatagccaa	840
cctttacttg	atgctgcctc	ccaccttaaa	tccaattgtc	tatggagtga	agaccaagca	900
gatacgtgaa	ggagtgatca	aattgttttt	tagagagaaa	ggtattttta	gtatgacata	960
aatctatgat	atagaagtct	gaat				984

<210> 395

<211> 903

<212> DNA

<213> Unknown (H38g244 nucleotide)

<220>

<223> Synthetic construct

<400> 395

atggccagta	caaataatgt	gactgagtca	atgatcacca	gcctttttcca	ggatccagca	60
gtgcagagag	tgtgctttgt	ggtgtttctc	cccgtgtact	ggccatggag	gtgggcaatg	120
gcctcatcgt	tctgacggtc	agtatcagca	agagtctgca	ttcccctgtg	tacttcttcc	180
tgagctacct	gtcattgatg	gagatcagtt	acttcactgt	tgtccctaaa	ttcatcacag	240
acttacttgc	caagattaaa	gccatctctc	tggagggcta	tctggctcag	atattcttgc	300
acttctttgg	catcccctgg	atctttctgc	tcccactgat	gaccaatgac	caatataatg	360
ccaactgcaa	actttattac	tacacaacca	tcatgagctg	cctgtctgtc	accttctggt	420
ggctggtttc	tggctgaggg	gcataattca	ctcaatgggt	cagatccttg	tctctgtcca	480
attgttcttc	tgtgggtccca	acatgattga	ccactcattc	tgtgacctcc	aggtcttatt	540
caagcttgcc	tgcactgaca	cctttgtgga	gggggttatt	gtgttggcca	acagtgaatt	600
agtatctgtc	ttcttcctta	tcttgggtgc	ctcttaatat	catcatccta	gtcaacttga	660
ggaaccattc	tcagagaggg	aggtgcaaa	ccctctccac	ctgtgcctct	tatcttgtat	720
tttgaacttg	ccattttcct	ctacgtgtga	ctctcctcca	cctttactaa	agataaactc	780
gtggctgtat	tttacgtggt	catcaccccc	atgctgaacc	ccttcactta	cacgcttggg	840
aatgcagaga	tgaaaatcac	catgaggaga	ttgttgggca	ggacagtga	ctcaggaatg	900
gaa						903

<210> 396

<211> 972

<212> DNA

<213> Unknown (H38g245 nucleotide)

<220>

<223> Synthetic construct

<400> 396

gggagctgaa	agcaatgaaa	gtcttgacct	cctatctgtc	ttcctgactg	gcatccagg	60
actggaggcc	caacatgggt	ggctctccat	ccctttcttc	accatgtaca	ttgtggccat	120
tgtgggaaac	atcctaatta	tggcagcagt	gcaggaagac	tctgccctac	atgagcccat	180
gtacttattt	ctctccatgt	tggctgtcac	tgaggtgggc	gtctctgtgt	ctacactgct	240
actgttacag	gcattctttg	gtttgatgcc	cacagagttg	actttgatgg	ctgcctggcc	300
cagatgttct	tcattcacac	cttctcctgc	atggagtcag	gggtcctact	agccatgagc	360
tatgaccgct	ttgtagccat	ctacaacctc	ctgcgctata	cagccatcct	gaccctgccc	420
cgtattatct	gcatgggtct	gggcattaca	ctgaagagtg	tggcactcat	ggccccactt	480
ccaatccttt	tgaggcaact	gccctattgc	cacactaatg	tcctctcaca	ctcctactgc	540
ctccactcag	atctgatcca	gctgccttgt	gcagatacta	aactcaacag	catcctgggc	600
ttagccattg	ttctcgcaaa	tttcgggctg	gactcattgc	ttatcgtggt	ctcttatgtc	660
ttgattcttt	atacagtgat	gggcattgct	tctggagagg	gacggtgga	ggctctcaac	720
acatgtgtgt	cacatatttg	tgcagtgcct	atatattatg	tgcccatgat	tgggggtgtct	780
gtgatgcac	gtgctgccaa	acatgcttct	cccattgtcc	acacacttat	gtctagcatc	840
tgcccttttg	tgccacctgt	acttaatccc	atcatctata	gtgttaagac	ccagacaata	900
agacagggaa	ttctcacctt	gttttcctgc	aagagggaa	tgctctgaat	cactgcaagg	960
agtcaggaac	tg					972

<210> 397
 <211> 874
 <212> DNA
 <213> Unknown (H38g246 nucleotide)

<220>
 <223> Synthetic construct

<400> 397
 acttttgttta ttatttcaaa atttcaaggc tgctgaaagg taggtcttta tacacagtca 60
 cttttatttgc tagctgagta ttttcatcgg gggcaactga tgaaaatgtt gacttccact 120
 aacctaagcc tgtccgttgt tactatcgta tcttccagtt caacgtcagg gaaatagttt 180
 ttggtgcttt ccttgtttat atacagatgt ttatgactta tctatgcact ggcctggaat 240
 ctgggggtact gataatcctg gccatagacc actatgtcgt aattcgcaat ccactgagat 300
 ataccatgat tctcatgaac aatgtggtag ccaccctagg aagtcatgat aattagatct 360
 ttaatcttta tcatcccttt tgagtttctc atcttgctgt tgcattctg tgctgcccac 420
 atcatccccc acaccaaagt tgagcacatg ggcattgccc atctttcctg tgccagtgtc 480
 agagccaata atatgtttgg gatggttgcc tttttgtggg atttattgac cttattgcaa 540
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 ttcgaggctc tcaatacctg tggttcccat gtttgtcatg ctcattctt acatcccag 660
 atttttttct tgatacactg cttggtgaaa gcatccctgc tatattcgta tatttctggc 720
 caatgtatat acggttggtc tacctgtatt caaccctgtt atctatggga tcaggaaaaa 780
 acagatccca gactagggta tagacctaaa gacatttgat gatcagtcac ttctagtcac 840
 gatgatatat atattgggat atatatgcaa atat 874

<210> 398
 <211> 936
 <212> DNA
 <213> Unknown (H38g247 nucleotide)

<220>
 <223> Synthetic construct

<400> 398
 atggatgaag ccaatcactc tgtggtctct gagtttgtgt tcttgggact ctctgactcg 60
 cggaagatcc agctcctcct ctctcctttt ttctcagtggt tctatgtatc aagcctgatg 120
 ggaaatctcc tcatttgtgt aactgtgacc tctgaccctc gtttacagtc ccccatgtac 180
 ttctgtctgg ccaacctttc catcatcaat ttggtatttt gttcctccac agctcccaag 240
 atgatttatg accttttcag gaagcacaag accatctctt ttgggggctg tgtagttcag 300
 atcttcttta tccatgcagt tgggggaact gagatggtgc tgctcatagc catggctttt 360
 gaccgatatg tggccatatg taagcctctc cactacctga ccatcatgaa cccacaaagg 420
 tgcattttgt ttttagtcat ttcttggtat ataggtatta ttactcagt gattcagttg 480
 gcttttgttg tagacctgt gttctgtggc cctaataaat tagatagttt cttttgtgat 540
 ctctctcgat ttatcaaact ggcttgcata gagacctaca cattgggatt catggttact 600
 gccaatagtg gatttatttc tctggtctct tttttaattc tcataatctc ttacatcttt 660
 attttggtga ctgttcagaa aaaatcttca ggtggtatat tcaaggcttt ctctatgctg 720
 tcagctcatg tcattgtggt ggttttggtc ttggggccat taatcttttt ctatattttt 780
 ccatttccca catcacatct tgataaattc cttgccatct ttgatgcagt tatcactccc 840
 gttttgaatc cagtcatact tactttttaga aataaagaga tgatggtggc aatgagaaga 900
 cgatgctctc agtttgtgaa ttacagtaaa atcttt 936

<210> 399
 <211> 503
 <212> DNA
 <213> Unknown (H38g248 nucleotide)

<220>
 <223> Synthetic construct

<400> 399
 aagcagtcga gtggtgacag tgggaaccag accacctggc tgatcctagt gggcttcggg 60

gagctgcaat	acctgggctt	ccttcccttc	actctcttcc	tggccatcta	tgtggtgaca	120
gttggggcaa	tgccctcatc	atgctggctg	tggcctctag	tgggacactg	caccacacaa	180
tgtacttctt	cctctgccac	ttctccctgc	tggagattgg	ctatacctcc	aacgtcatac	240
tatggctgtt	gcagagtttc	ttggagggga	aggaagtcac	ctctctagtc	agctgtctgg	300
ctcagttcta	cgtgttttcc	tcgrtggctg	cagctgagtg	cctcctgcta	tctgccgtgt	360
cctatgactg	ttacttggcc	atctgctgcc	cccttcacta	tctgacctg	atgagcacct	420
ggttttgtca	ctgcctggcc	gctgggtgct	ggttcagtg	cttcttctcc	tctgccttca	480
ctatggccct	ggcagcacct	ctg				503

<210> 400

<211> 963

<212> DNA

<213> Unknown (H38g249 nucleotide)

<220>

<223> Synthetic construct

<400> 400

atgctaacac	tgaataaaac	agaccttaata	ccagcttcat	ttattctgaa	tggagtccca	60
ggactggaag	acacacaact	ctggatttcc	ttcccattct	gctctatgta	tgttgtggct	120
atggtaggga	attgtggact	cctctacctc	attcactatg	aggatgccct	gcacaaaccc	180
atgtactact	tctggcccat	gctttccttt	actgaccttg	ttatgtgctc	tagtacaatc	240
cctaaagccc	tctgcactct	ctggtttcat	ctcaaggaca	ttggatttga	tgaatgcctt	300
gtccagatgt	tcttcatcca	caccttcaca	gggatggagt	ctgggggtgct	tatgcttatg	360
gccctggatc	gctatgtggc	catctgctac	cccttacgct	attcaactat	cctcaccaat	420
cctgtaattg	caaagggttg	gactgccacc	ttcctgagag	gggtattact	cattattccc	480
tttactttcc	tcaccaagcg	cctgccctac	tgcagaggca	atatacttcc	ccatacctac	540
tgtgaccaca	tgtctgtagc	caaattgtcc	tgtggtaatg	tcaagggtcaa	tgccatctat	600
ggctctgatg	tggcctcct	gattgggggc	tttgacatac	tgtgtatcac	catctcctat	660
accatgatcc	tccgggcagt	ggtcagcctc	tcctcagcag	atgctcggca	gaaggccttt	720
aatacctgca	ctgccacat	ttgtgccatt	gttttctcct	atactccagc	tttcttctcc	780
ttcttttccc	accgctttgg	ggaacacata	atccccctt	cttgccacat	cattgtagcc	840
aatattttatc	tgtctctacc	accactatg	aaccctattg	tctatggggg	gaaaacccaa	900
cagatacgag	actgtgtcat	aaggatcctt	tcaggttcta	aggataccaa	atcctacagc	960
atg						963

<210> 401

<211> 945

<212> DNA

<213> Unknown (H38g250 nucleotide)

<220>

<223> Synthetic construct

<400> 401

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttccct	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttctct	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccccgtg	actacctgct	cagcctcctc	tcctgtctgg	acatcgtgct	ctgccctact	240
gtcatcccca	aggtcctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgttctctcc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcggtta	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtcaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctgcccaccc	ccatcctttc	agcacaaatc	cgttattgtg	gaagaaatgt	cattgagaac	540
tgcatctgtg	ccaatatgtc	tgtttccaga	ctctcctgcg	atgatgtcac	catcaatcac	600
ctttaccaat	ttgctggagg	ctggactctg	ctaggatctg	acctcatcct	tatcttctct	660
tcctacacct	tcattctgcg	agctgtgctg	agactcaagg	cagagggtgc	cgtggcaaaag	720
gccctaagca	catgtggctc	ccacttcatg	ctcatcctct	tcttcagcac	catccttctg	780
gtttttgtcc	tcacacatgt	ggctaagaag	aaagtctccc	ctgatgtgcc	agtcttgctc	840
aatgtttctc	accatgtcat	tcctgcagcc	cttaacccca	tcatttacgg	ggtgagaacc	900
caagaaatta	agcaggggaat	gcagagggtg	ttgaagaaag	ggtgc		945

<210> 402
 <211> 906
 <212> DNA
 <213> Unknown (H38g251 nucleotide)

<220>
 <223> Synthetic construct

<400> 402
 ttgagctcta tgtgtctcac cattgtgatg cattgtgaat tcttcctcat ggacttgact 60
 gatgacctc agcttcatcc cacttctctt gccctcttcc tccccatcta tgtagtcag 120
 gtgatggaaa cctgggctc cttgccttca ttgtggtcag tccccaattc ctcaccccca 180
 tgtatttctt cctcagcaac tggctctctg ttgacttctg ttattcttca gtaacagtcc 240
 caaaaatata aatgggggtt ttttctgact gccaaagtct ctccttctct gggtgcatgg 300
 cccagttaa ctgcttttaa aatatttgcg gacaccgagt tcttcctcct ggctccatg 360
 gtctattacc gctaagaggg cgtctgcaat cctctgctct accatatcac catgtcccca 420
 aagctctgct tgcagctggg ggccaccagc tatgaacatg gtgctcccta gtagcacaat 480
 ctttcatctg atcttctgta agtctgtgac atcattcatt aattctgtta tttcctcccc 540
 caccgaggct ttaaaaactc tctgctctg acatgcaagg ccttcaactt cttacctttg 600
 cctctagttag ctttaattgta tcgggtgtcc ggacaatctt ccttgtctcc atttaattat 660
 gagaatgccc tcggtttgag gcaaacactt gtgcttccca cctgacagca gtcagcctgt 720
 gctatggaac cacagtgttc cttcacctgc acctatcctt gaagtgttca ccagacagag 780
 atatgctggg ctctgtttta cacagtgggt attctcatgc tcaaccccat ggtccaaagt 840
 ctgaggaaca aggatgtgaa gaaaacattt gggacttcct catgaagggt tacaattcct 900
 ctcctt 906

<210> 403
 <211> 972
 <212> DNA
 <213> Unknown (H38g252 nucleotide)

<220>
 <223> Synthetic construct

<400> 403
 atgcctctat ttaattcatt atgctgggtt ccaacaattc atgtgactcc tccatctttt 60
 attcttaatg gaatacctgg tctggaaaga gtacatgtat ggatctccct cccactctgc 120
 acaatgtaca tcacttctct tgtggggaat cttggctctg tgtacctcat ttattatgag 180
 gagtccctac atcatccgat gtattttttt tttggccatg ctctctccct cattgacctc 240
 cttacctgca ccaccactct acccaatgca cctctgcatc tctgggttcag tctcaaagaa 300
 attaaacttca atgcttgctt ggcccagatg ttctttgttc atgggttcac aggtgtggag 360
 tctgggggtgc tcatgctcat ggctctagac cgctatgtag ccatttgcta ccttttgctg 420
 tatgtaccac cactcaccaa cctatcatt gccaaaggct agcttgccac cttcctgagg 480
 ggtgtattgc tgatgattcc tttcccatc ttgggttaagc gtttgccctt ctgccaagc 540
 aatattatct cccatacgta ctgcgaccac atgtctgtag taaagctatc ttgtgccagc 600
 atcaagggtca atgtaatcta tgggtctaag gttgctctcc tgattggagt gtttgacatt 660
 tgttgatat ctttgtctta cactttgatc ctcaaggcag cgatcagcct ctcttcatca 720
 gatgctcggc agaaggcttt cagcacctgc actgccata tatctgccat catcatcacc 780
 tatgttccag cattcttca tttctttgac caccgttttg ggggacacac aattccccct 840
 tctcttcaca tcattgtggc taatctttat cttcttcttc cccaactct aaacctatt 900
 gtttatggag taaagacaaa acagatacgc aagagtgtca taaagttctt ccagggtgat 960
 aagggtgcag gt 972

<210> 404
 <211> 821
 <212> DNA
 <213> Unknown (H38g253 nucleotide)

<220>
 <223> Synthetic construct

<400> 404

gagagaaatc	ccagtgtagc	agaaaagtgc	cttcaaaggga	tgactgattc	ctctcaccat	60
tatcttttagc	ttaactccct	ctcttcaggc	tgtaaatcct	cttgatatact	atcattacga	120
tagggaattt	gggcacgggc	attctcattg	ggatcagtct	cggtttatat	gtctgtctcg	180
cctagatttc	tgctattcac	tttttccatg	ctcagagtc	tagtaaaatg	tttttgaagt	240
acagtgcctgc	ccttctcttt	ctggagtcct	gaagcgcaga	ttaacttctt	cagcatcttg	300
tgtatcacag	agttctttcc	cttggccaca	atggcctatg	atgacaatgt	tgccacttgt	360
gaacctttat	tccacctttt	caccagtttg	agactcaact	ggcatttggt	tgagaaaaac	420
tgtatcttag	agccttcacc	tcagccctcc	cctcaactct	tccgttccac	ctccccctct	480
tcaattccca	cttggtgctca	cttcagtgac	attactttct	gggtcaagtt	gtcctctgaa	540
acatgactcc	caactttaaa	ctccctgatt	tctctaactc	caatgtgaac	ttagtaagcc	600
tgtgctgtcc	aaccatctgc	tgctacccca	tcattttaag	gtcattatca	tcccataact	660
aatctgaaaa	acaaattatt	gataatcatt	tttttccaga	attccactca	ttgctcttta	720
ttttctgttc	agatgaaaat	gtttattaaa	ccatttgagg	tatcactgac	tagttcatta	780
aaagtaaaca	ttgtgtacat	attcccttaa	tcagattctt	t		821

<210> 405

<211> 945

<212> DNA

<213> Unknown (H38g254 nucleotide)

<220>

<223> Synthetic construct

<400> 405

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aggattggaa	gctgcacaac	gctggctagg	ctttcccttc	tgtgttggtat	atctgattgc	120
tcttgttgga	aatcttatca	ttctatttgt	tatctggact	gataaaaacc	ttcaccaacc	180
catgtttctac	tttctggcca	tgctgtcagt	catgacctga	gtctttctac	atctactatc	240
cccaagatgt	tgggcatctt	ctgggtcagc	cttcaggagt	tgtgcttttg	gtgctgtggt	300
gctcaagtct	tttttatcca	ttttttttgc	agtcattggag	agcattgtac	ttcttgtcat	360
gggatttgat	cgctatgtgg	ctatttgcaa	ccccttcagg	tagaccaaga	tcctcaccaa	420
cagaattact	ggtgtgattg	ctatgggtgt	ggttcttaga	agcttatgta	tgattgctcc	480
catcattttt	ctctctcatga	ggctgcctta	ctgtggacat	agaatcatcc	cttataccta	540
ttgtgagcac	atgggagtg	ctcgtctggc	ttgtgccagc	atcagtgtca	atgtctctca	600
tggtcttgga	aatattttta	tcttgtttct	ggatatgttt	cttatcatca	tctcctatgc	660
tagaatttta	tgcacagtct	ttcacctccc	ttcccaagag	gcccacctga	aggctcttaa	720
tacctgtagc	tcccatatct	gtgtcatctt	agcatttttt	ggcccagctc	tcttctctct	780
tctcactcat	cgctttggtc	atggcatccc	acagtatata	catattctcc	tggctaattct	840
ctatatatag	tcattccccc	tgctcttaac	ccagtcattt	atggagttag	gaccaagcaa	900
atccaggagc	gggtagaaaag	tctctttact	aaaaattgat	tgaat		945

<210> 406

<211> 970

<212> DNA

<213> Unknown (H38g255 nucleotide)

<220>

<223> Synthetic construct

<400> 406

gtggaaaatt	cacccatggg	gactgacttc	atcttttctc	gcatgacaga	taactctcag	60
cttgaagtcc	tgctatttgg	agtctttctt	attgcttaca	tcactactgt	gttggagaat	120
ctaggccttg	tggttctgat	cagagtcagc	tcccgcctcc	acaccccatg	tactttttcc	180
tctctaatac	gtccttcctt	gatgtctggt	tctcttccat	tacaattcca	cagaatttag	240
cacatttggt	ttctaagctg	cagtatgttt	ctttcctttt	cccgtataac	ttaaatgagc	300
ttgtttgtaa	tctttgcctc	tgctgaatgc	aattttttta	acttgcatgg	cctatgaccg	360
ctttactgcc	atctgtcacc	cactgttcta	ccacattacc	atgtcaagag	gccattatct	420
tttcttggtg	gcaggatgct	accttggtgg	gttagttaag	atggtcactg	tgacaacttc	480
catcacacaa	ctatcgcttt	gtcaaccatg	tgctctccct	gccttcttct	gtgacattcc	540

ctcattgttg	gtactgggtt	gctcagatcc	ttggatcacc	tcccgatctt	ggtgggttggc	600
tgtgggggat	tcaccctggg	cacctctgtt	gtggatgacc	ttgtctccta	catgtcttcc	660
ctcatgacta	tcctaggaat	tcccttagct	tctggaaaac	agagagcctt	ctccacctgt	720
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gcctcgcgac	atggatccgg	ggcaggaaat	cagattgtgt	cagtatttta	tacaatggtg	840
atccccatgt	taaatcctct	catctatagt	ttgagaaatg	aggaagtgaa	agttgcctta	900
tgaaaaacat	tgagacatag	tcttaaatct	tctattgagt	gtctcaaaaa	tgcaaaatat	960
tctgtgaaga						970

<210> 407

<211> 934

<212> DNA

<213> Unknown (H38g256 nucleotide)

<220>

<223> Synthetic construct

<400> 407

tggcttgatg	aaaaaaaaaaca	agattctaac	gtgacagaac	ttgttcttct	gggcctatca	60
tcttcttggg	agctgcagct	atttctctta	ttactatttt	tgttttttta	cattgctatt	120
gtcctgggaa	acctcttgat	agtggtaaca	gtgcaagccc	atgctcatct	gctccaatct	180
cctatgtatt	attttttagg	tcatctctct	ttcattgacc	tatgcctaag	ctgtgttact	240
ctgccaaaaga	tgtaggggga	tttctacag	cagggcaaga	gcatctcttt	ttcaggatgc	300
ctggcccaga	tctacttcct	ccactttcta	ggagccagtg	agatgttttt	gctgacagtt	360
atggcctatg	acaggatgtg	tgccatctgt	aaccctttgc	gctaccttat	aagtcatgaa	420
ccccagcta	tgcctttggg	tggttcttgc	ctgctgggtg	gggggtttta	tccactctat	480
catgcaggtc	atactagtca	tccagctgcc	tttctgtggc	cccaatgaac	tggacaactt	540
ctactgtgat	gtcccacagg	tcatcaagct	ggcctgcatg	gacacctatg	tggtagaggt	600
gctgatgata	gccaacagtg	gtctgctctc	tcttgtctgc	ttcttgggtc	tactattctc	660
ttatgctgtc	atcctgatca	ccctgagaac	acacttcggc	cagggccaga	acaagttcct	720
ctctacctgt	gcttctcacc	tgacagtggg	cagcctgacg	ttcatgccat	gtatattcat	780
ctatttgagg	cctttctgca	gcttctctgt	ggataagata	ttctccatgt	tttacacagt	840
gatgacacct	atgttgagcc	ccctcatcta	cacactcaga	aatgctgata	tgaagacagc	900
tatgaagaag	ctgaggataa	aacctatgta	catt			934

<210> 408

<211> 954

<212> DNA

<213> Unknown (H38g257 nucleotide)

<220>

<223> Synthetic construct

<400> 408

atgatgggtg	atcccaatgg	caatgaatcc	agtgtacat	acttcatcct	aataggcctc	60
cctgggttag	aagaggctca	gttctgggtg	gccttcccat	tgtgtccct	ctaccttatt	120
gctgtgctag	gtaacttgac	aatcatctac	attgtgcgga	ctgagcacag	cctgcatgag	180
cccattgata	tatttctttg	catgctttca	ggcattgaca	tcctcatctc	cacctcatcc	240
atgccccaaa	tgctggccat	cttctgggtc	aattccacta	ccatccagtt	tgatgcttgt	300
ctgtacaga	tgtttgccat	ccactcctta	tctggcatgg	aatccacagt	gctgtggccc	360
atggcctttg	accgctatgt	ggccatctgt	cacccactgc	gccatgccac	agtacttacg	420
ttgcctcgtg	tcacaaaaat	tgggtgtggc	gctgtgggtg	ggggggctgc	actgatggca	480
ccccttctctg	tcttcatcaa	gcagctgccc	ttctgcccgt	ccaatatcct	ttcccattcc	540
tactgcctac	accaagatgt	catgaagctg	gcctgtgatg	atatccgggt	caatgtcgtc	600
tatggcctta	tgctgcctta	ctccgccatt	ggcctggact	cacttctcat	ctccttctca	660
tatctgctta	ttcttaagac	tgtgttgggc	ttgacacgtg	aagcccaggc	caaggcattt	720
ggcacttgcg	tctctcatgt	gtgtgctgtg	ttcatattct	atgtaccttt	cattggattg	780
tccatgggtg	atcgcttttag	caagcggcgt	gactctccgc	tgcccgtcat	cttggccaat	840
atctatctgc	tgggttctcc	tgtgtctaac	ccaattgtct	atggagtga	gacaaaggag	900
attcgacagc	gcacccctcg	acttttccat	gtggccacac	acgcttcaga	gccc	954

<210> 409
 <211> 959
 <212> DNA
 <213> Unknown (H38g258 nucleotid)

<220>
 <223> Synthetic construct

<400> 409

atgtcttcca	gactaatgaa	tgtgttcagc	atggaaacta	tcaattttgt	tagctgcctt	60
atcctcatgg	gctttccctc	aagcccagaa	atgcagctcc	tctacttcgg	tctcttctca	120
gtagcctata	ctctcaccce	gatgggaaat	gcagccattg	tctgtgctgt	gtggtaggac	180
cagcaccttc	acactcccat	gtacaccctc	ttgggaaatt	tctctctcct	ggaaatatgt	240
tatgttactg	caactaaact	gctggccaac	ttcctctcca	caagcaagtc	catctcattc	300
atgagttgtt	ttgcacagtt	ctacttcttc	tctttgggggt	atgatgaggg	cttcttcctt	360
tgcacacagg	cctttgacag	gtatcttgcc	atctgccgcc	ctctacgtta	tccatgcac	420
atgactaaac	aagtatgcac	tggcctcatc	atcttttgc	ggatcatgtg	ctttgtaatc	480
ttcctaactc	tgggtgattct	catttcacag	ctatcctact	gtggcccaaa	tattatcaac	540
cattttattt	gtgatcccg	cccattgaag	atgctgtcct	gttctgaaga	catcatcatc	600
accagctcca	tttactccac	attcaattct	gtcttcataa	ttggcacctt	tctctttatc	660
ctttgttcct	atgctctgg	gattctggct	ataatacgg	tgccttcaga	ggcttgcaaa	720
cgaaaagctt	tctccacttg	tgcctctcat	ttggcagttg	tcaccttatt	ttatggctct	780
atcatgggtga	tgtatgtag	tcctggatca	gcacaccag	taaaaatgaa	aaaatcatta	840
ccttggtctt	ttctgtgata	acaccactct	gtaatcctct	aatatatagt	ctcaggaaca	900
aagagatgaa	agattatctg	aggaaaatct	tcaggactgg	aaaagatggt	aataaaata	959

<210> 410
 <211> 926
 <212> DNA
 <213> Unknown (H38g259 nucleotide)

<220>
 <223> Synthetic construct

<400> 410

atgctgaata	caacctcagt	cactgaattt	ctccttttgg	gagtgacaga	cattcaagaa	60
ctgcagcctt	ttctcttcgt	tggtttccct	accatctact	tcacagtggt	ggctgggaat	120
ggagccattc	tgatgattgt	catctctgat	cctagactcc	attcccctat	gtattttctc	180
ctgggaaacc	tgtcctgcct	ggacatctgc	tactccagcg	taacactgcc	aaaaatgctg	240
cagaacttcc	tctctgcaca	caaagcaatt	tctttcttgg	gatgcataag	ccaactccat	300
ttcttccact	tcctgggcag	cacagaggcc	atgttggttg	ccgtgatggc	atttgaccgc	360
tttgtggcta	tttgcaagcc	acttcgctac	actgtcatta	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	gatgattggt	ttttccatg	ccctgctgca	ctccctaagt	480
acctctcgct	tgaacttctg	tggttctaac	cgtatctatc	acttcttctg	tgatgtgaag	540
ccattgctaa	agctgagctt	aatcagtggt	tgctcagtac	tgtcacaggg	acaatcgcca	600
tgggcccctt	ctttctcaca	ttactctcct	atctctacat	tatcaccat	ctcttcttca	660
agactcattc	ttttagcatg	ctccgcaaag	cactgtccac	ttgtgcctcc	cacttcattg	720
tagttattct	tttgtatgca	cctgttctct	tcacctatat	tcacatgccc	tcagggacct	780
ccatggacca	ggaccggatc	actgccatca	tgtatactgt	ggtcactcca	gtactaaacc	840
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ggtggccttg	gcctaaagaa	atcttg				926

<210> 411
 <211> 994
 <212> DNA
 <213> Unknown (H38g260 nucleotide)

<220>
 <223> Synthetic construct

<400> 411

atggaaagcg	agaacagAAC	agtgataaga	gaattcatcc	tccttcgttt	gacccagttt	60
cgagatattt	agctcctggt	ctttgtgcta	gttttaatat	tctacttctt	catcctccct	120
ggaaattttc	tcattatttt	caccataagg	tcagaccctg	ggctcacagc	ccccctctat	180
ttattttctgg	gcaacttggc	cttcctggat	gcatcctact	ccttcattgt	ggctcccagg	240
atgttggtgg	acttcctctc	tgagaagaag	gtaatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcacttctt	tggaggaggg	gagggattac	tccctgttgt	gatggccttt	360
gaccgctaca	tcaccatctg	cctgcctctg	cagtatttca	ctgtcatgaa	ctctagagcc	420
tgtatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatca	tccgcttgcc	ttttgtggc	ccaaaccagc	tggacaactt	cttctgtgat	540
gtccgacagg	tcataagct	ggcttgacc	gacatgtttg	tggaggagct	tctgatggtc	600
ttcaatagtg	gcctgatgac	actcatgtgc	ttctctgggac	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagc	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacatgc	720
accacccata	tcattgttat	attcttcatg	tttggacctg	gcatcttcat	ctacacgtgc	780
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ttgttgaaatc	ctgtcattta	tacccttcat	aaccaggaag	tgaaagcttc	catgaaaaag	900
gtgtttaata	aacacatagc	ctgaaaaagg	gcaaaaaaaa	aaagaagaaa	aatagactgt	960
agaattttat	ctgaaattga	tttgtttatt	tcca			994

<210> 412

<211> 945

<212> DNA

<213> Unknown (H38g261 nucleotide)

<220>

<223> Synthetic construct

<400> 412

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggcttctat	60
gacatccctg	aactgcattt	cttgtttttt	attgtattca	ctgctgtcta	tgtcttcate	120
atcatagggg	atatgctgat	tattgtagca	gtggtagct	cccagaggct	ccacaaaccc	180
atgtatattt	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
ccaaaaatgc	tggagggtct	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggcccaga	420
cggtacatgg	ggctgggtgg	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
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ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgct	gagagtctct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgctcct	cccacctagc	tgtagtgacc	acattctatg	gaacgctcat	gatcttttat	780
gttgacacct	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctcctt	gctctacact	840
gtggtcaccc	ctctcttcaa	tctgtgatc	tataccatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

<210> 413

<211> 936

<212> DNA

<213> Unknown (H38g262 nucleotide)

<220>

<223> Synthetic construct

<400> 413

atgagtgcAA	acacctccat	ggtgactgag	tttcttcttc	tgggttcttc	ccacctggcc	60
gacctccagg	gcttgctctt	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatttcctca	ttgtgggtgct	ggtctccact	gatgctgccc	tccagtcccc	tatgtacttc	180
ttctctgcga	ccctctcggc	cttggagatt	ggctatacgt	ctgtcacggg	ccccctgcta	240
cttcaccacc	tccttactgg	cgggcgccac	atctctcgct	ctggatgtgc	tctccagatg	300
ttcttcttcc	tcttcttttg	cgccacggag	tgctgcctcc	tggcagccat	ggcctatgac	360
cgctatgcag	ccatctgtga	acccctccgc	taccactgc	tgctgagcca	ccgggtgtgt	420
ctacagctag	ctgggtcggc	gtgggcctgt	ggggtgctgg	tggggctggg	ccacaccctt	480

ttcatcttct	ctttgccctt	ctgcgccccc	aataccatcc	cgcagttctt	ctgtgagatc	540
cagcctgtcc	tgcagctggg	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
gcaacagccc	tcctcaccct	ctgccccctt	ggcctcatcc	tgggctccta	cgggcgtatc	660
ctcgttacca	tcttcgggat	cccatctgtt	gcgggccgcc	gcaaggcctt	ctccacctgc	720
tcttcccacc	tgatcgtggg	ctccctcttc	tatggcaccg	cactctttat	ctatatctgc	780
cctaaggcca	gctacgatcc	ggccactgac	cctctggtgt	ccctcttcta	tgctgtggtc	840
acccccatcc	tcaaccccat	catctacagc	ctgcggaaca	cagagggtcaa	agctgcccta	900
aagagaacca	tccagaaaac	ggtgcctatg	gagatt			936

<210> 414

<211> 948

<212> DNA

<213> Unknown (H38g263 nucleotide)

<220>

<223> Synthetic construct

<400> 414

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ctggaaagga	ctctctttgt	ggttgtcttc	acttctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tctgtctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttgtgtccc	ccagatgctg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttctctg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctcctga	cagtgatggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctggttcaat	cgatagtcca	gacaccatcc	480
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tctctgattc	gactctcctg	tggagatacc	tcctacaatg	aaatccagtt	ggctgtgtcc	600
agtgtcatct	tctgtggtgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtgc	tgaggattaa	ctctgccaca	gcatggagaa	aggcctttgg	gacctgtctc	720
tcccatctca	ctgtgggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcaact	840
ccttcaacta	accctctcgt	atacacctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaaag	agactccagg	gaaagctgga	gagctgct		948

<210> 415

<211> 954

<212> DNA

<213> Unknown (H38g264 nucleotide)

<220>

<223> Synthetic construct

<400> 415

atgaagagcg	aactgaacag	gaattactca	gaggtgacag	agttttattct	gctgggattc	60
agaacatcgc	cagaagcaca	gattctctta	ttcttctctg	tcttgcttat	ctacatggtc	120
attgtgttga	gaaatctcag	catgttagtt	gtcattgaaa	tagactccag	acttcacaca	180
cctgtgtatt	tctttctcag	aaatttgtcc	tatttggatc	tccgctactc	cacagttatt	240
gcttccaaaa	ctgactactt	tattttccaa	ggaaaagaaa	atttcttaca	atggttgagc	300
aacacagttg	tttttctttg	ctctctttgt	tgggactgaa	ggtttttttc	tggatatgat	360
ggcatatgat	cgcttctcag	ctatttgttc	acctttcttc	tatactgtat	gtatgtctca	420
gcaagcttgt	gtttgtttgg	tggttggtc	ctctatctgt	ggatgcatca	actccatgat	480
acaaacaggt	tttaccttca	gtttgcattt	ctgtggagaa	aacagattag	agcacttttt	540
ctgtgatgtc	tcagtcatga	tcaagatctc	atgtattgac	atccttgtga	atgaggtagt	600
actgtttatt	ctctctgtct	tcatcaccac	caccacaact	gtcattctgg	cttccctatgt	660
gcatactctc	tccactgtcc	tgaagattct	ctcaaccac	ggcagaagga	agactttctc	720
cacttgcagc	tctcacatca	ctgtggtgag	tttattctat	ggaactgtat	tcttcatgta	780
tgcccaacct	ggggccatct	ccaaagagca	aggttatagt	tgtattctaa	actcttgtca	840
tccctatgtt	aaatatctga	tttatagtct	aagaaatagg	tgcaaaatgc	tttgaaaagg	900
acattgataa	gaaaaatata	ttttcattgg	cctctagcca	tctataaaac	tata	954

<210> 416
 <211> 531
 <212> DNA
 <213> Unknown (H38g265 nucleotide)

<220>
 <223> Synthetic construct

<400> 416
 atgagcccaa gaatgtgcct ttcatttctg gctgttgccct ggacccttgg tgtcagtcac 60
 tccctgttcc aactggcatt tcttgtaaat ttacccttct gtggccctaa tgtgttggac 120
 agcttctact gtgaccttcc tcggcttctc agactagcct gtaccgacac ctacagattg 180
 cagttcatgg tcaactgttaa cagtgggttt atctgtgtgg gtactttctt catacttcta 240
 atctcctaca tcttcatcct gtttactgtt tggaaacatt cctcaggtgg ttcattccaag 300
 gccctttcca ctctttcagc tcacagcaca gcggctcttt tgttctttgg tccacctatg 360
 tttgtgtata catggccaca ccctaattca cagatggaca agtttctggc tattttttgat 420
 gcagttctca ctcttttctt gaatccagtt gtctatacat tcaggaataa ggagatgaag 480
 gcagcaataa agagagtatg caaacagcta gtgatttaca agaagatctc a 531

<210> 417
 <211> 965
 <212> DNA
 <213> Unknown (H38g266 nucleotide)

<220>
 <223> Synthetic construct

<400> 417
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 cctgaactgc agcccgctct ctttgggctg ttcctgtcca tgtacctggt cacggtgctg 120
 gggaacctgc tcatcattct ggccgtcagc tctgactccc acctccacac ccccatgtac 180
 ttcttctctc ccaacctgtc ctttgttgag atctgtttca tctccaccac agtccccaag 240
 atgctagtga gcatccaggc acggagcaaa gacatctcct acatgggggtg cctcactcag 300
 gtgtattttt taatgatgtt tgctggaatg gatactttcc tactggccgt gatggcctat 360
 gaccggtttg tggccatctg ccaccactg cactacacgg tcatcatgaa cccctgcctc 420
 tgtggcctcc tggttctggc atcttggttc atcattttct ggttctccct ggttcatatt 480
 ctactgatga agagggtgac ctctccaca ggcactgaga ttccgcattt cttctgtgaa 540
 ccggctcagg tcctcaagggt ggctgtctct aacaccttcc tcaataacat tgtcttgtat 600
 gtggccacgg cactgctggg tgtgtttcct gtagctggga tcctcttctc ctactctcag 660
 attgtctcct ccttaattggg aatgtcctcc accaagggca agtacaaagc cttttccacc 720
 tgtggatctc acctctgtgt ggtctccttg ttctatggaa caggacttgg ggtctatctg 780
 agttctgctg tgaccattc ttcccagagc agctccaccg cctcagtgat gtacgccatg 840
 gtcaccccca tgctgaacct ctcatctac agcctgagga acaaggatgt gaagggggcc 900
 ctggaaagac tcctcagcag ggccgactct tgtccatgac aaatcagggc ctcagaacta 960
 agagg 965

<210> 418
 <211> 967
 <212> DNA
 <213> Unknown (H38g267 nucleotide)

<220>
 <223> Synthetic construct

<400> 418
 tacacagagc cagagaatct cacaggtgtc ttagaattcc tgctcctggg actcccagat 60
 gatccagaac tgcagcccggt cctcttttggg ctgttctctgt ccatgtacct ggtcatggtg 120
 ctggggaacc tgctcatcat tctggccgtc agctctgact cccatctcca cagcccatg 180
 tactttctcc tctccaacct gtccttgggt gacatcgggt ttgcctctac tactgtcccc 240
 aagatgattg tggacatcca ggctcatagt agactcatct cttacgtggg ctgcctgact 300
 cagatgtctt ttttgcattt tttgcagatg atggaaagtc tgctcctgat tgtgatggcc 360

tatgaccggt	tctgtggccat	ctgtcacccc	ctgcactacc	aagtcacat	gagcccacga	420
ctctgtggct	tcttagtttt	ggtgtctttt	tttcttagcc	ttttggactc	tcagctgcac	480
gatttqattg	tgttacaact	tacctgcttc	aacgatgtgg	aaatctctaa	tttttttctg	540
tgacccttct	taactttctca	agctggcctg	ttctgacacc	tccattaata	acatgggtgt	600
atattttatt	ggtgccatat	ttggttttct	ccctctctta	gggacccctt	tctcttacta	660
taaaattggt	tcttccatc	tgagagttct	ctcttcaggt	gggaagtata	aagccttctc	720
cacctgcagc	tctcacctgt	cagttgtttg	cttactttat	ggaacagccc	ttggagggtta	780
cctcagttca	gctgtgtccc	tttctccag	gaaggggtgca	gtggcctcag	taatgtacat	840
ggtggtcacc	cccatgctga	accccttcat	ctacagcctg	agaaacaggg	acattcaaag	900
tgccctgcag	aggctgcacg	gcagaataat	gtaatctcct	tatctgttgc	atcttttttg	960
tagtatt						967

<210> 419

<211> 924

<212> DNA

<213> Unknown (H38g268 nucleotide)

<220>

<223> Synthetic construct

<400> 419

atgagacaga	taaatcagac	acaagtgaca	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atztatcgta	ttattgggtg	tctacctggg	cactgtgctt	120
ggaaatctgc	ttctaacttc	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgtc	tctggctgac	ctctgtttct	ctaccaacat	agttcctcag	240
gcactagtcc	acctgctttc	cagaaagaag	gtcattgcat	tcacactttg	cgcagctcga	300
cttctctttt	tcctcatatt	tgggtgtacc	cagtgcgccc	ttcttgacag	gatgtcctat	360
gatcgctatg	ttgcaatctg	caatcctctg	cgttaccctg	acatcatgac	ctggaaagtg	420
tgtgtccagc	tggcaacagg	atcatggacc	agtggcattc	tgggtgtctg	ggtagacacc	480
accttcacac	tgaggctacc	ctaccgaggc	agtaacagca	ttgctcattt	cttttgtgag	540
gcccctgcac	tattgatctt	agcatccaca	gacacccatg	catcagagat	ggccattttt	600
cttacggggg	ttgtgattct	cctcatacct	gtttttctga	ttctgggtatc	ctatggccgt	660
atcatagtaa	ctgtgggtcaa	gatgaagtca	actgtgggga	gtctcaaggc	attttctacc	720
tgtggctccc	acctcatggg	ggtcatactt	ttttatggat	cagcaattat	cacttacatg	780
acacccaagt	cttccaaaca	gcaggaaaaa	tgggtgtctg	ttttctatgc	aatagtgcct	840
cccatgctga	atccccctcat	ctatagcctg	agaaacaagg	atgtgaaggc	agctctgagg	900
aaagtagcca	caaggaattt	ccca				924

<210> 420

<211> 954

<212> DNA

<213> Unknown (H38g269 nucleotide)

<220>

<223> Synthetic construct

<400> 420

atgcccatac	ttatggctat	aggaaactgg	acagaaataa	gtgaatttat	cctcatgagc	60
ttctcttccc	tacctactga	aatacagtca	ttgctcttcc	tgacatttct	aactatctat	120
ttggttactc	tgaaggga	cagcctcatc	attctgggta	ccctagctga	ccccatgcta	180
cacagcccga	tgtacttctt	cctcagaaac	ttatctttcc	tggagattgg	cttcaacctta	240
gtcatttgtc	ccaaaatgct	ggggaccctg	cttgcccagg	acacaacccat	ctccttctct	300
ggctgtgcca	ctcagatgta	tttcttcttc	ttctttgggg	tagctgaatg	cttctctctg	360
gctaccatgg	catatgaccg	ctatgtggcc	atctgcagtc	ccttgactta	cccagtcctc	420
atgaacaaa	ggacacgggc	caaactggct	gctgcttcc	ggttcccagg	ctttctctgta	480
gctactgtgc	agaccacatg	gctcttcagt	tttccattct	gtggcaccaa	caaggtgaac	540
cacttcttct	gtgacagccc	gcctgtgctg	aagctggctc	gtgcagacac	agcactgttt	600
gagatctacg	ccatcgctcg	aaccattctg	gtggtcatga	tcccctgctt	gctgatcttg	660
tgttctctata	ctcgctattg	tgtgctatc	ctcaagatcc	catcagctaa	agggagcatc	720
aaagccttct	ctacgtgtc	ctcacacctc	cttgttgtct	ctcttttcta	tatatcttct	780
agcctcacct	acttctggcc	taaatcaaat	aattctcctg	agagcaagaa	gttggttatca	840

ttatcctaca ctgttgtagac tcccatgttg aaccccatta tctacagctt gagaaatagc 900
gagggtgaaga atgccctcag caggaccttc cacaaggtcc tagccctcag aaac 954

<210> 421

<211> 780

<212> DNA

<213> Unknown (H38g270 nucleotide)

<220>

<223> Synthetic construct

<400> 421

gcccaccttt	ccttcctgga	cctcagtttc	accaccagct	ccatcccca	gctgctctac	60
aaccttaatg	gatgtgacaa	gaccatcagc	tacatgggct	gtgccatcca	gctcttcctg	120
ttcctgggtc	tgggtgggtg	ggagtgcctg	cttctggctg	tcatggccta	tgaccgggtg	180
gtggctatct	gcaagcccct	gcactacatg	gtgatcatga	accccaggct	ctgccggggc	240
ttgggtgcag	tgacctggag	ctgtgggggtg	gccaactcct	tggccatgtc	tcctgtgacc	300
ctgcgcttac	cccgcgtgtg	gcaccacgag	gtggaccact	tcctgcgtga	gatgcccgcc	360
ctgatccgga	tggcctgcgt	cagcactgtg	gccatcgaag	gcaccgtctt	tgtcctggcg	420
gtgggtgttg	tgctgtcccc	cttgggtgtt	atcctgctct	cttacagcta	cattgtgagg	480
gctgtgttac	aaattcgggc	agcatcagga	aggcagaagg	ccttcggcac	ctgcggctcc	540
catctcactg	tgggtctcct	tttctatgga	aacatcatct	acatgtacat	gcagccagga	600
gccagttctt	cccaggacca	gggcatgttc	ctcatgctct	tctacaacat	tgtcaccccc	660
ctcctcaatc	ctctcatcta	caccctcaga	aacagagagg	tgaagggggc	actgggaagg	720
ttgcttctgg	ggaagagaga	gctaggaaag	gagtaaaggc	atctccacct	gacttcactt	780

<210> 422

<211> 985

<212> DNA

<213> Unknown (H38g271 nucleotide)

<220>

<223> Synthetic construct

<400> 422

gaagagatat	tatgaataat	atcccagcat	gtacacacag	ggtgtgtaca	gattaagaac	60
tgcagcccat	cctctttggg	ctgttctctg	ccatgtgcct	ggtcatgggtg	ctggggaacc	120
ttctcatcat	cctggccgtc	agctctgact	cccacctcca	cacccccacg	tactttttcc	180
tctccaacct	gtccttggtg	gacatcggtt	tcccctccac	cactgtcccc	aagatgattg	240
tggacatcca	gtctcacagc	agagtcacat	cctatgcggg	ctgcctgact	cagatatctc	300
tttttgcgtg	ttttggatgc	atggaagaca	tgcttctgag	tgtgatgggt	tatgaccggt	360
ttgtggccat	ctgtcaccc	ctggattatc	cagtcacatc	gaacccatgt	ttctgtgggt	420
tcctgggttt	gttgtctttt	ttttctcagt	cttttagact	tccagctgca	caattggatt	480
gccttacaaa	ttacctgctt	caaggatgtg	gaaattccca	gtttcttctg	tgacctttct	540
caactcccc	accttgccctg	ttgtgacacc	ttcaccaaca	acatagtcac	gtatttctct	600
gctgccatac	ttgggtttct	tcccatctcg	gggatctttt	ctcttactat	aaaattgttt	660
cctccattct	gaaggtttca	tcatcagggtg	ggaagtataa	agccttctcc	acctgtgggt	720
ctcacctgtc	agttgtttgc	ttattttatg	gaacagccct	tggagggtac	ctcagttcag	780
acatgtcttc	ttatcccaga	aagggtgcag	tggcttcagt	gatgtacaca	gtggtcgccc	840
ccatgctgaa	cccgttcatc	tacagcctga	gaaaaaggga	cattaaaagt	gccctgcagc	900
agctgcatgg	cagaatagtc	taatctcatg	atcttattat	cggttccatt	ctttagcatg	960
ggttggaaaa	ggcagcaagg	tcaaa				985

<210> 423

<211> 963

<212> DNA

<213> Unknown (H38g272 nucleotide)

<220>

<223> Synthetic construct

<400> 423

atggaatctc	ctaatacacac	tgatgttgac	ccttctgtct	tcttctctct	gggcatccca	60
ggtctggaac	aatttcaatt	gtggctctca	ctccctgtgt	gtggcttagg	cacagccaca	120
attgtgggca	atataactat	tctgggtgtt	gttgccactg	aaccagtctt	gcacaagcct	180
gtgtaccttt	ttctgtgcat	gcctcaacc	atcgacttgg	ctgcctctgt	ctccacagtt	240
cccaagctac	tggtatctt	ctgggtgga	gcggacata	tatctgcctc	tgctgacctg	300
gcacagatgt	tcttcatlca	tgcttctgc	atgatggagt	ccactgtgct	actggccatg	360
gcctttgac	gctacgtggc	catctgccac	ccactccgt	atgccacaat	cctcactgac	420
accatcattg	cccacatagg	ggtggcagct	gtagtgcgag	gctccctgct	catgctccca	480
tgtcccttcc	ttattgggag	tttgaacttc	tgccaaagcc	atgtgatcct	acacacgtac	540
tgtgagcaca	tggtgtgggt	gaagctggcc	tgtggagaca	ccaggcctaa	ccgtgtgtat	600
gggtgacag	ctgcactgtt	ggtcattggg	gttgacttgt	tttgattgg	tctctctat	660
gccctaagtg	cacaagctgt	ccttcgcctc	tcattccatg	aagctcggtc	caaggcccta	720
gggacctgtg	gttcccattg	ctgtgtcctc	ctcatctctt	atacaccagc	cctcttctcc	780
ttttttacac	accgctttgg	ccatcacgtt	ccagtccata	ttcacattct	tttggccaat	840
gtttatctgc	ttttgccacc	tgctcttaat	cctgtggtat	atggagttaa	gaccaaagag	900
atccgtaaaa	gagttgtcag	ggtgtttcaa	agtgggcagg	gaatgggcat	caaggcatct	960
gag						963

<210> 424

<211> 982

<212> DNA

<213> Unknown (H38g273 nucleotide)

<220>

<223> Synthetic construct

<400> 424

atgacatgga	gtggcggaac	catagtggga	gagtgagtga	gtttgtgttg	ctggggcttc	60
cctgtctctg	cgccactaca	ggtactattg	tttgcccttt	tgctgctggc	ctatgtgttg	120
gtgctgactg	agaacacact	catcattatg	gcaattagga	accattccac	cctccacaaa	180
cccatgtact	tttttctagc	taatatgtcc	tttctggaga	tctgggtatg	cactgtcact	240
attcccaaga	tgcttgctgg	ctttgttgga	tccaaacagg	atcatggaca	gctaattctcc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggtc	tggtgctgac	tgagtgtgtc	360
cttctcgctg	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420
gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tgagggtttt	480
ggcatctcca	tggtcaaaag	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtcaacc	tctcatgcac	tgatatgtcc	600
acagcagagc	ttacagattt	catcctggcc	atttttatte	ttctaggggc	actctctgtc	660
actggggcct	cctatgtggc	cattactggt	gctgtgatgc	acataccttc	ggctgtgtga	720
cgctataagg	ccttttccac	ctgtgcctct	catctcactg	ttgtgataat	cttctatgca	780
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gtctctgtac	tgtatgtgtg	cattgtacca	ttgtcaatc	ccatcattta	ctgcctgcgc	900
aatcaagagg	tcaagagagc	cctatgctgt	actctgcacc	ctgtaccagc	accaggatcc	960
tgaccccaag	aaagctagca	ga				982

<210> 425

<211> 936

<212> DNA

<213> Unknown (H38g274 nucleotide)

<220>

<223> Synthetic construct

<400> 425

atggaagcag	gaaaccaaac	aggattttta	gagtttatcc	ttctcggact	ctctgaggat	60
ccagaactac	agccgttcat	atttgggctg	ttcctgtcca	tgtacctggt	gacgggtgctg	120
ggaaacctgc	tcattatcct	ggccatcagc	tctgactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ctgggttgac	atctgtttca	gcatttgcac	cgtccccaag	240
atgctggtga	atcatccagc	cgagaacaaa	gccatctcct	acatggactg	cctcacacag	300
gtctattttc	ccatgttttt	tcctattctg	gacacgctac	tcctgaccgt	gatggcctat	360

gaccggtttg	tggtgtgtctg	ccaccctctg	cactatatga	tcatcatgaa	ccccacctc	420
tgtggcctcc	tggtttttgt	cacctggctc	attggtgtca	tgacatccct	cctccatatt	480
tctctgatga	tgcatctaat	cttctgtaaa	gattttgaaa	ttccacattt	tttctgcgaa	540
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tttatgacgg	gtgtgctggg	cgtttttccc	ctccttggga	tcattttctc	ttattcacga	660
attgcttcaa	ccataaggaa	gatgtcctca	tctgggggaa	aacaaaaagc	actttccacc	720
tgtgggtctc	acctctccgt	cgtttcttta	ttttatggga	caggcattgg	gggccacttc	780
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gtcaccccca	tggtgaaccc	cttcatctac	agcctgagga	acaaggatgt	gaagggagcc	900
ctggggagtc	tcctcagcag	ggcagcctct	tgtttg			936

<210> 426

<211> 960

<212> DNA

<213> Unknown (H38g275 nucleotide)

<220>

<223> Synthetic construct

<400> 426

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ggcatggagg	acaaacacag	atggatatct	atccccctct	cctccatgta	tttcattatg	120
gtgcttggga	actgcaccat	cctcctcacc	atctccacag	agcgctccct	gcacaaaccc	180
atgttcctgc	tcctctgtct	gttggccctc	acagacctgg	gcattgtctac	aaccaccatt	240
cccaagggtgc	tgtgcatttt	ctggtttggc	cagagtggga	tcagctatga	aggatgcctg	300
gttcagctgt	tcttcatcca	ctccatctct	gccatgcagt	cagctgtcct	gatgaccatg	360
gcctttgacc	actatgtggc	catctgcaag	cccttgcgct	atgccaccat	cctttccaat	420
agttgcactg	gactcattgg	cttagtgagt	ttggtgagag	ctatcctctt	tattctcccc	480
atgcccattc	tccttcagca	aatgccttat	catgccaatc	gtgtcatccc	caccacctcc	540
tgtgagcaca	tggtgtgggt	gaagatgggt	tgtgtagata	ctacagtcaa	caggatatat	600
ggcctgggtg	tggccttggt	ggttgctggc	tagatctctc	agctattgct	tcattcttatg	660
tgctaattcat	ccaggctata	atgcatctct	cttctaagga	agcccaccac	aaagcagtea	720
acacctgcac	cacacacatc	tgtgtcatgc	ttatttctta	tactccctca	cttttctctt	780
ttctcgctca	ccgctttggc	caaggcattc	caccccatgt	ccacatcatt	cttgggaacc	840
tttacttctt	tgtacctcca	atgctcagtc	ctataattta	tggagtgaag	actaaggagt	900
tctggggacaa	agtgaccaaa	taggggttgct	ggaaagaaga	accacaaccc	actgaccatg	960

<210> 427

<211> 948

<212> DNA

<213> Unknown (H38g276 nucleotide)

<220>

<223> Synthetic construct

<400> 427

atggagctct	ggaacttcac	cttgggaagt	ggcttcattt	tggtggggat	tctgaatgac	60
agtgggtctc	ctgaactgct	ctgtgtcaca	attacaatcc	tatacttggt	ggccctgac	120
agcaatggcc	tactgtctct	ggctatcacc	atggaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	tctcatggac	ctcctgttca	catctgttgt	cactcccaag	240
gcccttgccg	actttctgcy	cagagaaaaac	accatctcct	ttggaggctg	tgcccttcag	300
atgttcctgg	cactgacaat	gggtggtgct	gaggacctcc	tactggcctt	catggcctat	360
gacagggtatg	tggccatttg	tcatcctctg	acatacatga	ccctcatgag	ctcaagagcc	420
tgctggctca	tggtggccac	gtcctggatc	ctggcatccc	taagtgcctt	aatatatacc	480
gtgtatacca	tgactatccc	cttctgcagg	gccaggaga	tcaggcatct	tctctgtgag	540
atcccacact	tgctgaagg	ggcctgtgct	gatactcca	gatatgagct	catggtatat	600
gtgatgggtg	tgaccttctt	gattccctct	cttctgctca	tactggcctc	ctatacaca	660
attctactca	ctgtgtctca	tatgccatca	aatgagggga	ggaagaaagc	ccttgctcacc	720
tgctcttccc	acctgactgt	ggttgggatg	ttctatggag	ctgccacatt	catgtatgtc	780
ttgccaggtt	ccttccacag	caccagacaa	gacaacatca	tctctgtttt	ctacacaatt	840
gtcactccag	ccctgaatcc	actcatctac	agcctgagga	ataaggaggt	catgcggggc	900

ttgaggaggg tcctgggaaa atacatgctg ccagcacact ccacgctc

948

<210> 428

<211> 936

<212> DNA

<213> Unknown (H38g277 nucleotide)

<220>

<223> Synthetic construct

<400> 428

atgaaagcag	gaaacttctc	agacactcca	gaattctttc	tcttgggatt	gtcaggggat	60
ccggagctgc	agcccatcct	cttcattgctg	ttcctgtcca	tgtacctggc	cacaatgctg	120
gggaacctgc	tcatcatcct	ggcgtcaac	tctgactccc	acctccacac	ccccatgtac	180
ttcctcctct	ctatcctgtc	cttggtcgac	atctgtttca	cctccaccac	gatgcccagg	240
atgctggtga	acatccaggc	acaggctcaa	tccatcaatt	acacaggctg	cctcacccaa	300
atctgctttg	tcctgggtttt	tgttggattg	gaaaatggaa	ttctgggtcat	gatggcctat	360
gatcgatttg	tggccatctg	tcacccactg	aggtacaatg	tcatcatgaa	ccccaaactc	420
tgtgggctgc	tgttctgct	gtccttcac	gtagtgctcc	tggatgctct	gctgcacacg	480
ttgatggctg	tacagctgac	cttctgcata	gacctggaaa	ttccccactt	tttctgtgaa	540
ctagctcata	ttctcaagct	cgctgttct	gatgtcctca	tcaataacat	cctgggtgat	600
ttggtgacca	gcctgttagg	tgttgttct	ctctctggga	tcattttctc	ttacacacga	660
attgtctcct	ctgtcatgaa	aattccatca	gctgggtggaa	agtataaagc	tttttccatc	720
tgcgggtcac	atttaatcgt	cgtttccttg	ttttatggaa	cagggtttgg	ggtgtacctt	780
agttctgggg	ctacccactc	ctccaggaag	ggtgcaatag	catcagtgat	gtataccgtg	840
gtcaccacca	tgtgaaacc	actcatttac	agcctgagaa	acaaggacat	gttgaaggct	900
ttgaggaaac	taatatctag	gataccatct	ttccat			936

<210> 429

<211> 984

<212> DNA

<213> Unknown (H38g278 nucleotide)

<220>

<223> Synthetic construct

<400> 429

aaaatctcca	atagctccaa	attccaggtc	tctgagttca	tcctgctggg	attcccgggc	60
attcacagct	ggcaacactg	gctatctctg	cccctggcac	tactgtatct	ctcagcactt	120
gctgcaaaca	ccctcatcct	catcatcctc	tggcagaacc	cttctttaca	gcagcccatg	180
tatatcttcc	ttggcatcct	ctgtatggta	gacatgggtc	tggccactac	tatcatccct	240
aagatcctgg	ccatcttctg	gtttgatgcc	aaggttatta	gcctccctga	gtgctttgct	300
cagattttatg	ccattcactt	ctttgtgggc	atggagtctg	gtatcctact	ctgcattgct	360
tttgatagat	atgtggctat	ttgtcaccc	cttcgctatc	catcaattgt	caccagttcc	420
ttaatcttaa	aagctaccct	gttcatgggtg	ctgagaaatg	gcttatttgt	cactccagtg	480
cctgtgcttg	cagcacagcg	tgattattgc	tccaagaatg	aaattgaaca	ctgcctgtgc	540
tctaaccttg	gggtcacaa	cctggcttgt	gatgacagga	ggccaaacag	catttgccag	600
ttgggttctgg	catggcttgg	aatggggagt	gatctaagtc	ttattatact	gtcatatatt	660
ttgattctgt	actctgtact	tagactgaac	tcagctgaag	ctgcagccaa	ggccctgagc	720
acttgtagtt	cacatctcac	cctcatcctt	ttcttttaca	ctattgttgt	agtgatttca	780
gtgactcatc	tgacagagat	gaaggctact	ttgattccag	ttctacttaa	tgtgttgac	840
aacatcatcc	ccccttccct	caaccctaca	gtttatgcac	ttcagaccaa	agaacttagg	900
gcagccttcc	aaaagggtgt	gtttgccctt	acaaaagaaa	taagatctta	gagaccttct	960
ccatgatgta	catgaacctc	agct				984

<210> 430

<211> 947

<212> DNA

<213> Unknown (H38g279 nucleotide)

<220>

<223> Synthetic construct

<400> 430

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agtgggtctc	ctgaactgct	ctatgctaca	tttacaatcc	tatacatgtt	ggcactgacc	120
agcaatggtc	tgtctgctcc	ggccaacacc	atagaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	ctcatgggac	ctcctgttca	catctgttgt	cactcccaag	240
gccttgcgga	ctttctgcgc	agagaaaaca	ctatctcctt	tggaggctgt	gcacttcaga	300
tgttcctggc	actgacaatg	ggtagcgctg	aggacctcct	actggccttc	atggcctatg	360
acaggatatg	ggccatttgt	catcctctga	aatacatgac	cctcatgagc	ccaagagtct	420
gctggatcat	ggtggccaca	tcctggatcc	tggcatccct	gattgctata	ggacatacca	480
tgtacactat	gcacctccct	ttctgtgtgt	cctgggaaat	caggcatctg	ctctgtgaga	540
tcccaccctt	gctgaagttg	gcctgtgctg	atacctccag	gtatgagctt	ataatatacg	600
tgacagggtg	gactttcctc	ttgctcccca	tttctgccat	tgtggcctcc	tacacactag	660
tcctattcac	tgtgcttcgt	atgccatcaa	atgaggggag	gaagaaagcc	cttgtcacct	720
gctcttccca	cctgattgtg	gtcgggatgt	tctatggagc	tgccacattc	atgtatgtct	780
tgcccagttc	cttccacagc	cccaaacaag	acaacatcat	ctctgttttc	tacacaattg	840
tcactccagc	cctgaatcca	ctcatctaca	gcctgaggaa	taaggaggtc	atgcgggcct	900
tgaggagggg	cctgggaaaa	tacatactgc	tggcacattc	cacgctc		947

<210> 431

<211> 897

<212> DNA

<213> Unknown (H38g280 nucleotide)

<220>

<223> Synthetic construct

<400> 431

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tacctcttag	ctctcagtgc	caacatcctt	atcctgatca	tcatacaaaa	agaggcagca	120
ctgcaccagc	ctatgtacta	tttcttgggc	atcttggcta	tggcagacat	aggcctggct	180
accaccatca	tgccctaagat	tttggccatc	ttatgggtca	atgctaagac	catcagtctc	240
ctggagtgtc	ttgtctcagat	gtatgccata	cattgctttg	tggccatgga	atcaagtacc	300
tttgtctgca	tggctattga	tagatatgta	gccatttgtc	gaccgctacg	atatccatca	360
atcatcactg	aatcttttgt	tttcaaagca	aatgggttca	tggcactgag	aaacagcctg	420
tgtctcatct	cagtgcctct	gttggctgcc	cagaggcatt	actgctccca	gaatcaaatt	480
gagcactgtc	tttgttctaa	ccttggagtc	actagcctat	cttgtgatga	tcgaagaatc	540
aatagcatta	accaggctct	tttggcttgg	acactcatgg	gaagtgcctt	gggtttgtat	600
attttatcat	atgctctaat	actttactct	gtcctgaagc	tgaactctcc	agaagctgca	660
tccaaggcct	taagtacctg	cacctcccac	ctcatcttaa	tcctttttct	ctacacagtc	720
atcattgtga	tttccattac	tcgtagtaca	ggaatgagag	ttccccttat	tccagttcta	780
cttaattgtc	tacacaatgt	cattccccct	gccctgaacc	ccatgggtata	tgcactcaag	840
aacaaggaac	tcaggcaagg	cttataacaag	gtacttagac	tgggagtga	gggcacc	897

<210> 432

<211> 980

<212> DNA

<213> Unknown (H38g281 nucleotide)

<220>

<223> Synthetic construct

<400> 432

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tgctgactga	gaacacactc	atcattatgg	caagtaggaa	ccattccacc	ctccacaaac	180
ccatgtactt	tgttctagct	aatatgtcct	cctctggaga	tctgggtatgt	cactgtcact	240
attcccaaga	tgcttgctgg	ctttgttgga	tccaaacagg	atcatggaca	gctaattctcc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggct	tgggctgcac	tgagtgtgtc	360
cttctcgtct	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420

gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tggagggttt	480
ggcatctcca	tgggtcaaagt	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtcaacc	tctcatgcac	tgatatgtcc	600
acagcagagc	ttacagattt	catectggcc	atttttatct	ttctaggggc	actctcgtc	660
actggggcct	cctatgtggc	cattactggg	gctgtgatgc	agactctctc	ggctgctgga	720
cgctataaag	ccttttccac	ctgtgcctct	catctcactg	ttgtgataat	cttctatgca	780
gccagtatct	tcatctatgc	tcgccaaagg	cactctcagc	ttttgacacc	apcaagttgg	840
tctctgtact	gtatgctgtc	attgtaccat	tgctcaatcc	catcatttac	tgectgogca	900
atcaagaggt	caagagagcc	ctatgctgta	ctctgcacct	gtaccagcac	caggatcctg	960
acccaagaa	agctagcaga					980

<210> 433

<211> 998

<212> DNA

<213> Unknown (H38g282 nucleotide)

<220>

<223> Synthetic construct

<400> 433

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tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccccctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggacce	ttgttgtcag	tcactccctg	ttccaactgg	480
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cacaccctaa	ttcacagatg	gacaagtttc	tggctatatt	tgatgcagtt	ctcactcctt	840
ttctgaatct	agttgtctat	acattcagga	ataaggagag	gaaggcagca	ataaagagag	900
tatgcaaac	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacaatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 434

<211> 840

<212> DNA

<213> Unknown (H38g283 nucleotide)

<220>

<223> Synthetic construct

<400> 434

atgctgctgg	gcaacctggc	catcatcagc	ttcatttgcc	ttgattcccc	ccttcactca	60
cccattgtact	tcttctctg	caacttctcc	ctcatggaga	tgggtgtcac	ctccactgtg	120
gtacatagga	tgctggcaga	cctgctatcc	actcacaaga	ccatgtccct	ggccaaatgc	180
ctaaccagct	ctttctttta	cttctccctg	ggctctgcc	acttctgat	actcatggtc	240
atggcctttg	atcgctacgt	ggccatctgc	cacccccctg	gctacccaac	catcacgaat	300
ggtccagtgt	gtgtgaagct	ggtgggtggc	tggtgggtgg	ttggtttctt	ctccattgtc	360
tctcccacac	tgcaaaaaac	acgactctgg	ttctgtggcc	ctaacaatcat	cggccactac	420
ttctgtgact	ctgccccgct	gctcaagctt	gcctgctctg	acaccggcca	cattgagcgc	480
atggacctct	tcctgtccct	gctctttgtg	ctgaccacca	tgctgcttat	catectctcc	540
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actgcaatgg	taaccctttt	cctcaacccc	ttcatcttca	ccttccggaa	tgagaaggctc	780
aaggagggtca	ttgaggatgt	gactaaaagg	atcttccttg	gagaccacag	agcctgtagg	840

<210> 435
 <211> 939
 <212> DNA
 <213> Unknown (H38g284 nucleotide)

<220>
 <223> Synthetic construct

<400> 435
 atggaaactg caaattacac caaggtgaca gaatttgttc tcaactggcct atcccagact 60
 ccagagggtcc aactagtcct atttggtata tttctatcct tctatttgtt catcctacca 120
 ggaaatatcc ttatcatttg caccatcagt ctagaccctc atctgacctc tcctatgtat 180
 ttccctgttg ctaatctggc cttccttgat atttggtact cttccattac agcccctgaa 240
 atgctcatag acttcttctt ggagaggaag ataatttctt ttgatggatg cattgcacag 300
 ctcttcttct tacactttgc tggggcttcg gagatgttct tgctcacagt gatggccttt 360
 gacctctaca ctgctatctg ccgacccctc cactatgcta ccatcatgaa tcaacgtctc 420
 tgctgtatcc tgggtggctct ctccctggagg gggggcttca ttcattctat catagagggtg 480
 gctctcattg ttcgacttcc tttctgtggg cccaatgagt tagacagtta cttctgtgac 540
 atcacacagg ttgtccggat tgccctgtgcc aacaccttcc cagaggagtt agtgatgatc 600
 tgtagtagtg gtctgatctc tgggtgtgtt ttgattgtc tgtaaatgtc ctatgccttc 660
 cttctggcct tgttcaagaa actttcaggc tcagggtgaga ataccaacag ggccatgtcc 720
 acctgctatt cccacattac cattgtggtg ctaatgtttg ggccatccat ctacatttat 780
 gctcgcccat ttgactcgtt ttccctagat aaagtgggtg ctgtgttcaa tactttaata 840
 ttccctttac gtaatcccat tatttacaca ttgagaaaca aggaagtaaa ggcagccatg 900
 aggaagtggg tcaccaaata tattttgtgt aaagagaag 939

<210> 436
 <211> 640
 <212> DNA
 <213> Unknown (H38g285 nucleotide)

<220>
 <223> Synthetic construct

<400> 436
 tgcttgttgt aactgtacca ggtatgcctg ctcaccagag acccgatctt gcaagacctc 60
 cattaagaagc ctctgtatcta ttgttctcct tgtctctgag tctattcttt gggtttggac 120
 aggtgaggtg gtttctcaca atgacacaga gtgtactgtg aatgagcctg tttgttctat 180
 gttctcctag atgcccttct gcctcagcta gatcttgccc tagacctact atgagcaagt 240
 ggtcatgctg aatctgggat gtgcagacat cacatatata gtccatacct gtggtctctt 300
 atggcctttt ctgtggatgg atttgatata tttggcatta ttatccacag atatcagaca 360
 ttgcaggctg tactgtagct acctgcaaaa gaatctgtgc ccaaagtatt tagcatatat 420
 gccttccata tttgcgtcac cctgtacctg ctcatgatag gattctactc ctttttttct 480
 tgttgcttta gctaccatac actcacagtg attcccatct ccttgctcat ccttttactc 540
 attagtgcct tccatgttca ataccatcac ctgtggggtg aagagtaagc atatccaaga 600
 aaacatggta cagagatttt gtgggaaaat ttcctgcat 640

<210> 437
 <211> 989
 <212> DNA
 <213> Unknown (H38g286 nucleotide)

<220>
 <223> Synthetic construct

<400> 437
 atgtgtctct tgaccttgca ggtcactggc ccaatgaatg tctctgagcc aaattccagc 60
 tttgcttttag taaatgaatt tatactccaa gatttatctt ttgagtggac aattcagatc 120
 ttcctcttct cactcttcac tacaacatat gcactgacca taacaggaaa cggagccatt 180
 gcttgcgccc tgtggtgtga ccggcgacgt cacactccca tgtacatgtt cctgggaaat 240

ttctcctttt	tagagatatg	gtatgtctct	tctacagttc	ccaagatggt	ggccaacttc	300
ctttcagaga	aaaaaaccat	ctcctttgct	ggatgttttc	tccaatttta	tttcttcttc	360
tctttgggta	catctgaatg	cttgattttg	actgtgatgg	cctttgatca	gtaccttggt	420
atctgccatc	ccttgcacta	tcctaataaa	tcagtactgg	gcattctctgt	gccaaactgg	480
tcatactgtg	ctgggtttgt	ggatttctgt	gtttcctgat	cccactgtt	ctcatctctc	540
agatgccctt	ctgtgggtcca	aacattaatg	accatgttgt	gtgtgaccca	gggccactat	600
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tagttatttt	tggtaaacttc	ctctttatta	ttggatccta	tactcttggtc	ctgaaagctg	720
tgttgggtat	gccttcgagc	actgggaaac	ataaagcctt	ctctacctgt	gggtctcatt	780
tggctgtggt	atcactgttc	tatggctctc	ttatggtcac	gtgtgtgagt	ccaggacttg	840
gacactctat	ggggatgcag	aaaatcaaaa	ctttgttcta	tgctatgggtg	acccactctc	900
tcaatccctt	tatctatagc	ctccagaata	aggagataaa	ggcagccctg	aggaaagtgc	960
tggggagttc	caacataatc	taagccata				989

<210> 438

<211> 930

<212> DNA

<213> Unknown (H38g287 nucleotide)

<220>

<223> Synthetic construct

<400> 438

atgatggaca	accactctag	tgccactgaa	ttccaccttc	taggcttccc	tgggtcccaa	60
ggactacacc	acattctttt	tgctatatcc	ttttcttct	atttagtgac	attaatggga	120
aacacgggtca	tcatttgtgat	tgtctgtgtg	gataaacgtc	tgcagtcccc	catgtatttc	180
ttcctcagcc	acctctctac	cctggagatc	ctggtcacaa	ccataattgt	ccccatgatg	240
ctttggggat	tgtcttctct	gggatgcaga	cagtatcttt	ctctacatgt	atcgctcaac	300
ttttctctgtg	ggaccatgga	gtttgcatta	cttggagtga	tggctgtgga	ccgttatgtg	360
gctgtgtgta	accctttgag	gtacaacatc	attatgaaca	gcagtacctg	tatttgggtg	420
gtaatagtgt	catgggtgtt	tggatttctt	tctgaaatct	ggcccatcta	tgccacattt	480
cagtttacct	tccgcaaata	aaattcatta	gaccattttt	actgtgaccg	agggcaattg	540
ctcaaactgt	cctgcgataa	cactcttctc	acagagttaa	tccttttctt	aatggctgtt	600
tttattctca	ttggttcttt	gatecctacg	attgtctcct	acacctacat	tatctccacc	660
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ttcacctgtg	ttgtgattgg	ctatggcagc	tgcttgtttc	tctacgtgaa	acccaagcaa	780
acacagggag	ttgagtacaa	taagatagtt	tccctgttgg	tttctgtgtt	aaccccttc	840
ctgaatcctt	tcattctttac	tcttcggaat	gacaaagtca	aagaggccct	ccgagatggg	900
atgaaacgct	gctgtcaact	cctgaaagat				930

<210> 439

<211> 915

<212> DNA

<213> Unknown (H38g288 nucleotide)

<220>

<223> Synthetic construct

<400> 439

atgtccaaca	caaattggcag	tgcaatcaca	gaattcattt	tacttgggct	cacagattgc	60
ccggaactcc	agtctctgct	ttttgtgctg	tttctgggtg	tttacctcgt	cacctgcta	120
ggcaacctgg	gcatgataat	gttaatgaga	ctggactctc	gccttcacac	gccccgttac	180
ttcttctctca	ctaacttagc	ctttgtggat	ttgtgtctata	catcaaattg	aaccccgag	240
atgtcgacta	atatcgatc	tgagaagacc	atttcctttg	ctggttgctt	tacacagtgc	300
tacattttca	ttgcccttct	actcactgag	ttttacatgc	tggcagcaat	ggcctatgac	360
cgctatgtgg	ccatatatga	ccctctgcgc	tacagtgtga	aaacgtccag	gagagtttgc	420
atctgcttgg	ccacatttcc	ctatgtctat	ggcttctcag	atggactctt	ccaggccatc	480
ctgaccttcc	gcctgacctt	ctgtagatcc	agtgtcatca	accacttcta	ctgtgctgac	540
ccgcccgtca	ttagcttttc	ttgttctgat	acttatgtca	aagagcatgc	catgttcata	600
tctgtctggct	tcaacctctc	cagctccctc	accatcgtct	tgggtgtccta	tgccttcatt	660
cttctgtgcca	tcctccggat	caaatcagca	gaggggaaggc	acaaggcatt	ctccacctgt	720

ggttcccata	tgatggctgt	caccctgttt	tatgggactc	tcttttgcac	gtatataaga	780
ccaccaacag	ataagactgt	tgaggaatct	aaaataatag	ctgtctttta	cacctttgtg	840
agtccggtac	ttaatccatt	gatctacagt	ctgaggaata	aagatgtgaa	gcagggcttg	900
aagaatgtcc	tgaga					915

<210> 440

<211> 939

<212> DNA

<213> Unknown (H38g289 nucleotide)

<220>

<223> Synthetic construct

<400> 440

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ctgcaggccc	ttctgtatgg	ccccttcctc	atgctttatc	ttctcgccct	catgggaaac	120
accatcatca	tagttatgg	catagctgac	acccacctac	atacaccat	gtacttcttc	180
ctgggcaatt	tttccctgct	ggagatcttg	gtaaccatga	ctgcagtggc	caggatgctc	240
tcagacctgt	tggtccccc	caaagtcatt	accttcactg	gctgcatggg	ccagttctac	300
ttccactttt	ccctgggggc	cacctcttc	ctcatcctga	cagacatggc	ccttgatcgc	360
tttgtggcca	tctgccaccc	actgcgctat	ggcactctga	tgagccgggc	tatgtgtgtc	420
cagctggctg	gggctgctg	ggcagctcct	ttcctagcca	tggtacccac	tgctctctcc	480
cgagctcatc	ttgattactg	ccatggcgac	gtcatcaacc	acttcttctg	tgacaatgaa	540
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gccttgacct	ttgtcctcag	ctccttcctg	gtgacctca	tctcctatgg	ctacatagtg	660
accactgtgc	tgcggtatcc	ctctgccagc	agctgccaga	aggctttctc	cacttgccgg	720
tctcacctca	cactgggtctt	catcggtac	agtagtacca	tctttctgta	tgtcaggcct	780
ggcaaagctc	actctgtgca	agtcaggaag	gtcgtggcct	tggtgacttc	agttctcacc	840
ccctttctca	atccctttat	ccttaccttc	tgcaatcaga	cagttaaaac	agtgtctacag	900
gggcagatgc	agaggctgaa	aggcctttgc	aaggcacia			939

<210> 441

<211> 948

<212> DNA

<213> Unknown (H38g290 nucleotide)

<220>

<223> Synthetic construct

<400> 441

atgaagatag	caaacaacac	agtagtgaca	gaatttatcc	tccttgggtc	gactcagtc	60
caagatatcc	agctcttgg	ctttgtgctg	atcttaattt	tctaccttat	catcctccct	120
ggaaattttc	tcattatttt	caccataaag	tcagaccctg	ggctcacagc	ccccctctat	180
ttattttctg	gcaacttggc	cttcctggat	gcatcctact	ccttcattgt	ggctcccagg	240
atgttgggtg	acttctctc	tgagaagaag	gtaatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcaattcct	tggaggagg	gagggtattac	tccttgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggcctctg	cactgttcaa	ctgtcatgaa	ccctagagcc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatcc	tcgccttgcc	tttttgtggc	ccaaaccagc	tggaacaact	cttctgtgat	540
gtccgacagg	tcataaagct	ggcttgcacc	gacatgtttg	tggtggagct	tctgatggtc	600
ttcaacagtg	gcctgatgac	actcctgtgc	tttctggggc	ttctggcttc	ctatgcagtc	660
atcctctgcc	atgttcgtag	ggcagcttct	gaagggaaga	acaaggccat	gtccacgtgc	720
accactcgtg	tcattattat	acttcttatg	tttggacctg	ctatcttcat	ctacatgtgc	780
cctttcaggg	ccttaccagc	tgacaagatg	gtttctctct	ttcacacagt	gatctttcca	840
ttgatgaatc	ctatgattta	tacccttcgc	aaccaggaag	tgaaaacttc	catgaagagg	900
ttattgagtc	gacatgtagt	ctgtcaagtg	gattttataa	taagaaac		948

<210> 442

<211> 1034

<212> DNA

<213> Unknown (H38g291 nucleotide)

<220>

<223> Synthetic construct

<400> 442

atggaaccttc	ccaattcttc	tgaaattgcg	attaccacct	tctttctgat	tggaatacca	60
gggctggagc	atgcccatat	atggatatct	gtcccatct	gcctcatgta	cttggttagcc	120
atcctaggca	attgcacaat	cctctttgtt	atcaggactg	agccctcact	ccatgcaccc	180
atgtactatt	tcctttccat	gttggctgtc	tctgatctgg	gcctgtccct	ctcctaccta	240
cccactatgc	tgaggatctt	tgtattcaat	gccacaggaa	tctcctcaaa	tgctcgcttt	300
gctcaagaat	tctttattca	tggattcaca	gatatggagt	cctcagtgtc	tctcgctcatg	360
tcttttgacc	ggttttggcc	atatgccacc	ctctgaggta	catatctgag	gtactgggtga	420
gctgtatcct	caccagtgcc	agagttgcca	aaatggggct	gttgtttctc	attaaaagag	480
aaacaacact	aaactcatta	aaagaaacaa	ctaactcatg	ctgttagtac	tcccatttcc	540
tttactctt	acaagggtga	catattgtag	gaaaagccta	ctctctcatt	cctattgtct	600
ccatcaggat	gtcaggaagc	tggcctgtc	cgacaacact	gtcaacttct	tctatggttt	660
ctttcttgcc	ctctgtatga	tgtcagaaag	tgtgttcatt	actgtgtctt	atgtgctcat	720
cctgaagacg	atcatgggaa	ttggatccca	tagggagcgg	ctcaaggccc	tcaacacctg	780
tgtctcccat	atctgtgtctg	tgtttatctt	ctatgcgccc	gtcattgctt	tggcatccat	840
gcactgcttt	ggcatccatg	aactgctttg	gcaagcacag	gtccccactg	gccatgatcc	900
tcattgctga	tgttttcttg	ctagtgccac	ctcttatgaa	tcccatgtga	tattgtgtga	960
agacacagca	aattcatgaa	aaagttttag	gaaaactggg	tctacaacaa	cgggtgcagt	1020
aaacgtggta	caag					1034

<210> 443

<211> 713

<212> DNA

<213> Unknown (H38g292 nucleotide)

<220>

<223> Synthetic construct

<400> 443

ccacttattt	gaccagatcc	attcatcttt	acacaattgt	gttcattcct	taataaatat	60
gtagcgtcaa	ctcggttaa	tgatcataac	atagatcagg	ctccataatc	caggagcata	120
atcctaaatc	tgtccttatt	tcctttggga	ttaaaggcat	gtggagcaat	gttaattctt	180
gtttcccttc	tagccttccc	agagagaaag	agctaggatt	gaaacagcga	ggggaactac	240
tctagtgtca	ctcaattctg	tctcctgggc	ttcccaggct	ttgaggaact	gccccatttc	300
cttttggtta	acttcttctt	tcaattgatg	agattaatgg	gaaatgcagt	catttacatg	360
gttgaattga	tgaagtcttc	agtctcccgg	ggatttcttc	ctcagtcaac	tcttcatctt	420
ttcacacagt	ctattaatgg	acatttccat	tgttattgct	tctttgatcc	agattgatcc	480
ctactccagt	atcccctcag	cgtctggcca	aaaaataatc	cttctccact	catgcctccc	540
atttcacctg	tgtggggatt	gactatgaca	gctgtctgtt	tctctacgtg	aaacccaagc	600
aaatttgggc	agcagaataa	aacaaggtag	ttttcctgtt	tattttcctg	ttgacccctt	660
ttctgaacct	tcttacaggt	cagatttact	gacctaaatc	agtttttaggt	ggg	713

<210> 444

<211> 931

<212> DNA

<213> Unknown (H38g293 nucleotide)

<220>

<223> Synthetic construct

<400> 444

cccattgaaag	tggccaacaa	tgtcactgag	tttatattcc	tgggactttc	ccaagattct	60
ggaatgcaat	tgatgttctt	tgtcttattt	ctcctcttct	acgtcgtgat	catgggtggga	120
aatttgctca	ttttgcttat	ggtcttttct	gactcccagc	tacacacacc	catgtatttc	180
ttcctcagta	acctgtcttt	tgtggacatt	gcctgttccct	cagccacagc	accaagatg	240
attgaagact	ttgtttctga	gaaaaagact	atttcttact	ggggctgtat	aactcagatg	300
tttaccttcc	acttttttgg	ttgtgctgag	atttttgttt	tgactgtcat	ggctttttgat	360

cgctatgctg	ctatctgcc	acccctccgt	tacactgtca	tcatgagtgc	taatgcttat	420
actgtgctgg	catcactgtc	ctgggtgggg	gccctgggtc	attcctttgt	tcagaccctc	480
ctgaccttcc	agctgccctt	ctgtaatgct	cagggtatag	accattactt	ttgtgatgtc	540
caccagtgcc	taaaacttgc	ctgtgctgat	acaactctgg	taaatatgtt	ggtgggttgc	600
aacagtgggc	tcattctcct	gggggtgttc	ctcattcttt	tggcctccta	cacagtcatt	660
ctgttttagtc	ttcaaaaaca	gtctgcagag	agctgacaca	aagttctctc	tacctgtgga	720
tctcatctga	ctatagtaac	tttcttcttt	gttccgtgta	tctttattta	tctccatcca	780
ctactttccc	attggataaa	gctgtgtctg	tgttctatac	caccatcacc	ccaatgctga	840
acccactcat	ctatactctg	aggaatgagg	agtaaagaat	gccatgaggc	ggctatggag	900
tagcaagatc	tccttgaagg	aaaagcagag	a			931

<210> 445

<211> 968

<212> DNA

<213> Unknown (H38g294 nucleotide)

<220>

<223> Synthetic construct

<400> 445

atggaaatcc	taagcaactc	aacatctaaa	tttccaacct	tcttgttgac	eggcattcct	60
ggcctagagt	ctgcccatgt	ctggatctcc	attcctttct	gctgttttta	tgccattgcc	120
ctctctggga	acagcgtgat	cctgtttgtc	atcattaccc	agcagagtct	ccatgaaccc	180
atgtattatt	tcctctccat	gctatcagcc	actgatctgg	gcttgactgt	ttcttcattg	240
tcaacaacat	taggtatcct	ctggtttgag	gcagtgaat	cagtctatac	agctgcattg	300
tccagatgtt	ttttcttcat	ggattcactt	ttatggaatc	tggagtgtcg	gtggctacag	360
cctttgaccg	ttatgtggcc	atctgtgatc	ctctgaggta	cactaccatt	ctcactaatt	420
ccagaatcat	tcaaattggg	cttctgatga	ttacacgtgc	tatagtacta	atattaccac	480
tacttttget	ccttaagcct	ctctatttct	gtagaatgaa	tgccctttct	cactcctatt	540
gttaccatcc	agatgtgatt	caattagcat	gttcagacat	tcgggcaaat	agcatctgtg	600
gattaattga	tctcatcctg	accactggaa	tagatacacc	atgcattgtc	ctgtcatata	660
tcttaattat	tcgctttgtc	ctcagaattg	cctcccctga	agaatggcac	aaggtcttca	720
gcacctgtgt	ctccacgtg	ggagcagttg	ctttcttcta	catccacatg	ctgagcctgt	780
ccttggtgta	tcgctatggg	cggtcagccc	ccagagtagt	ccattcagtg	atggctaacg	840
tatacctgct	tttaccctct	gtgctcaacc	ccatcatcta	cagtgtaaaa	acaaaacaaa	900
tccgcaaggc	tatgctcagt	ctgctgctta	caaatgaac	agacatagtt	ttatttgata	960
caaacctg						968

<210> 446

<211> 963

<212> DNA

<213> Unknown (H38g295 nucleotide)

<220>

<223> Synthetic construct

<400> 446

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gaccagaac	tgcagcctat	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acggtgctga	ggaacctgct	cagcatcctg	gctgtctgct	ctgactcccc	cctccacacc	180
cccaggtaact	tcttctctct	caacctgtgc	tgggctgaca	tcgggtttcac	ctccgccacg	240
gttcccaaga	tgattgtgga	catgcagctg	catagcagag	tcacgtctca	tgcggtgtgt	300
ctgacgcaga	tgtctttctt	ggtccttttt	gcattgtatg	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
cctcacctct	gtgtcttctg	tttggtgtcc	ttttctctta	gcctgttgga	ttcccagctg	480
cacagttgga	ttgtgttaca	attcaccatc	gtctagaatt	tggaaatctc	taattttgtc	540
tgtgacccct	ctcaacttct	caaacttgcc	tgttctgaca	gcgtcatcaa	tagcatattc	600
atatattttc	atagtactat	gtttgggttt	cttcccattt	cagggatcct	atggtcttac	660
tataaaatca	tcccctccat	tctaaggatt	tcacgtctag	atgggaagta	taaagccttc	720
tccacctgtg	gctctcacct	agccgttggt	tgctgatttt	atggaacagg	cattggcatg	780
tacctgactt	cagctgtgtc	acaaccccc	aggaatgggt	tgggtggcatc	agtgtatgtat	840

gctgtggtca ccccatgct gaaccttttc atctacagcc tgagaaacag gaacatacaa 900
 agtgcctgt ggaggctgca cagcagaaca gtcgaatctc atgatttgtt ccatcctttc 960
 tct 963

<210> 447

<211> 975

<212> DNA

<213> Unknown (H38g296 nucleotide)

<220>

<223> Synthetic construct

<400> 447

atggcaatat tcaataacac cacttcgtct tcctcaaact tcctcctcac tgcattccct 60
 gggctggaat gtgctcatgt ctggatctcc attccagtct gctgtctcta caccattgcc 120
 ctcttgggaa acagtatgat ctttcttgtc atcattacta agcggagact ccacaaaccc 180
 atgtattatt tcctctccat gctggcagct gttgatctat gtctgaccat tacgaccctt 240
 cccactgtgc ttggtgttct ctgggtttcat gcccgggaga tcagctttaa agcttgcttc 300
 attcaaatgt tctttgtgca tgctttctcc ttgctggagt cctcgggtgt ggtagccatg 360
 gcctttgacc gcttcgtggc tatctgtaac ccaactgaact atgctactat cctcacagac 420
 aggatggtcc tggatgtagg gctggtcac tgcattagac cagcagtttt ctacttccc 480
 cttctttag tagcataaacac tgtgtctttt catgggggtc acgagctttc ccatccattt 540
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 ggactgtttc ttcagctcta cctgaatggc actgacgtat tgtttattct tttctcctat 660
 gtctgatcc tccgtactgt tctgggcatt gtggcccgaa agaagcaaca aaaagctctc 720
 agcacttggt tctgtcacat ctgtgcagtc actattttct atgtgccact gatcagcctc 780
 tctttggcac accgcctctt ccaactccacc ccaaggggtg tctgtagcac tttggccaat 840
 atttatctgc tcttaccacc tgtgctgaac cctatcattt acagcttgaa gaccaagaca 900
 atccgccagg ctatgttcca gctgctocaa tccaaggggt catgggggtt taatgtgagg 960
 ggtcttaggg gaaga 975

<210> 448

<211> 945

<212> DNA

<213> Unknown (H38g297 nucleotide)

<220>

<223> Synthetic construct

<400> 448

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 cacagtactg ctgaccttgt cctcttctcc gtggttatgg cggctctcac agtggccctc 120
 tgtgggaatg tcctcctcat cttcctcatc tacatggacc ctcacctca cacccecatg 180
 tacttcttcc tcagccagct ctccctcatg gacctcatgt tggctgtac caatgtgcca 240
 aagatggcag ccaacttctt gtctggcagg aagtcctctt cctttgtggg ctgtggcata 300
 caaattggcc tctttgtctg tcttgtggga tctgaggggc tcttgtctgg actcatggct 360
 tatgaccgct atgtggccat tagccaccca cttcactatc ccatcctcat gaatcagagg 420
 gtctgtctcc agattactgg gagctcctgg gcctttggga taatcgatgg cttgatccag 480
 atgggtggtat taatgaattt cccctactgt ggcttgagga aggtgaacca tttcttctgt 540
 gagatgctat ccttgttgaa gctggcctgt gtagacacat ccctgtttga gaaggtgata 600
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 cgcattctag ggactgtgct gcaaattgcac tctgtcagg cctggaaaaa ggccctggcc 720
 acctgtcctt cccacctgac agctgtcacc ctcttctatg gggcagccat gttcatctac 780
 ctgaggccta ggcactaccg ggccccagc catgacaagg tggcctctat cttctacacg 840
 gtccttactc ccatgctcaa cccctcatt tacagcttga ggaacagggg ggtgatgggg 900
 gcaactgagga aggggctgga ccgctgcagg atcggcagcc agcac 945

<210> 449

<211> 965

<212> DNA

<213> Unknown (H38g298 nucleotide)

<220>

<223> Synthetic construct

<400> 400

atgtcaccac	tcaaccaa	tactgaga	caccagag	tcttcacc	gactggg	60
ccaggaatgc	cagagaa	cttatgg	gccttgccc	tctgtctt	ttatagc	120
acgatcttgg	gaaatgtc	catccttg	gtcatcaa	ttgagcaa	tctccatg	180
cccatgtatt	tttctagc	tgtagctg	cactgacct	agcctttc	tgtcttcc	240
gcctaccatg	gtcagtg	actggttc	ctggcggt	ataacttt	atggctgc	300
tatccagatg	ttcttcat	acacattt	gggagtgg	tcaggtgt	tggtggcc	360
ggcctttgat	cgctttgt	ccatccgt	tcctttgc	tatgctac	ttctcact	420
cagtgtcatc	agcaagatt	cagcagcc	cctgttac	agtgtggg	ctgtgctc	480
tgtgcctttt	ctcatcaaa	ggttacct	ctgtcact	aatgtcct	cccatgc	540
ctgcctccat	caggatgcc	tgaggctt	ctgtgctg	actgggtg	atagcatc	600
tggcctgttg	gctgtgat	tcatcatt	actagatg	ttaatact	tggcctct	660
cattctaata	ctgcaggc	tattgagc	tgcttccc	gaagacag	tcaaggct	720
caacacctgt	ctctctca	tctgcagt	tgcttttc	tgtgcctc	attggtat	780
ccctaattca	tgcattgg	aagcattt	caccacta	acacacatt	atggcca	840
tctacctgt	tctccctc	gtgtcaat	ccattgtg	cagtgttag	accaagc	900
tctgatagca	gattgtcc	gccttttg	gggctagg	tagccctta	tggtcatc	960
tattt						965

<210> 450

<211> 936

<212> DNA

<213> Unknown (H38g299 nucleotide)

<220>

<223> Synthetic construct

<400> 450

atgtctgttc	tcaataact	cgaagtca	cttttcttc	tgattggg	cccaggact	60
gaacatgccc	acatttggt	ctccatccc	atttgccct	tgtacctg	tgccatcat	120
ggcaactgca	ccattctct	tattataaa	acagagccc	cgcttcat	gcccattgat	180
tatttccctg	ccatgttgg	tgtctctg	atgggcctg	ccctctct	ccttccctacc	240
atgttgaggg	tcttcttgt	caatgccat	ggaatttc	ctaatagc	ctttgtctca	300
gaattcttca	ttcatggat	cactgtcat	gaatcctc	tacttcta	tatgtctttg	360
gaccgctttc	ttgccattc	caatccctt	agatacagt	ctatcctc	tagcaacagg	420
gttgctaaaa	tggaacttat	tttagccat	aggagcatt	tcttagtg	tccatttccc	480
ttcaccttaa	ggagattaaa	atattgtca	aagaacttc	ttctcact	atactgtctt	540
catcaggata	ccatgaagc	ggcctgct	gacaacaag	ccaatgtc	ctatggcttc	600
ttcattgtct	tctgtactat	gctggactg	gcactgatt	ttttgtct	tgtgtgatc	660
ttgaagacta	tactcagcat	tgcactttg	gcagagagg	ttaaggcc	aaatacctg	720
gtctcccaca	tctgtgctg	gtcaccttc	tatgtgccc	tcataccct	ggctgccatg	780
catcactttg	ccaagcaca	aagccctct	gttgtgatc	ttattgcag	tatgttctg	840
ttggtgccgc	cccttatg	cccattgtg	tactgtgta	agactcgac	aatctgggag	900
aagatcttgg	ggaagttgt	taatgtatg	gggaga			936

<210> 451

<211> 923

<212> DNA

<213> Unknown (H38g300 nucleotide)

<220>

<223> Synthetic construct

<400> 451

atgaaaataa	atgacagct	aggggaag	ttcatcttag	ttggcttct	agaatatccc	60
caggctgagt	tcatacttc	tctgtttgt	tccgggttct	acaccatg	attcacagg	120
aacacagcca	tcactttggt	ctctctgct	gactaccgg	tccgcaccc	aatgtacttc	180

ttcctccgaa	agctctcatt	tctggacatg	tgtttcacca	cctgcattgt	ccttcagatg	240
ctgggtgaaca	tctggggaga	gagtaagaag	gtcagctatg	taggctgcat	ggttcagtat	300
tctgtagcct	tggtctcttg	ctccacagag	tgtgtgcttc	ttgctatcat	ggctgtggac	360
cgttatgttg	cgtccgctg	gccccctcac	tatgttacaa	tcatgcacca	acagatctgc	420
cactttctcg	cagccttgct	ctgggtttct	gggttagcca	actctctctt	tcactcttca	480
ctaaccacca	ttttgacct	gtgtggccac	cggctgtgg	accatttctt	tgtgaggtcc	540
tgctcattgt	caagctgtcc	tgcgtggaca	cgggccaac	tgaattgaag	atgttaattg	600
ctcgtgtgat	cacccttgcc	cttcagtggt	gcaccatcct	cacctcctat	gcctgcattg	660
ccagggctgt	gctgaggctg	cagtctgctg	aaggtcagca	gaaggccttt	gggacttggt	720
cctccacact	gatgggtggt	ttgctgttct	atggaaccat	catgttcatt	tgtcttcagc	780
tgaagagtaa	ctactctcag	attcagggaa	agctgcttcc	tcttgtttat	accattgctg	840
ccccaccta	gaaccaccta	atctatgcac	tgaggaacaa	agttgtaaag	agggcaattg	900
gaaaattgat	ctggaaggat	tca				923

<210> 452

<211> 951

<212> DNA

<213> Unknown (H38g301 nucleotide)

<220>

<223> Synthetic construct

<400> 452

atggaaatag	ataaccagac	gtgggtgaga	gaattttatc	tccttggctt	atccagtgc	60
tggtgcactc	agatatccct	gttttccctg	ttcttgggtc	catacctcat	gacagtgtg	120
gggaactgtc	tcattgtcct	tctgatcaga	ctggacagcc	gactccacac	tcccatgtat	180
ttctttctca	ccaacctctc	ccttgctgat	gtctcctatg	ccacaagcgt	agtccccag	240
ctgctggcac	attttcttgc	agaacataaa	gccatcccat	tccagagctg	tgcagcccag	300
ttatttttct	acctggcctt	gggtgggatt	gagtttggtc	tcctggcagt	gatggcctat	360
gaccgccatg	tggctgtgtc	tgaccgcctg	cgatactcgg	ccatcatgca	tggagggctg	420
tgtgctaggt	tggccatcac	atcctgggtc	agtggctcca	tcaactctct	tgtgcagact	480
gctatcacct	ttcagctgcc	catgtgcact	aacaagttta	ttgatcacat	atcctgtgaa	540
ctcctagctg	tggtcaggct	ggcttgtgtg	gacacctcct	ccaatgaggc	tgccatcatg	600
gtgtctagca	ttgttcttct	gatgacacct	ttctgcctgg	ttctgttggt	ctacatccgg	660
atcatctcca	ccatccataa	gatccagtcc	agagaaggaa	gaaagaaagc	cttccacacg	720
tgtgcctctc	acctcacggt	ggttgccctg	tgctacggca	caacgatttt	cacttacatc	780
cagccccact	ctggctccctc	agtccttcaa	gagaagctga	tctctgtctt	ctatgccatt	840
gttatgcctc	tgtgaaccc	tgtgatttat	agtctaagga	ataaagaggt	gaagggggcc	900
tggcataaac	tattagagaa	attctctggg	ttaacatcca	agctgggaac	t	951

<210> 453

<211> 918

<212> DNA

<213> Unknown (H38g302 nucleotide)

<220>

<223> Synthetic construct

<400> 453

atggaaggga	aaaatcaaac	caatatctct	gaattttctc	tcctgggctt	ctcaagttgg	60
caacaacagc	aggtgctact	ctttgcactt	ttcctgtgtc	tctatttaac	agggtgtgtt	120
ggaaacttac	tcattcttgc	ggccattggc	tcggtacact	gccttcacac	acccatgtat	180
ttcttctctg	ccaatctgtc	cttggttagac	ctctgccttc	cctcagccac	agtccccag	240
atgctactga	acatccaaac	ccaaacccaa	accatctcct	atcccggctg	cctgggtcag	300
atgtattttct	gtatgatgtt	tgccaatatg	gacaattttc	ttctcacagt	gatggcatat	360
gaccgttaag	tggccatctg	tcacccttta	cattactcca	ccattatggc	cctgcgcctc	420
tgtgcctctc	tggtagctgc	accttgggtc	attgccattt	tgaacctctc	cttgcacact	480
cttatgatgg	cccatctgca	cttctgctct	gataatgtta	tccaccattt	cttctgtgat	540
atcaactctc	tcctccctct	gtcctgttcc	gacaccagtc	ttaatcagtt	gagtggtctg	600
gctacgggtg	ggctgatctt	tgtggtacct	tcagtgtgta	tcctgggtatc	ctatatcctc	660
attgtttctg	ctgtgatgaa	agtccttctt	gccaaggaa	aactcaaggc	tttctctacc	720

tgtggatctc	accttgcctt	ggtcattctt	ttctatggag	caaacacagg	ggtctatatg	780
agcccttat	ccaatcactc	tactgaaaaa	gactcagccg	catcagtcac	ttttatgggt	840
gtagcacctg	tggtgaaacc	attcattttac	agtttaagaa	acaatgaact	gaagggggact	900
ttaaaaaaga	ccctaagc					918

<210> 454

<211> 933

<212> DNA

<213> Unknown (H38g303 nucleotide)

<220>

<223> Synthetic construct

<400> 454

atgggaccca	gaaaccaaac	agctgtttca	gaatttcttc	tcataaaagt	gacagaggac	60
ccagaactga	agttaatccc	tttcagcctg	ttcctgtcca	tgtacctggt	caccatcctg	120
gggaacctgc	tcattctcct	ggctgtcatc	tctgactccc	acctccacac	ccccatgtac	180
ttccttctct	ttaatctctc	ctttactgac	atctgtttaa	ccacaaccac	agtcccaaag	240
atcctagtga	acatccaagc	tcagaatcag	agtatcactt	acacaggctg	cctcaccag	300
atctgtcttg	tcttggtttt	tgctggcttg	gaaagtgtgt	ttcttgcatg	catggcctac	360
gaccgctatg	tggccatttg	ccaccactg	aggtacacag	tcctcatgaa	tgteccatttc	420
tggggcttgc	tgattcttct	ctccatgttc	atgagcacta	tggatgccct	ggttcagagt	480
ctgatgggat	tgcagctgtc	cttctgcaaa	aacgttgaaa	tccttttgtt	cttctgtgaa	540
gtcggtcagg	tcatacaagc	cgcctgttct	gacacctca	tcaacaacat	cctcatatat	600
tttgcaagta	gtgtatttgg	tgcaattcct	ctctctggaa	taattttctc	ttattctcaa	660
atagtcacct	ctgtttctgag	aatgccatca	gcaagaggaa	agtataaagc	gttttccacc	720
tgtggctgtc	acctctctgt	tttttccttg	ttctatggga	cagcttttgg	ggtgtacatt	780
agtctcgtcg	ttgctgagtc	ttcccgaatt	actgctgtgg	cttcagtgat	gtacactgtg	840
gtccctcaaa	tgatgaaccc	cttcatctac	agcctgagaa	ataaggagat	gaagaaagct	900
ttgaggaaac	ttattggtag	gctgtttcct	ttt			933

<210> 455

<211> 939

<212> DNA

<213> Unknown (H38g304 nucleotide)

<220>

<223> Synthetic construct

<400> 455

atggaagcga	gaaaccaaac	agctattttca	aaattccttc	tcctgggact	gatagaggat	60
ccggaactgc	agcccgctct	tttcagcctg	ttcctgtcca	tgtacttggt	caccatcctg	120
gggaacctgc	tcatectctt	ggctgtcatc	tctgactctc	acctccacac	ccccatgtac	180
ttcttctctt	ccaatctctc	ctttttggac	atttgtttaa	gcacaaccac	gatcccaaag	240
atgctgggtga	acatccaagc	tcagaatcgg	agcatcacgt	actcaggctg	cctcaccag	300
atctgctttg	tcttggtttt	tgctggcttg	gaaaattgtc	tccttgagc	aatggcctat	360
gaccgctatg	tggccatttg	tcacccctt	agatacacag	tcatacatgaa	ccccgcctc	420
tgtggcctgc	tgattcttct	ctctctgttg	actagtgttg	tgaatgccct	tcttctcagc	480
ctgatgggtg	tgaggctgtc	cttctgcaca	gacctggaaa	tcctgctctt	cttctgtgaa	540
ctggctcagg	tcataccaact	cacctgttca	gacacctca	tcaataacat	cctgatatat	600
tttgacagct	gcataatttg	tggtgttctt	ctgtctggaa	tcattttgtc	ttacactcag	660
atcacctcct	gtgtttttgag	aatgccatca	gcaagtggaa	agcacaaagc	agtttccacc	720
tgtgggtctc	acctctccat	tggtctcttg	ttctatgggg	caggtttggg	ggtgtacatt	780
agttctgtgg	ttactgactc	acctaggaag	gctgcagtgg	cttcagtgat	gtattctgtg	840
ttccctcaaa	tggtgaaccc	ctttatctat	agtctgagga	ataaggacat	gaaaggaacc	900
ttgagggaag	tcatagggag	gataccttct	cttctgtgg			939

<210> 456

<211> 939

<212> DNA

<213> Unknown (H38g305 nucleotide)

<220>

<223> Synthetic construct

<400> 456

atggaaccaa gaaaccaaac cagtgcattt caattcatcc tcttgggact ctcagaaaag	60
ccagagcagg agacgcttct cttttccctg ttcttctgca tgtacctggg catggtcgtg	120
gggaacctgc tcatcatcct ggccatcagc atagactccc acctccacac ccccatgtac	180
ttcttccctg ccaacctgtc cctgggtgat ttctgtctgg ccaccaacac catccctaag	240
atgctggtga gccttcaaac cgggagcaag gccatctctt atccctgctg cctgatccag	300
atgtacttct tccatttctt tggcatcgtg gacagcgtca taatcgccat gatggcttat	360
gaccggttct tggccatctg ccacccattg cactacgcca agatcatgag cctacgcctc	420
tgtcgcctgc tggctcggcg cctctggggc ttttccctgt tcatctcact cactcacatc	480
ctcctgatgg cccgtctcgt tttctgcggc agccatgagg tgcctcacta cttctgcgac	540
ctcactccca tctctcgact ttcgtgcacg gacacctctg tgaataggat cttcatcctc	600
attgtggcag ggatgggtgat agccacgccc tttgtctgca tcttggcctc ctatgctcgc	660
atccttgtgg ccatcatgaa ggtccccctt gcaggcggca ggaagaaagc cttctccacc	720
tgcagctccc acctgtctgt ggttgcctct ttctatggga ccaccattgg cgtctatctg	780
tgtccctcct cggctctcac cactgtgaag gagaaagctt ctgcggtgat gtacacagca	840
gtcaccacca tgctgaatcc cttcatctac agcttgagga acagagacct gaaaggggct	900
ctcaggaagc tgggtcaacag aaagatcacc tcatcttcc	939

<210> 457

<211> 295

<212> DNA

<213> Unknown (H38g306 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(295)

<223> n = A,T,C or G

<400> 457

atgtcagcct ccagtatcac ctcaacacat ccaacttctt tcttgttgat ggggattcca	60
ggcctggagc acctgcacat ctggatctcc atccccctt cagcatatac actggccctg	120
cttggaaact gcactctcct tctcatcacc caggctgatg cagccctcca tgaacctatg	180
tacctctttc tggccatggt ggcagccatc gaccagctct ctatctctc agcactgccc	240
ccgggacaga cgggtgattct ggttcacgga tcngaagaat aaaccctttg ccggg	295

<210> 458

<211> 960

<212> DNA

<213> Unknown (H38g307 nucleotide)

<220>

<223> Synthetic construct

<400> 458

atgccatctg cctctgccat gatcattttc aacctgagca gttacaatcc aggacccttc	60
attctggtag ggatcccagg cctggagcaa ttccatgtgt ggattggaat tcccttctgt	120
atcatctaca ttgtagctgt tgtgggaaac tgcattcttc tctacctcat tgtggtggag	180
catagtcttc atgaacctat gttcttcttt ctctccatgc tggccatgac tgacctatc	240
ttgtccacag ctggtgtgcc taaagcactc agtatctttt ggctaggggc tcgcgaaatc	300
acattcccag gatgccttac acaaagtgtc ttcttccact ataactttgt cctggattca	360
gccattctga tggccatggc atttgatcac tatgtagcta tctgttctcc cttgagatat	420
accaccatct tgactcccaa gaccatcatc aagagtgtca tgggcatctc ctttcgaagc	480
ttctgcatca tcttgccaga tgtattcttg ctgacatgcc tgcccttctg caggacacgc	540
atcatacccc acacatactg tgagcatata ggtgttgccc agctgcctg tgctgatatc	600
tccatcaact tctgggtatgg cttttgtgtt cccatcatga cggtcattctc agatgtgatt	660

ctcattgctg	tttctacgc	acacatcctc	tgtgctgtct	ttggccttcc	ctcccaagag	720
gcctgccaga	aagccctcgg	cacttggtgt	tctcatgtct	gtgtcatcct	catgttttat	780
acacctgcct	ttttctccat	cctcgcccat	cgtttggac	acaatgtctc	tcgcaccttc	840
cacatcatgt	ttgccaatct	ctacattgtt	atccacctg	cactcaaccc	catgggttac	900
ggagtgaaga	ccaagcagat	cagagataag	gttatactt	tgttttctaa	gggtacagga	960

<210> 459

<211> 936

<212> DNA

<213> Unknown (H38g308 nucleotide)

<220>

<223> Synthetic construct

<400> 459

atgagcggga	caaaccagtc	gagtgtctcc	gagttcctcc	tcctgggact	ctccaggcag	60
ccccagcagc	agcatctcct	ctttgtgttc	ttcctcagca	tgtacctggc	cactgtcctg	120
gggaacctgc	tcacatcctc	gtccgtaagc	atagactcct	gcctgcacac	ccccatgtac	180
ttcttctcca	gcaacctgtc	ttttgtggac	atctgtttct	ccttcaccac	cgtccccaag	240
atgctggcca	atcacatact	cgagactcag	accatctcct	tctgtggctg	tctcacacag	300
atgtatttgc	ttttcatgtt	cgtggacatg	gacaatttcc	tcctagctgt	gatggcctat	360
gaccactttg	tcgccgtgtg	ccacccttta	cattacacag	caaagatgac	ccatcagctc	420
tgtgccctgc	tggttgctgg	attatgggtg	gttgccaacc	tgaatgtcct	tctgcacacc	480
ctgctgatgg	ctccactctc	attctgtgca	gacaatgcca	tcactcactt	cttctgcgat	540
gtgactcccc	tactgaaact	ctcctgtctc	gacacacacc	tcaatgaggt	cataatcctt	600
agtgaggggt	ccctgggtcat	gatcacccca	tttctttgca	tcctggcttc	ttatatgcac	660
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aacctctgt	cctccactc	agctgagaaa	gacactatgg	ctactgtgtt	gtatacagta	840
gtgactccca	tgctaaaccc	tttcatctac	agcctgagga	acagggtactt	gaaaggggct	900
ctgaaaaaag	tagttggcag	ggtgggtgtt	tctgtc			936

<210> 460

<211> 762

<212> DNA

<213> Unknown (H38g309 nucleotide)

<220>

<223> Synthetic construct

<400> 460

atgtactttct	tcctgcgcca	actctcagtg	gtggagctct	tctacaccac	tgacatcgtg	60
cccaggaccc	tggccaatct	gggtccccc	catccccagg	ccatctcttt	ccagggctgt	120
gcagcccata	tgtacgtctt	cattgtcctg	ggcatctcgg	agtgtgcct	gctcactgcc	180
atggcctatg	accgatatgt	tgccatctgc	cagccccctac	gctattccac	cctcttgagc	240
ccacgggcct	gcatggccat	ggtgggtacc	tcctgggtca	caggcatcat	cacggccacc	300
acccatgcct	ccctcatctt	ctctctacct	tttcgcagcc	acccgatcat	cccgcacttt	360
ctctgtgaca	tcctgccagt	actgaggctg	gcaagtgtctg	ggaagcacag	gagcgagatc	420
tcctgtgatga	cagccaccat	agtcttctat	atgatcccc	tctctctgat	tgtcacctct	480
tacatccgca	tcctgggtgc	catactagca	atggcctcca	cccagagccg	ccgcaaggtc	540
ttctccacct	gtctctccca	tctgtctgtg	gtctctctct	tctttggaac	agccagcatc	600
acctacatcc	ggccgcaggc	aggctcctct	gttaccacag	accgcgtcct	cagtctcttc	660
tacacagtca	tcacacccat	gctcaacccc	atcatctaca	cccttcggaa	caaggacgtg	720
aggagggccc	tgcgacactt	ggtgaagagg	cagcgccctc	ca		762

<210> 461

<211> 998

<212> DNA

<213> Unknown (H38g310 nucleotide)

<220>

<223> Synthetic construct

<400> 461

atggatggag	agaatcactc	agtgggtatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccctctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttgttgtcag	tcactccctg	ttccaactgg	480
catttcttgt	taatttaccc	ttctgtggcc	ctaagtgtgt	ggacagcttc	tactgtgacc	540
ttcctcagct	tctcagacta	gcctgtaccg	acacctacag	attgcagttc	atggtcactg	600
ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactctc	tacgtcttca	660
tcctgtttac	tgtttgaaa	cattcctcag	gtgggtccat	caaggccctt	tccactcttt	720
cagctcaacag	cacagcggtc	cttttggtct	ttggtccacc	catgtttgtg	tatacatggc	780
cacaccctaa	ttcacagatg	gacaagtctc	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacaatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 462

<211> 933

<212> DNA

<213> Unknown (H38g311 nucleotide)

<220>

<223> Synthetic construct

<400> 462

atggaagagt	acaacacatc	ctctacagac	ttcactttca	tggggctgtt	caacagaaag	60
gaaacctcag	gtcttatttt	tgccatcatc	tctatcatct	tcttcaccgc	actgatggcc	120
aatgggggta	tgatcttctc	gatccaaaca	gatttgcgcc	ttcatacacc	catgtacttc	180
ctcctcagcc	acctttcctt	aattgacatg	atgtatattt	ccactattgt	gcctaagatg	240
ctgggttaatt	acctgctgga	tcaaaggacc	atttcctttg	tgggggtgcac	agctcaacac	300
ttcctctacc	ttacccttgt	gggagctgaa	ttcttctctg	tgggcctcat	ggcctatgac	360
cgctatgtgg	ccatttgcaa	ccctctgaga	tacctgtctc	tcattgagccg	ccgggtctgt	420
tggatgatta	tagcaggttc	ctgggttggg	ggctctttgg	atggcttctc	cctaaccctc	480
atcaccatga	gctttccctt	ctgcaattcc	cgggagatta	accacttctt	ctgcgaggca	540
ccagcagtc	tgaagttggc	atgtgcagac	acagccctct	acgagacagt	gatgtatgtg	600
tgctgtgttt	tgatgtctgt	gattcctttc	tctgtagtcc	ttgcttctta	tgcccgaatc	660
ctgactacag	ttcagtgcct	gagctcagtg	gagggcagga	agaaggcatt	tgccacttgc	720
tcattccaca	tgactgtggt	gtccttggtc	tacggggctg	ccatgtacac	ctacatgctg	780
ccacattctt	accacaagcc	agcccaggac	aaagtccctc	ctgtgtttta	caccattctc	840
acacccatgc	tgaacccctc	catctacagc	cttagaaca	aggatgtgac	tggagctctg	900
aagagggcct	tggggaggtt	caagggtcct	caa			933

<210> 463

<211> 883

<212> DNA

<213> Unknown (H38g312 nucleotide)

<220>

<223> Synthetic construct

<400> 463

atccaatgca	agggctaata	gaagtgaatt	aagacattct	ctgtaactcc	aatattaaat	60
ggaaaccggg	aaatagccag	attcctctcc	aacctgtcct	tggctggcat	cggtttcccc	120
tccaccatag	tctccaagat	gattgtggac	atccagtctc	acagcagagt	catctcctat	180
gcgggctgcc	tgactcaggt	atctcttttt	gccgtttttg	gatgcattga	agacatgctt	240
ctgagtgtga	tggcttatga	cgggtttgtg	gacatctgtc	accctctgga	ttatccagtc	300

atcatgaacc	catgtttctg	tggttccta	gttttgtgt	cttttttct	cagtcttta	360
gactcccagc	tgacaaattg	gattgcctta	caaattacct	gcttcaagga	tgtggaaatt	420
cccaatttct	tctgtgaccc	ttctcaactc	ccccaccctt	gcctgttgtg	acaccttcac	480
caatgacata	gtcatgtatt	tccttgctgc	catatttggt	ttcttccca	tttcggggcc	540
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ataaagcctt	ctccacctgt	ggctctcacc	tgctcagttg	ttgcttattt	tatggaacag	660
gctttggagg	ggacctcagt	tcagacatgt	cctcttatcc	cagaaaaggt	gcagtggcct	720
cagtgatgta	cacggtgggt	actcccatgc	tgaaccatt	catttacagc	ctaacagggg	780
aattaaaagt	gccctgcggc	agctgcactg	cagaatagtc	taatctcatt	ttcttattat	840
ctgttccatt	ccttccgtag	tgtgagttag	aaaaggcagc	aag		883

<210> 464

<211> 942

<212> DNA

<213> Unknown (H38g313 nucleotide)

<220>

<223> Synthetic construct

<400> 464

atgaccctgg	gatccctggg	aaacagcagc	agcagcgttt	ctgctacctt	cctgctgagt	60
ggcatccctg	ggctggagcg	catgcacatc	tggatctcca	tcccactgtg	cttcatgtat	120
ctggtttcca	tcccgggcaa	ctgcacaatt	ctttttatca	ttaaaacaga	gcgctcactt	180
catgaacctt	tgtatctctt	cctgtccatg	ctggctctga	ttgacctggg	tctctccctt	240
tgcactctcc	ctacagtcct	gggcatcttt	tgggttgagg	cacgagaaat	tagccatgat	300
gcctgctttg	ctcagctctt	tttcattcac	tgcttctcct	tcctcgagtc	ctctgtgcta	360
ctgtctatgg	cctttgaccg	ctttgtggct	atctgccacc	ccttgcaacta	tgtttccatt	420
ctcaccaaca	cagtcattgg	caggattggc	ctggctctct	tgggtcgtag	tgtagcactc	480
atttttccat	taccttttat	gtcmetaaga	ttccccctatt	gtggctcccc	agttctctca	540
cattcttatt	gtctccacca	agaagtgatg	aaattggcct	gtgccgacat	gaaggccaac	600
agcatctacg	gcatgtttgt	catcgctctt	acagtgggta	tagactcact	gctcaccctc	660
ttctcttatg	ctctgatcct	ggcaccgctg	ctgtccatcg	cctccagggc	tgagagattc	720
aaggccctta	acacctgtgt	ttcccacatc	tgtgtctgtc	tgctcttcta	cactcccatg	780
attggcctct	ctgtcatcca	tcgctttgga	aagcaggcac	cccacctggt	ccaggtgggc	840
atgggtttca	tgtatcttct	ctttctctct	gtgatgaatc	ccattgtcta	cagtgtgaag	900
accaaacaga	tccgggatcg	agtgcacgat	gccttttggt	ac		942

<210> 465

<211> 990

<212> DNA

<213> Unknown (H38g314 nucleotide)

<220>

<223> Synthetic construct

<400> 465

atgggactct	tcagacaatc	caaacatcca	atggccaata	tcacctggat	ggccaaccac	60
actggatggg	cggatttcat	cctgttgagg	ctcttcagac	aatccaaaca	tccagcacta	120
ctttgtgtgg	tcatttttgt	ggttttcctg	atggcgttgt	ctggaaatgc	tgctctgatc	180
cttctgatac	actgtgacgc	ccacctccac	acccccatgt	actttttcat	cagtcaattg	240
tctctcatgg	acatggcgta	catttctgtc	actgtgccc	agatgtctct	ggaccaggtc	300
atgggtgtga	ataagatctc	agcccctgag	tgtgggatgc	agatgttctt	ctacgtgaca	360
ctagcaggtt	cagaattttt	ccttctagcc	accatggcct	atgaccgcta	cgtggccatc	420
tgccatcttc	tccgttacct	tgctctcatg	aacctatagg	tgtgtctctt	cctgtcatca	480
ggctgtgggt	tctgggctc	agtggatggc	ttcacattca	ctcccatcac	catgaccttc	540
cccttccgtg	gatcccgga	gattcatcat	ttcttctgtg	aagttcctgc	tgtattgaat	600
ctctcctgct	cagacacctc	actctatgag	attttcatgt	acttgtgctg	tgctctcatg	660
ctcctcatcc	ctgtgggtgat	catttcaagc	tcctattttac	tcctcctcct	cacctccac	720
gggatgaact	cagcagaggg	ccggaaaaag	gcctttgcca	cctgtctctc	ccacctgact	780
gtgggtcatcc	tcttctatgg	ggctgccatc	tacacctaca	tgctccccag	ctcctaccac	840
acccctgaga	aggacatgat	ggtatctgtc	ttctatacca	tcctcactcc	agtggatgaac	900

cctttaatct atagtcttag gaataaggat gtcattggggg ctctgaagaa aatgttaaca 960
gtggaacctg cctttcaaaa agctatggag 990

<210> 466

<211> 591

<212> DNA

<213> Unknown (H38g315 nucleotide)

<220>

<223> Synthetic construct

<400> 466

gctgccatgg	cttaagaccg	gtacatagca	atctgtaacc	cgctgctcta	tacagtgatt	60
atgtccaaga	agggttggtg	ccagcttgca	attggagcat	ttttgggggg	cactatgagc	120
tcaattattc	ataccacgaa	cactttccat	ctgtcattct	gctccagaga	tattaacat	180
ttcttttgtg	atatctcccc	actcttctct	ctgtccctgca	ctgacacata	catgcatgac	240
atcattctgg	tgggtcttgc	cagttttgtg	gaagcaatct	gtcttctatc	agttctcctt	300
tcttatgtct	tcattatggc	agctattctt	agaacagggt	ctgtggaggg	aagaagaaga	360
gggttctcca	cttggtgctc	ccacctgact	gtgggtcacta	tgtatcatgg	taccttgatc	420
ttcatttatt	tgcgtcccag	cactggccat	tcactggata	ttgacaaagt	gacctctgtg	480
ttctatactt	tgattatacc	tatgttgaac	cctctaattt	acagtctaag	gaacaaagat	540
gtcaaaaatg	cttttagaaa	agtgattggc	cgaaaattac	ttccttaagg	t	591

<210> 467

<211> 938

<212> DNA

<213> Unknown (H38g316 nucleotide)

<220>

<223> Synthetic construct

<400> 467

atgatgactc	ttaagaactg	cactgtgttt	actgacttta	tattcttagg	actttcaggt	60
acacaggata	tacagcaggg	gctctttgtg	cttttcttcc	tgatttatgg	cataactgtg	120
attgtcaatc	tagggatgat	cctactgac	aagatggatc	tcagacttca	cacacccgtg	180
tattatttcc	tgagcaattt	gtctttctgt	gatgtctgct	actcttccac	gtctctccca	240
aatgctagct	gatttcttat	cggaccaaaa	gtggattccg	tataatttat	gtgccattca	300
gatgtattta	tttgaggtct	ttgcagatgt	ggaatgtctc	atggtggctg	tcattggccta	360
tgatcggtat	gttgccattt	gcaatccact	tctttatacg	atcactatgc	ccaggaggat	420
ctgcacccag	ctagtggctc	ttgcctatgt	tgtagggttg	gtggattctg	caatccacac	480
ctgctgcaca	ttcagattgt	cattctgcaa	ttctaattgc	atcaatcact	ttttctgtga	540
catccacccc	ttgctagccc	tcaatccctac	tattaattgc	tattaatgag	atagtgatgt	600
tcacattcgt	tggctgtgtt	gcgggggtgca	gcattgtcac	tgtcttcttc	tcctacagct	660
acatcataat	taccatcctt	aaaatgagct	cagctgaggg	cagacggaaa	gccttctcta	720
cctgcacctc	ccacttgatg	gccgtggctg	tatttcatgg	cacactcctg	ttcatgtatt	780
tccgacccag	ttcaagttac	tcaatggaaa	cagacaaaat	ggcctctgtt	ttctacacag	840
ttgtcatacc	tatgttaa	ccactgatct	acagcttaag	gaatagggat	gtgaaagggtg	900
ctctgaaaaa	agcaataagc	actaaattat	attctgtta			938

<210> 468

<211> 969

<212> DNA

<213> Unknown (H38g317 nucleotide)

<220>

<223> Synthetic construct

<400> 468

atgtcaacat	taccaactca	gatagccccc	aatagcagca	cttcaatggc	ccccaccttc	60
ttgctggtgg	gcatgccagg	cctatcaggt	gcacctcct	ggtggacatt	gccccctcatt	120
gctgtctacc	ttctctctgc	actgggaaat	ggcaccatcc	tctggatcat	tgccctgcag	180

cccgccctgc	accgcccacat	gcacttcttc	ctcttcttgc	ttagtggtgc	tgatattgga	240
ttggtcactg	ccctgatgcc	cacactgctg	ggcatcgccc	ttgctgggtgc	tcacactgtc	300
cctgcctcag	cctgccttct	acagatgggt	tttatccatg	tcttttctgt	catggagtc	360
tctgtcttgc	tcgccatgtc	cattgatcgg	gcactggcca	tctgccgacc	tctccactac	420
ccagcgctcc	tcaccaatgg	tgtaattagc	aaaatcagcc	tggccatttc	ttttcgatgc	480
ctgggtctcc	atctgcccct	gccattcctg	ctggcctaca	tgccctactg	cctcccacag	540
gtcctaacc	attcttattg	cttgcaccca	gatgtgggtc	gtttggcctg	cccagaagct	600
tgggggtgcag	cctacagcct	atttgtgggt	ctttcagcca	tgggtttgga	ccccctgctt	660
attttcttct	cctatggcct	gattggcaag	gtgttgcaag	gtgtggagtc	cagagaggat	720
cgctggaagg	ctgggtcaaac	ctgtgctgcc	cacctctctg	cagtgtcctc	cttctatata	780
cctatgatcc	tcctggcact	gattaaccat	cctgagctgc	caatcactca	gcatacccat	840
actcttctat	cctatgtcca	tttccttctt	cctccattga	taaaccctat	tctctatagt	900
gtcaagatga	aggagattag	aaagagaata	ctcaacaggt	tgcagcccag	gaaggtgggt	960
ggtgctcag						969

<210> 469

<211> 384

<212> DNA

<213> Unknown (H38g318 nucleotide)

<220>

<223> Synthetic construct

<400> 469

tctcgctcag	atacacaggt	caatgagtta	gtgttattca	cgtcttttgg	ttttattgaa	60
ctgagtacca	tttcaggagt	tttcatttct	tattgttata	tcattcctatc	agtcttggag	120
atacactctg	ctgaggggag	gttcaaagct	ctctctacat	gcacttccca	cttatctgcg	180
gttgcaattt	tccagggaac	tctgctcttt	atgtatttcc	ggccaagtcc	ttcctattct	240
ctagatcaag	ataaaatgac	ctcattgttt	tacacccttg	tggttcccat	gttgaacccc	300
ctgatttata	gcctgaggaa	caaggatgtg	aaagaggccc	tgaaaaaact	gaaaaataaa	360
attttatttt	aaggaaatag	taaa				384

<210> 470

<211> 946

<212> DNA

<213> Unknown (H38g319 nucleotide)

<220>

<223> Synthetic construct

<400> 470

atgtttctgc	tcaatacctc	agaagttgaa	gtctccacat	tcctattgat	tgggatacca	60
ggacttgagc	atgcacacat	ttggatctct	atccccatct	gccttatgta	cctcatggcc	120
atcctgggca	actgcacccat	cctatttggt	atcagaacag	agcattccct	gcaagagccc	180
atgtactatt	tcctctccat	gctggccctg	tccgacctgg	gcctgtcttt	ctcctcccta	240
cccacgatgc	tgagaatctt	cttgttcaac	aacatgggga	tttctgctga	tacatgcatt	300
gcccaggaat	tcttcatcca	tggattcaca	gacatggagt	cttcagttct	cctaatacatg	360
tcctttgatc	acttagtagc	catttgcaac	cccctaagat	atagctctat	tctcaccage	420
ttcagggttt	tgcaaatggg	actggctttt	gccattaaaa	gcattctcct	agtgtacccc	480
cttttacttt	aaagagactc	agatactgta	ataaacacct	tttatcccac	tcctactgcc	540
ttcaccagga	tgtaatgaag	ctggcctgct	ctgacaacag	ggttaacttt	tactatgggt	600
tgttcgttgc	actctgcatg	atgtcagaca	gtgtttttat	tgctatttcc	tatatgtgtt	660
catcctgaag	actgtgttgg	gtattgcac	ccatggggag	tgccctgaag	ctcttgacac	720
ctgtgtgtct	catatctgtg	ctgtactcgt	cttctatgtg	cccatcatca	ccttggctac	780
catgcgtcgc	tttgctaagc	ataaatcccc	tttagctatg	attctgatag	cagatgcatt	840
cttgctggta	ccacccttga	tgaatcccat	tgtgtattgt	gtaaaaactc	ggcagattag	900
agtaaagggtc	ctggaaaaat	tggctctgaa	gcctaaatga	tggggc		946

<210> 471

<211> 942

<212> DNA

<213> Unknown (H38g320 nucleotide)

<220>

<223> Synthetic construct

<400> 471

atgatggcat	ct,aaagaaa	tcaaagcagc	acacccactt	ttattctctt	gggtttttca	60
gaatacccg	aaatccagg	tccactcttt	ctggttttct	tggtcgtcta	cacagtcact	120
gtagtggga	acttgggcat	gataataatc	atcagactca	attcaaaact	ccatacaatc	180
atgtgctttt	tccttagtca	cttgtccttg	acagacttct	gtttttccac	tgtagttaca	240
cctaaactgt	tggagaactt	ggttgtggaa	tacagaacca	tctctttctc	tggttgcac	300
atgcaatttt	gttttgcttg	catttttgga	gtgacagaaa	ctttcatgtt	agcagcgatg	360
gcttatgacc	gttttgctgc	agtttgtaaa	cccttgctgt	ataccactat	tatgtctcag	420
aagctctgtg	ctcttctggt	ggctgggtcc	tatacatggg	ggatagtgtg	ctccctgata	480
ctcacatatt	ttcttcttga	cttatcggtt	tgtgaatcta	ccttcataaa	taattttatc	540
tgtgaccact	ctgtaattgt	ttctgcctcc	tactcagacc	cctatatcag	ccagaggcta	600
tgctttatta	ttgccatatt	caatgagggtg	agcagcctaa	ttatcattct	gacatcatat	660
atgcttattt	tactaccat	tatgaagatg	cgatctgcaa	gtgggcgcca	gaaaactttc	720
tccacctgtg	cctccacact	gacagccatc	actatcttcc	atggaactat	ccttttccct	780
tactgtgttc	ctaatacctaa	aacttctagc	ctcatagtta	cagtgggttc	tgtgttttac	840
acagtggcga	ttccaatgct	gaacccattg	atctacagcc	ttaggaacaa	agatatcaat	900
aacatgtttg	aaaaattagt	tgtcaccaaa	ttgatttacc	ac		942

<210> 472

<211> 965

<212> DNA

<213> Unknown (H38g321 nucleotide)

<220>

<223> Synthetic construct

<400> 472

cacacagagc	cacggaatca	cacaggggtc	tgagaatttc	tctctctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctgtccctgt	cctgtcccat	gtatctgggc	120
acgggtgctga	ggaacctgct	cagcatcctg	gctgtccgct	ctgactcccc	cctccacaac	180
cccatgtact	tcttctcttc	caacctgtgc	tgggctgaca	tgggtttcac	ctcgccacag	240
gttgccaaga	tgattgtgga	atgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgcttttga	gccatctgtc	gtcctctgca	ctaccagtc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttggtgt	cctttttcct	tagcctgttg	gattcccagc	480
tgcacagttc	gattgtgtta	caattcacca	tcataaagaa	tgtggaaatc	tctcattttg	540
tctgtgaccc	ctctcatctt	ctcaaacttg	cctgttctga	cagcgtcatc	aatagcatat	600
tcatataatt	cgatagtact	atgtttggtt	ttcttcccat	ttcagggatc	ccttggtctt	660
actataaaat	cgtccctctc	attctaagga	tttcatcatc	agatgggaag	tataaagcct	720
tgcgccactg	tggctctcac	ctagcagttg	tttgctgatt	tgatggaaca	ggcattggta	780
tgtacctgac	ttcagctgtg	gcaccacccc	ctaggaatgg	agtgggtggc	tcagtgatgt	840
aggctgtggt	cacccccatg	ctgaaccttt	tcacttacag	cctgagaaac	agggacatac	900
aaagtgcctt	gcggaggctg	ctcagcagaa	cagtcgaatt	tcatgatctg	tttcattctt	960
tttct						965

<210> 473

<211> 990

<212> DNA

<213> Unknown (H38g322 nucleotide)

<220>

<223> Synthetic construct

<400> 473

atgtcgggtcc	tcaataatac	cattgctgag	cctctgatct	tctctctgat	gggcattcca	60
ggcctgaaag	ccaccagta	ctggatctcc	atcccttttt	gtctctata	tgttgttgcc	120

gtctctggaa	atagcatgat	cctgtttgtg	gtctctgtg	aacggagcct	ccataagcct	180
atgtactatt	tcctctctat	gctttcagcc	acagacctga	gcttgccct	gtgtacactt	240
tctactaccc	ttggtgtctt	ctggtttgaa	gcccagaaaa	tcaacctaaa	tgccctgcatt	300
gcccagatgt	tctttctaca	cggatttact	ttcatggagt	ctgggggttct	actggccatg	360
gcctttgatc	gttttgtggc	catctgttac	ccactgagat	acactaccat	ccttaccaat	420
gcccgaattg	ccaagattgg	gatgagcatg	ttgataagaa	atgttgccgt	catgttgcca	480
gtcatgctct	ttgtcaagag	gttgctcttc	tgcagttcta	tggtcctttc	acattcttac	540
tgctaccatg	ttgatctcat	ccaactctcc	tgacagaca	ataggatcaa	cagcatcctt	600
ggtctgtttg	cgttttgtc	cactacaggg	tttgactgcc	cttgcatcct	gctctcctat	660
atcctgatca	ttcgatctgt	cctcagcatt	gcttcctcag	aagagaggcg	gaaagccttc	720
aacacctgca	catcccacat	cagtgtctgt	tccatcttct	acctccctct	catcagtttg	780
tctcttgtcc	atcgctatgg	ccattcagca	cctccatttg	tccacatcat	catggccaat	840
gtctttctgc	taatccctcc	tgtgtcaac	cctattattt	acagtgtaaa	gattaagcag	900
attcaaaagg	ccattatcaa	ggtcttaatt	cagaagcact	ccaaatctaa	tcacagcta	960
tttctgatta	gagataaagc	catttatgaa				990

<210> 474

<211> 942

<212> DNA

<213> Unknown (H38g323 nucleotide)

<220>

<223> Synthetic construct

<400> 474

atgatgatgg	ttttaaggaa	tctgagcatg	gagccacact	ttgccctttt	aggtttcaca	60
gattacccaa	agcttcagat	tcctctcttc	cttgtgtttc	tgctcatgta	tgttatcaca	120
gtggtaggaa	accttgggat	gatcataata	atcaagatta	accccaaatt	tcacactcct	180
atgtactttt	tccttagtca	cctctctttt	gttgattttt	gttactcttc	cattgtcact	240
cccaagctgc	ttgagaactt	ggtaatggca	gataaaagca	tcttctactt	tagctgcatg	300
atgcagtact	tcctgtcctg	cactgtctgtg	gtgacagagt	ctttcttgct	ggcagtgatg	360
gcctatgacc	gctttgtggc	catctgcaat	cctctgcttt	atacagtggc	catgtcacag	420
aggctctgtg	ccctgctggt	ggctgggtca	tatctctggg	gcatgtttgg	ccccttggta	480
ctcctttgtt	atgctctccg	gttaaaacttc	tctggacctt	atgtaataaa	ccacttcttt	540
tgtgagtata	ctgctctcat	ctctgtgtct	ggctctgata	tactcatccc	ccacctgctg	600
cttttcagct	tcgccacctt	caatgagagt	tgtacactac	tgatcatcct	cacttcctat	660
gttttcattt	ttgtgactgt	actaaaaatc	cgttctgtta	gtgggcgcca	caaagccttc	720
tccacctggg	cctccacact	gactgctatc	accatcttcc	atgggaccat	ccttttcctt	780
tactgtgtac	ccaactccaa	aaactctcgg	caaacagtca	aagtggcctc	tgtattttac	840
acagttgtca	accccatgct	gaacctccg	atctacagcc	taaggaataa	agacgtgaag	900
gatgctttct	ggaagttaat	acatacacia	gttccatttc	ac		942

<210> 475

<211> 942

<212> DNA

<213> Unknown (H38g324 nucleotide)

<220>

<223> Synthetic construct

<400> 475

atggtgctgg	cttcagggaa	cagctcttct	catcctgtgt	ccttcatacct	gcttgggaatc	60
ccaggcctgg	agagtttcca	gttgtggatt	gcctttccgt	tctgtgccac	gtatgctgtg	120
gctgttgttg	gaaatatcac	tctcctccat	gtaatcagaa	ttgaccacac	cctgcatgag	180
cccatgtacc	tctttctggc	catgctggcc	atcactgacc	tggtcctctc	ctcctccact	240
caacctaaaga	tgttggccat	attctggttt	catgctcatg	agattcagta	ccatgcctgc	300
ctcatccagg	tgttcttcat	ccatgccttt	tcttctgttg	agtctggggg	gctcatggct	360
atggccctgg	gttctactgc	ggctacctgc	tcccactcc	gacactctag	catcctgacc	420
ccatcggtcg	tgatcaaact	ggggaccatc	gtgatgtcga	gagggctgct	gtgggtgagc	480
cccttctgct	tcatgggtgc	taggatgccc	ttctgccaac	accaagccat	tccccagtca	540
tactgtgagc	acatggctgt	gctgaagttg	gtgtgtgctg	atacaagcat	aagtcgtggg	600

tatgggctct	ttgtggcctt	ctctgtggct	ggctttgata	tgattgtcat	tggtatgtca	660
tacgtgatga	ttttgagagc	tgtgcttcag	ttgccctcag	gtgaagcccg	cctcaaagct	720
tttagcacac	gtgcctccca	tatctgtgtc	atcttggtc	tttatatccc	agcccttttt	780
tctttcctca	cctaccgctt	tggccatgat	gtgccccgag	ttgtacacat	cctgtttgct	840
aatctctatc	tactgatacc	tcccatgtct	aaccccatca	tttatggagt	tagaaccaaa	900
cagatcgggg	acagggttat	ccaaggatgt	tgtgggaaca	tc		942

<210> 476

<211> 860

<212> DNA

<213> Unknown (H38g325 nucleotide)

<220>

<223> Synthetic construct

<400> 476

tatatattgt	tagacatata	tatatgtcta	aacaacactc	atgtctaatt	gtgtgtagag	60
tcactagagg	caatttaaaa	taagttttta	tttttctttt	tttctattgg	caataacatg	120
attttagtga	taaattttta	taattatgaa	aacataacag	tactttttta	aacataaaca	180
tttaaagaaa	aagttttcat	gattcttgta	tacatcttaa	catacatact	ctccctttta	240
agtaagttct	ttgcattgtt	taaattcttg	cagacaaagc	ttttcaagag	caagtcagtg	300
gaaactagta	gagcaggagt	tgagaaagcc	ctgtgcatta	tacactcacc	atgtcccaga	360
agttttgtct	catccatcca	gcaggatggt	agaccagggc	atataatcta	tcccgggtca	420
ctcattttct	cattgtattg	cctattgtgg	gcacaatgta	gttaatatat	tttaaaataa	480
atattctgtt	gccatttcag	attcgtgagt	tcactctggat	agcggatttt	tgtttgtttg	540
tttgttttgc	tttagtcaat	tttgattaat	taaggaatct	cagagtcctc	actccttagc	600
tttcattttc	aacttgtcta	aaaggcactt	tctgccagtg	cacatcaacc	ttctccaccc	660
atttcccaca	tttccaccat	ccttcctcac	tctagtgcac	taactccaaa	aactcacagg	720
caactgtgaa	agcacactct	gtatgttatg	ccatgttaat	ccccatgctg	aactcacaga	780
cttgtagcat	gcggtacaaa	aatgtgaatg	aatctctgca	gaagctgatg	gacttcaaaa	840
tatttttagca	ttgaaagcaa					860

<210> 477

<211> 966

<212> DNA

<213> Unknown (H38g326 nucleotide)

<220>

<223> Synthetic construct

<400> 477

agtcacacag	agccatagaa	tctcacaagt	gtctcagaat	tccttctcca	gggactctca	60
gaggatccag	aactgcagcc	cgctctcgct	gggctgtccc	tgtccatgta	cctgggtcacg	120
gtgctgagga	acctgctcat	catcctggct	gtcagctctg	actcccacct	ccacaccccc	180
atgtacttct	tctctctcaa	cctctcctgg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcagtcgcat	agcagagtca	tctcttaagc	gggctgcctg	300
acacagatgt	ctttctttgt	cctttttgca	tgtatagaag	acatgtcctc	gactgtgatg	360
gcctatgacc	aatttggtggc	catctgtcac	ccctgcacta	cccagtcac	atgaatcctc	420
acctctgtgt	cttcttagtt	ttggtttctt	ttttccttag	cctgttggat	tcccagctgc	480
acagttggat	tgtgttacaa	ttcaccttct	tcaagaatgt	ggaaatctct	aattttttct	540
gtgatccatc	tcaacttctc	aaccttgcc	gttctgacgg	catcatcaat	agcatattta	600
tatatcttaga	tattattctg	ttcagttttc	ttcccatctc	agggatcctt	ttgtcttact	660
ataaaaattgt	cccctccatt	ctaagaatct	catcgtcaga	tgggaagtat	aaagccttct	720
ccatctgtgg	ctctcacctg	gcagttgttt	gcttatttta	tgggaacaggc	attggcgtgt	780
acctaacttc	agctgtgtca	ccacccccag	gaatgggtgtg	gtggcgtcag	tgatgtatgc	840
tgtgggcacc	cccattgtga	actcttttat	ctacagcctg	agaaacaggg	acattcaaag	900
cgccctgtgg	aggctgcgca	gcagaacagt	cgaatctcat	gatctgttcc	atccttatct	960
ttgtgt						966

<210> 478

<211> 951

<212> DNA

<213> Unknown (H38g327 nucleotide)

<220>

<223> Synthetic construct

<400> 478

atgcaaccat	ataccaaaaa	ctggacccag	gtaactgaat	ttgtcatgat	gggcttttgc	60
ggcatccatg	aagcacacct	cctcttcttc	atactcttcc	tcaccatgta	cctgttcacc	120
ttgggtggaga	atttggccat	catttttagtg	gtgggttttg	accaccgact	acggagaccc	180
atgtatttct	tcctgacaca	cttgtcctgc	cttgaaatct	ggtacacttc	tgttacagtg	240
cccaagatgc	tggctgggtt	tattgggggtg	gatgggtggca	agaatatctc	ttatgctggt	300
tgcctatccc	agctcttcat	cttcaccttt	cttggggcaa	ctgagtgttt	cctactggct	360
gccatggcct	atgatcgta	tgtggccatt	tgtatgcctc	tccactatgg	ggcttttgtg	420
tcctggggca	cctgcatccg	tctggcagct	gcctgttggc	tggtagggtt	cctcacaccc	480
atcttgccaa	tctacctctt	gtctcagcta	acattttgtg	gccccaaatg	cattgaccat	540
ttctcctgtg	atgcctcacc	cttgctagcc	ttgtcgtgct	cagatgtcac	ttggaaggag	600
actgtggatt	tcctgggtgc	tctggctgtg	ctactggcct	cctctatggt	cattgctgtg	660
tcctatggca	acatcgctctg	gacactgctg	cacatccgct	cagctgctga	gcgctggaag	720
gcccttctta	cctgtgcagc	tcacctgact	gtggtgagcc	tcttctatgg	cactcttttc	780
tttatgtatg	tccagaccaa	ggtgacctcc	tccatcaact	tcaacaaggt	ggtatctgtc	840
ttctactctg	ttgtcacgcc	catgctcaat	cctctcatct	acagtcttag	gaacaaggaa	900
gtgaagggag	ctctgggtcg	agtcttttct	ctcaactttt	ggaagggaca	g	951

<210> 479

<211> 936

<212> DNA

<213> Unknown (H38g328 nucleotide)

<220>

<223> Synthetic construct

<400> 479

atggatggag	agaatcactc	agtgggtatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tcctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccttc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atctttcttca	tccacgtcgt	tgggtgggtg	gagatgggtg	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcctttcat	ttctggctgt	tgcctggacc	cttgggtgtc	gtcactccct	gttccaactg	480
gcattttctg	tttaatttacc	cttctgtggc	cctaattgtg	tggacagctt	ctactgtgac	540
cttccctcagc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catgtgcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacatcttc	660
atcctgttta	ctgtttggaa	acattcctca	ggtgggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagcgg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacatgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagaag	atctca			936

<210> 480

<211> 668

<212> DNA

<213> Unknown (H38g329 nucleotide)

<220>

<223> Synthetic construct

<400> 480

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aggaacccca	tcatgacctc	gtgtttctgt	ggctttctag	ttttgtcttt	tttttttttt	120

ttctcagtc	tttagacgcc	cagctgcaca	acttgattgc	cttacaaatg	acctgcttcc	180
aggatgcgga	aattcctagt	ttcttctgtg	acccttctca	actcccccat	cttgcattgt	240
gtgacacctt	caccaataac	ataatcatgt	atttgccctg	tgccatat	ggttttcttc	300
ccatctcggg	gacccttttc	tcttactata	aaattgtttc	ctccattctg	aggggttcat	360
catcacgtgg	gaagtataag	gccttctcca	cctgtgggtc	tcacctgtca	gttggttgct	420
gattttacgg	aacaggcttt	ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	480
aggctgcagt	ggcctcagtg	atgtacacgg	tgatcacctc	catgctganc	cccttcatct	540
acagcctgag	aaacagggat	attaaagggtg	tcctgcggca	gccgcacggc	agcaccgtcc	600
aatttcagta	tcttcttata	tgttccattc	ctttttagtg	gtgggttaaa	aaaggcagca	660
aggtcaaa						668

<210> 481

<211> 840

<212> DNA

<213> Unknown (H38g330 nucleotide)

<220>

<223> Synthetic construct

<400> 481

atgtacctgg	tcacgggtgct	gaggaacctg	ctcatcatcc	tggctgtcag	ctctgactcc	60
cacctccaca	cccccatgtg	cttcttcctc	tccaacctgt	gctgggctga	catcgggttc	120
acctcggcc	tggttcccaa	gatgattgtg	gacatgcagt	cgcatagcag	agtcattctc	180
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ctcctgacag	tgatggccta	tgaccgattt	gtggccatct	gtcaccacct	gcactaccca	300
gtcatcatga	atcctcacct	tggtgtcttc	ttagtttttg	tgctcctttt	cctcagcctg	360
ttggattccc	agctgcacag	ttggattgtg	ttacaattca	ccttcttcaa	gaatgtggaa	420
atctccaatt	ttgtctgtga	cccatctcaa	cttctcaacc	ttgcctgttc	tgacagtgtc	480
atcaatagca	tattcatata	tttagatagt	attatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttacgctaa	caatgtcccc	tccattctaa	gaatttcata	atcagatagg	600
aagtctaaag	ccttctccac	ctgtggctct	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gcgtgtacct	gacttcagct	gtgtcaccac	ccccaggaa	tggtgtgggtg	720
gcatcagtga	tgtacgctgt	ggtcaccccc	atgctgaacc	ctttcatcta	cagcctgaga	780
aatagggaca	ttcaaagtgc	cctgtggagg	ctgcgcagca	gaacagtcga	atctcatgat	840

<210> 482

<211> 924

<212> DNA

<213> Unknown (H38g331 nucleotide)

<220>

<223> Synthetic construct

<400> 482

atggaaacac	agaacctcac	agtggtgaca	gaattcattc	ttcttgggtc	gacctcagtc	60
caagatgctc	aacttctggg	ctttgtgcta	gtcttaattt	tctaccttat	catcctccct	120
ggaaatttcc	tcatcatttt	caccataaag	tcagaccttg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttggc	cttactggat	gcacccact	ccttcattgt	ggttcccagg	240
atgttgggtg	acttctcttc	tgagaagaag	gtaatctctc	atagaagctg	catcactcag	300
ctctttttct	tgcattttct	tgagcgggga	gagatgttcc	tcctcgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggccttta	cactattcaa	ccatcatgaa	ccctagagcc	420
tgctatgcat	tatcgttggg	tctgtggctt	gggggcttta	tccattccat	tgtacaagta	480
gcccttatcc	tgcacttgcc	tttctgtggc	ccaaaccagc	tcgataactt	cttctgtgat	540
gttccacagg	tcatcaagct	ggcctgcacc	aatacctttg	tggtggagct	tctgatggtc	600
tccaacagtg	gcctgtcag	cctcctgtgc	ttcctgggce	ttctggcctc	ctatgcagtc	660
atcctctgtc	gtataaggga	gcactcctct	gaaggaaaga	gcaaggctat	ttccacatgc	720
accacccata	ttatcattat	atcttctcatg	tttggacctg	ctattttcat	ctacacttgc	780
cccttccagg	ctttcccagc	tgacaaggta	gtttctcttt	tccatactgt	catctttcct	840
ttgatgaacc	ctgttattta	tacgtttcgc	aaccaggagg	tgaaagcttc	catgaggaag	900
ttgttaagtc	aacatatggt	ttgc				924

<210> 483
 <211> 457
 <212> DNA
 <213> Unknown (H38g332 nucleotide)

<220>
 <223> Synthetic construct

<400> 483
 gggatgagaa aggaacaagc tgtctgtggt agtcatccat gattgagatg atgtgtggac 60
 cctgagtcag actacctggt tcaaatgcag gctctctact ttttaccat ttgatcttgg 120
 cctgtggctc tctacttctt atccatttca tcttggactt gtggcctctc atacctcacc 180
 ttcccttacag tctcccatat gaaatcccc taaagtagga acaaagcttt ggccaactgc 240
 tctcccatc tttccgtggt ctttacttag gaactgtgtg tttaataatg gtgacacagg 300
 gtttctccca catccctgag cagaaacaag ctgtgtctgt attttgcact gtactcacc 360
 ccatgctaaa cccctcacc tacatcctga gaaacaagga tgtggtggg ctcttcagaa 420
 agttctggga acacatcaag tctctaaaca gaacaca 457

<210> 484
 <211> 972
 <212> DNA
 <213> Unknown (H38g333 nucleotide)

<220>
 <223> Synthetic construct

<400> 484
 atgtctttct tctttgtaga cttaagaccc atgaacaggt cagcaacaca catcgtgaca 60
 gagtttatcc tcttgggatt ccctggttgc tgggaagattc agattttcct cttctcattg 120
 tttttggtga tttatgtctt gaccttgctg ggaaatggag ccatcatcta tgcagtgaga 180
 tgcaaccac tactacacac cccatgtac tttctgctgg gaaattttgc cttccttgag 240
 atctggtatg tgtcctccac tattcctaac atgctagtca acattctctc caagaccaag 300
 gccatctcat tttctgggtg cttcctccag ttctatttct tcttttact gggaacaact 360
 gaatgtctct tcttggcagt aatggcttat gatcgatacc tggccatctg ccacctactg 420
 cagtaccctg ccatcatgac tgtaagggtc tgtggttaagc tgggtgtctt ctgttggctt 480
 attggattcc ttggataccc aattcccatt ttctacatct cccaactccc cttctgtggt 540
 cctaatatca ttgatcactt cctgtgtgac atggacccat tgatggctct atcctgtgcc 600
 ccagctccca taactgaatg tattttctat actcagagct cccttgtcct ctttttact 660
 agtatgtaca ttcttcgac ctatctcctg ttactaacag ctgtttttca ggtccctct 720
 gcagctggtc ggagaaaagc cttctctacc tgtggttctc atttggttgt ggtatctctt 780
 ttctatggga cagtcattgt aatgtatgta agtcctacat atgggatccc aactttattg 840
 cagaagatcc tcacactggt atattcagta acgactctc tttttaatcc tctgatctat 900
 actcttcgta ataaggacat gaaactcgct ctgagaaatg tctgttttg aatgagaatt 960
 cgtcaaaatt cg 972

<210> 485
 <211> 945
 <212> DNA
 <213> Unknown (H38g334 nucleotide)

<220>
 <223> Synthetic construct

<400> 485
 atggccaaca tcaccaggat ggccaaccac actggaaagt tggatttcat cctcatggga 60
 ctcttcagac gatccaaaca tccagctcta cttagtgtgg tcatctttgt ggttttcctg 120
 aaggcggtgt ctggaaatgc tgtcctgac cttctgatac actgtgacgc ccacctccac 180
 agcccatgt actttttcat cagtcaattg tctctcatgg acatggcgta catttctgtc 240
 actgtgcca agatgtctct ggaccagggtc atgggtgtga ataaggctct agccctgag 300
 tgtgggatgc agatgttct ctatctgaca ctagcaggtt cggaattttt cttctagcc 360
 accatggcct atgaccgcta cgtggccatc tgccatcctc tccgttacct tgcctcatg 420

aaccataggg	tctgtctttt	cctggcatcg	ggctgctggg	tcctgggctc	agtggatggc	480
ttcatgctca	ctcccatcac	catgagcttc	cccttctgca	gatectggga	gattcatcat	540
ttcttctgtg	aagtccctgc	tgtaacgatc	ctgtcctgct	cagacacctc	actctatgag	600
accctcatgt	acctatgctg	tgtcctcatg	ctcctcatcc	ctgtgacgat	catttcaagc	660
tcctattttac	tcatectctc	caccgtccac	aggatgaact	cagcagaggg	ccggaaaaag	720
gcctttgcca	cctgctctc	ccacctgact	gtggtcaccc	tcttctatgg	ggctgccgtc	780
tacacctaca	tgctccccag	ctcctaccac	acccttgaga	aggacatgat	ggatatctgc	840
ttctatacca	tcctcactcc	gggtgctgaac	cctttaatct	atagtcttag	gaataaggat	900
gtcatggggg	ctctgaagaa	aatgttaact	gtgagattcg	tcctt		945

<210> 486

<211> 759

<212> DNA

<213> Unknown (H38g335 nucleotide)

<220>

<223> Synthetic construct

<400> 486

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gattatctca	tgggcgaggg	gaccatctct	ttcatcgcc	gcactgctca	gtgctttctc	120
tacatgggct	ttatgggggc	tgaattcttc	ctgctggggc	tcattggccta	tgaccgctac	180
gtggccatct	gcaacccact	gcgctatcct	gtcctcatca	gctggcgggt	ctgctggatg	240
atcctggcca	gctcttgggt	cggtggggct	ttggacagtt	ttctcctcac	ccccattacc	300
atgagtctcc	cgttctgtgc	ctctcaccaa	atcaatcact	ttttctgtga	ggcaccacc	360
atgctgaggg	tggcctgtgg	ggacaaaacc	acctatgaaa	cagtgatgta	tgtgtgctgc	420
gttgcaatgc	tgctgatccc	cttctcgggt	gtgactgcat	cctacaccag	gattctcatc	480
acagtgcac	agatgacatc	ggctgaaggg	aggaagaagg	cctttgccac	ctgctcttca	540
cacatgatgg	tgggtgacatt	gttctatggg	gctgccttgt	atacgtatac	gcttccccaa	600
tcttaccaca	cccacatcaa	agataaggtc	ttctctgcct	tttataccat	cctcaccccc	660
ttattaaacc	ctctcatcta	cagtctgagg	aacagggatg	tgatgggtgc	cttgaagaga	720
gttgtggcaa	gatgttaggg	gacatgtggg	gtgatgagg			759

<210> 487

<211> 857

<212> DNA

<213> Unknown (H38g336 nucleotide)

<220>

<223> Synthetic construct

<400> 487

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ttttttttgt	ccccctcatg	cccatctcct	atcgagtggt	ctaagagtgc	agtcagcttc	120
gtgtcacaga	gcaggcgcat	tagatttttg	ggctgtgaca	ttcaaacggg	atgtgttctc	180
gggcccctgg	gggaactgaa	gcccttctct	ttggttttat	gtcttatgat	cgctatgtag	240
ctatctgtca	ccctttacat	tatcctatgc	ttatgagcaa	gaagatctgc	tgccctatgg	300
ttgcatgtgc	atgggccagt	ggttctatca	atgctttcat	acatacattg	tatgtgtttc	360
agcttccatt	ctgtaggtct	cggtcatta	accacttttt	ctgtgaagtt	ccagctctac	420
tatcattggg	gtgtcaggac	acctcccagt	atgagtatac	agtcctcctg	agtggactta	480
ttatcttgct	actaccattc	ctagccattc	tggcttccca	tgctcgtgtg	cttattgtgg	540
tattccagga	gagctcagga	aaaggacagg	caaaagctgt	ttccacttgt	tcctcccacc	600
tgattgtggc	aagcctgttc	tatgcaacca	ctctctttac	ctacacaagg	ccacactcct	660
tgcgttcccc	ttcacgggat	aaggcggtgg	cagtatttta	caccattgtc	acacctctac	720
tgaacccatt	tatctacagc	ctgagaaata	aggaagtgc	gggggcagtg	aggagactgt	780
tgggatattg	gatatgctgt	agaaaatatg	acttcagatc	tctgtattga	ttgagcatta	840
acaacataaa	aagctgt					857

<210> 488

<211> 812

<212> DNA

<213> Unknown (H38g337 nucleotide)

<220>

<223> Synthetic construct

<400> 488

agaagggaca	ttttctattt	tgccttcatt	tgtagctatt	catgactgac	tctccgttct	60
tttgtctact	tgttcatccg	tccatccatc	catccatcca	tccactcagc	cattcttttg	120
ttcaacagtg	atttactgaa	ttccttacta	tgactcttct	atatttgaca	tgccacacga	180
tgttcagcaa	tgacttctac	tcaagagcta	gttttttagt	tcacactgct	tttctcttgt	240
tctttatctt	ttgcttttgt	agctcagaac	agaaaaatct	atagaaaaga	tcttgctacc	300
aggctatggg	accctcttgt	ccatggcgat	atcttactgt	ctttgtgtct	ttgggctgag	360
caatcctgca	gcatgggtga	tgctcaataa	tgctcatgga	acaaaatggg	gtgggttcctc	420
ttccaggaag	tgctgccatc	tctcttttga	ttgagaatag	gtttacctag	gtgattacat	480
cactaacatt	gtattcctgt	gatttcttcc	tcatgatagg	acagatttta	ctaaaaagtc	540
aaaaattatt	tattacatta	tgccgttcct	cttacttttc	atgccagatt	aaattttctt	600
ggtccttcaa	tgcccacttc	taatatcaat	aaacaagtaa	cctttcccca	acctactgaa	660
gtcgccatgt	ggaattggtc	attctttctg	ttgattccat	atcatccctt	tcattcttct	720
gtctgcccg	ttgtccatcc	atttatccat	ccacttagct	attcgttcgt	tcaacaatga	780
tttagtgaat	acctacttac	tgtgacccta	tt			812

<210> 489

<211> 931

<212> DNA

<213> Unknown (H38g338 nucleotide)

<220>

<223> Synthetic construct

<400> 489

atgtcattag	ctgaaggaaa	tcagagttct	ggagccgcat	ttaccctctt	gggcttctca	60
gaatatgcag	acctccaggt	tctctgttcc	ctggctctcc	tgaccatcta	cacaatcact	120
gtattgggaa	acctgggcat	gatcatgac	atcaggatca	accccaaact	ccacaccgcg	180
atgtactttt	tctcagcca	cttgtccttt	gttgatttct	gttattccac	cacagttaca	240
cccaaactgc	tggagaactt	ggttgtggaa	gacagaacca	tctccttcac	aggatgcatc	300
atgcaattct	tcctggcgtg	tatatgtgca	gtggcagaaa	cattcatgct	ggcagtgatg	360
gcctatgatt	gatacgtggc	ggtgtgtaac	cctttgctct	acacagttgt	caggtcccag	420
aaactctgtg	catcattagt	ggcagggccc	tacacatggg	gtataatctc	ttctctgaca	480
ctcacctatt	tcctcttgtc	attatccttc	tgtgggtcta	acatcatcaa	taattttgtc	540
tgtgagcact	ctgtcatcat	ctctgtctcc	tgctctgacc	cctacatcag	ccaaatgctt	600
tgttttgtca	ttgcaatatt	caatgagggt	agcagcttgg	gagtcatcct	cactaccctat	660
attttcatct	ttattgctgt	cataaaaaatg	ccttctgtctg	ttgggcacca	aaaagctttc	720
tctacctgtg	cttcccacct	gactgccatc	actattttcc	acgggactgt	cctgttccctt	780
tattgtgtac	ccaactccaa	aaactcatgg	ctcatagtca	aagtaggttc	tgtgttttat	840
acagtcatca	tccccacggt	gaacccttta	acctacagcc	tcaggaacaa	agacgtgaaa	900
gagagtgttc	gaaagttaat	gaatcactca	a			931

<210> 490

<211> 651

<212> DNA

<213> Unknown (H38g339 nucleotide)

<220>

<223> Synthetic construct

<400> 490

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ttcttcattt	tgggtgtcctt	tttcccttagc	ctgttggatt	cccagctgca	tagctggatt	180
gtgtttacaat	tcaccatcat	caagaatgtg	gaagtctcta	attttgtctg	tgaccctctt	240
caactttctca	aacttgccctg	ttctgacagc	gtcatcaata	gcatattcat	atatttcgat	300

aatactatgt	ttgggttttct	tcccatttca	gggatccctt	ggctcttacta	taaaatcgtc	360
ccctacattc	tcaggatttc	atcgtcagat	gggaagtata	aagccttcgc	cacctgtggc	420
tctcacctgg	cagttgcttg	ctgattttat	ggaacaggca	ttggcatgta	cctgacttca	480
gctgtgtcac	cacccccag	gaatgggtgtg	gtggcatcag	tgatgtacgc	tgtggtcacc	540
cccattgtga	acctttttat	ctacagcctg	agaaacaggg	acatacaaaag	tgccctgcgg	600
aggctgcgcc	ccagaacagt	cgaatctcat	gatctgttcc	atcctttttc	t	651

<210> 491

<211> 933

<212> DNA

<213> Unknown (H38g340 nucleotide)

<220>

<223> Synthetic construct

<400> 491

atgggcaagg	aaaactgcac	cactgtggct	gagttcattc	tccttggact	atcagatgtc	60
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gccaatctgg	gcatgactgc	actgattcag	gtcagctctc	ggctccacac	ccccgtgtac	180
tttttctca	gccacttgct	ctttgtagat	ttctgctact	cctcaataat	tgtgccaaaag	240
atgttggtca	atatctttaa	caaggacaaa	gccatctcct	tcctaggggtg	catgggtgcaa	300
ttctacttgt	tttgacatg	tggagtcact	gaggctcttc	tgctggccgt	gatggcctat	360
gaccgctttg	tggccatctg	taacccccctg	ctgtacatgg	tgaccatgtc	tcagaagctg	420
cgtgtggagc	tgacctcttg	ctgctacttc	tgtgggacgg	tgtgttctct	gattcactcg	480
tccttagctc	ttaggatcct	cttctataga	tctaattgtga	ttaaccactt	cttctgtgat	540
ctacccccctc	tcctaagtct	tgcttgctct	gatgtcactg	tgaatgagac	actgctgttc	600
ctgggtggcca	ctttgaatga	gagtgttacc	atcatgatca	tcctcacctc	ctacctgcta	660
attctcacca	ctatcctgaa	gatacactct	gcagagagca	ggcacaaaagc	tttctccacc	720
tgtgcctccc	acctcacagc	catcactgtc	tcccatggaa	caatccttta	catttattgc	780
aggccgagtt	caggcaacag	tggagatgtt	gacaaagtgg	ccaccgtgtt	ctacacagtt	840
gtgattccca	tgctgaaccc	cctgatctac	agcctgagaa	ataaggatgt	gaacaaagct	900
ctcagaaaag	tgatgggctc	caaaattcac	tcc			933

<210> 492

<211> 963

<212> DNA

<213> Unknown (H38g341 nucleotide)

<220>

<223> Synthetic construct

<400> 492

atgtttctga	cagagagaaa	tacgacatct	gaggccacat	tcactctctt	gggctttctca	60
gattacctgg	aactgcaaat	tcccctcttc	tttgatattc	tggcagtcta	cggcttcagt	120
gtggtaggga	atcttgggat	gatagtgate	atcaaaatta	acccaaaatt	gcatacccc	180
atgtattttt	tcctcaacca	cctctccttt	gtggatttct	gctattcctc	catcattgct	240
cccattgatgc	tggatgaacct	ggttgtagaa	gatagaacca	tttcattctc	aggatgtttg	300
gtgcaattct	ttttcttttg	cacctttgta	gtgactgaat	taattctatt	tgcggtgatg	360
gcctatgacc	actttgtggc	catttgcaat	cctctgctct	acacagttgc	catctcccag	420
aaactctgtg	ccatgctggt	ggttgtattg	tatgcatggg	gagtcgcatg	ttccctgaca	480
ctcgctgtgct	ctgcttttaa	gttatctttt	catggtttca	acacaatcaa	tcatttcttc	540
tgtgagttat	cctccctgat	atcactctct	taccctgact	cttatctcag	ccagttgctt	600
cttttctactg	ttgccacttt	taatgagata	agcacactac	tcattcattct	gacatcttat	660
gcattcatca	ttgtcaccac	cttgaagatg	ccttcagcca	gtgggcaccg	caaagtcttc	720
tccacctgtg	cctcccacct	gactgccatc	accatcttcc	atggcaccat	cctcttcttc	780
tactgtgtac	ccaactccaa	aaactccagg	cacacagtca	aagtggcctc	tgtgttttac	840
accgtggtga	tccccttggt	gaatcccctg	atctacagtc	tgagaaataa	agatgttaag	900
gatgcaatcc	gaaaaataat	caatacaaaa	tattttcata	ttaaacaatag	gcattgggtat	960
cca						963

<210> 493

<211> 303
 <212> DNA
 <213> Unknown (H38g342 nucleotide)

<220>
 <223> Synthetic construct

<400> 493
 tgttgcccac tccaccacca ttacctgcct agacagtcac tggatcagct cacataactta 60
 attgctttga ttttcaattt tctctttgtt tttggcctcc agagtccctt tattttctta 120
 aaggcatgac agtgctttcc aaaggatata cactatattt tcgttaaggc gagaagggtc 180
 tcagggtatc taacctacca tattgctgga aatagaagtt aaaccgtttt tttcctagtc 240
 tgtaactgcc actattatgg tgatgatata ggctaagtct gaatatttta tgtgaacata 300
 tta 303

<210> 494
 <211> 957
 <212> DNA
 <213> Unknown (H38g343 nucleotide)

<220>
 <223> Synthetic construct

<400> 494
 atgcctgtgg ggaaacttgt cttcaaccag tctgagccca ctgagtttgt gttccgtgcg 60
 ttcaccacag ccactgaatt ccaggttctt ctcttccttc tcttcctcct cctctacttg 120
 atgacccctt gtggcaacac agccatcatc tgggtggtgt gcacacacag caccctccgc 180
 accccgatgt atttcttctt gtccaacctg tctttcctgg aactctgcta caccaccgtg 240
 gtagtaccct tgatgctttc caacattttg gggggccaga agcccatttc gttggctgga 300
 tgtggggccc aaatgttctt ctttgtcacc ctccggcagc cggactgttt cctcttggtg 360
 atcatggcct atgaccgcta tgtggctatc tgccaccgcg tgcactacac cctcatcatg 420
 accgcgcagc tgtgcacgca gatgctgggt ggggcccctg gcctggccct cttccccctc 480
 ctgcagctca ccgccttaat cttcaccctg cccttttgcg gccaccacca ggaaatcaac 540
 cacttcctct gcgatgtgcc tcccgctctg cgccctggcct gcgctgacat ccgctgacac 600
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 gtctcctacg tgttcacac ctgtgccatc ctgagcatcc gttctgcca gggccgcgcg 720
 cgggccttct ccacctgctc cttccacctc accgtggctc tgcctgcagta tggctgctgc 780
 agcctcgtgt acctgcgtcc tcgggtccagc acctcagagg atgaggacag ccaaatcgcg 840
 ttgggtctaca cctttgtcac ccccttactc aaccctttgc tttacagcct taggaacaag 900
 gatgtcaaag gtgctctgag gagtgccatt atccgtaaaag cagcctctga cgccaac 957

<210> 495
 <211> 624
 <212> DNA
 <213> Unknown (H38g344 nucleotide)

<220>
 <223> Synthetic construct

<400> 495
 atggagctgg agaatggcac tgtgaagact gggttctttc tcttgggatt cagcgaccat 60
 ctggaacttc agagtctcct ttttgagaa tttttttcca tctactctgt tactctgatg 120
 gggaaccttg gaatgatttt attaatacaca atcagttccc acttgacac tcctatgtac 180
 tttttcctct gtgtgttgc cttcatagat gcatgctact cttctgtcat tgctccaaa 240
 ttacttgtga acttggtttc tgaaaagaag accatttctt acaatggctg tgttgacag 300
 ttatatttct tctgtctttt agttgacaca gaatctttcc tcttggtgc catggcttaa 360
 gaccggtaca tagcaatctg taaccgcgtg ctctatacag tgattatgtc caagaaggtt 420
 tgttgccagc ttgcaattgg agcatttttg gggggcacta tgagctcaat tattcatacc 480
 acgaacactt tccatctgtc attctgtctc agagatatta accatttctt ttgtgatata 540
 tccccactct tctctctgtc ctgcaactgc acatacatgc atgacatcat tctgggtggtc 600
 tttgccagtt ttgtggaagc aatc 624

<210> 496
 <211> 963
 <212> DNA
 <213> Unknown (H38g345 nucleotide)

<220>
 <223> Synthetic construct

<400> 496
 cacacagagc cacggaatct cacaggtgtc tcagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcagcctgt cctccctggg ctgtccctgt ccatgtatct gctcacggtg 120
 ctgaggaacc tgctcatcat cctggctgtc agctctgact cccacctcca ccccccatg 180
 tacttcttcc tctccaaccc gtcacgggct gacatcgctt tcacctcggc cacagttccc 240
 aagatgattg tggacatgca gtcgcatagc agtcatctct tatgcaagct gcctgacaca 300
 gatgtctttc tttgcccttt ttgcatgcat agaagatcat gctcctgatt gtgatggcct 360
 atgaccgatt tgtagccgtc tgtcactccc cacactaccc agtcatcatg aatcctcgcc 420
 tcggtgtctt ctctgctttg gtgtcctttt tccttagcct gttggattcc cagctgcaca 480
 gttggactgt gttacaattc accttcttca agaattgtgga aatctctaat tttgtctgtg 540
 acccatctca acttctcaac cttgcctgtt ctgacagcgt catcgatagc atattcatat 600
 atttagatag tactatgttt cgttttcttc cgatttcagg gatccttttg tcttactcta 660
 acattgtccc ctccattcta agaatttcat catcagatgg gaagtctaaa gccttctcca 720
 cctgtcgtc tcacctggca gttgtttgtt tattttatgg aacaggcatt ggcgtgtacc 780
 tgacttcagc tgtggcaca cccccaggag tgggtgtggt gtgtcagtga tgtacactgt 840
 ggtcaccccc atgctgaacc ctttcatcta ctgcctgaga aacagggaca ttcaaagcgc 900
 cctgtggagg ctgcccagca gaacagtcga atctcatgat ctgttccatc ctttttcttg 960
 tgt 963

<210> 497
 <211> 932
 <212> DNA
 <213> Unknown (H38g346 nucleotide)

<220>
 <223> Synthetic construct

<400> 497
 gaaaagaatc tcatctctat gaatggggtt atgaacttca ctgattaccc agagttggaa 60
 atgcccttgt tcttagtggt tctcagttgc ttccctggcca ttattttgag aaatatggaa 120
 tgggtcattc tgacccaagt gaatgtgcat ctcttcaccc tatatacttc ttccctaaca 180
 atgtcaccc tttgggatacc tcagtcacat tgcctcagat cctggccatt ctggccacag 240
 gcaagacaac catttccctat ggccgctaataaaaagcaatg aggtcctttt tcttcatttg 300
 tgtaggaact tagtggttcc tgccaacagc aatgaccata agcagcccac tgccccacac 360
 tacaagccat gaacttcaag acatgtttggg gttttttttt ggtggggatt tgttgttgta 420
 catgctgggt tttgatgggt aacgtgggtga atgcctacac ctgaggacta tcaggagcca 480
 ctttcaacac catctgcaca tttgcccgtc tcttctgtga tgacaattag atcaaattct 540
 gtcacatcct gccctgtctg aagctcattt gaaatacttc aggaaacagc aagataatta 600
 ttgtgatctt tgacagcttt tatgattata gctggcacta gggtcaccc gatctcttac 660
 ctgctaataca tcagggtctt gaggatgaaa tcatcgagt gcaaagccaa taattttatc 720
 catccacttg tgccctccac ctaactgcta tgacctcct tttggatccc catcttcaga 780
 catgtgaagt acctcagata aatcactgac agaagacaag ttggcatcat gacttgcacc 840
 atctttatc ctatgctaga acttttgatc caaagtctaa agaaggatat acaagttgcc 900
 ttcaaaaagg ccataggtaa cttctgggtt tt 932

<210> 498
 <211> 1005
 <212> DNA
 <213> Unknown (H38g347 nucleotide)

<220>
 <223> Synthetic construct

<400> 498

tctacagacc	cacagaatct	aacagatgtc	tctatatattcc	tcctccgaga	acctcagagg	60
atccagaatg	gcagctgggc	cttgctgggt	tggttcctgtc	catgtgcctg	gtaacgggtgc	120
tggygaacct	gctcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acttcttcc	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acggtagcca	240
agatgattgt	ggacatccaa	tctcacagca	gagtcattctc	ctatgcaggc	tgcttgactc	300
agatgtctcc	ctttgccatt	tttgagtgca	tggaagagag	acacgctcct	gagtggtgatg	360
gcctctgacc	gctttgtagc	catctgtcac	cctctatatac	attcagccat	catgaacccg	420
tggtttctgtg	gctttctagt	tttggtgtct	tttttttttt	tttctgtctt	ttagatgccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctgtga	cccttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaataaca	600
taatcatgta	tttccctgt	gccatatttg	gttttcttcc	catctcggtg	tcccttttct	660
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ccttctcttc	ctgttggtct	cacctgtcag	ttgtttgtctg	attttatgga	acagggcttg	780
gaggtacctc	agttgagatg	tgctatcttc	cccgaggaag	gttgagtggtg	cctcagtgat	840
gtacatgggtg	gtcaccctta	tgctgaaccc	ctttgtctac	agcctgagaa	acagggatat	900
taaaagtgtc	ctgcggtggc	cgcacggcag	cacggtctaa	tctcaatata	ttcttatctg	960
ttccattcct	ttttagtgt	aggttaaaaa	ggcagcaagg	tcaaa		1005

<210> 499

<211> 975

<212> DNA

<213> Unknown (H38g348 nucleotide)

<220>

<223> Synthetic construct

<400> 499

atgaagactt	ttagttcctt	tcttcagatc	ggcagaaata	tgcatcaagg	aaaccaaacc	60
accatcactg	aattcattct	cctgggattt	ttcaagcagg	atgagcatca	aaacctcttc	120
tttgtgcttt	tcttgggtat	gtacctgggc	actgtgattg	ggaacgggct	catcattgtg	180
gctatcagct	tggtacgta	ccttcatacc	cccatgtatc	tcttccttgc	caatctatcc	240
tttgcgtata	tttctccat	ttccaactca	gtccccaaaa	tgctgggtgaa	tattcaaacc	300
aagagtcaat	ccatctctta	tgagagctgc	atcacacaga	tgtacttttc	tattgtgttt	360
gtcgtcattg	acaattttgt	cttggggacc	atggcctatg	accactttgt	ggcgatctgc	420
cacctctga	attatacaat	tctcatgcgg	cccagggttcg	gcatttttgc	cacagtcac	480
tcattggttc	tcagtaatat	tattgtctctg	acacacaccc	ttctgtctcat	ccaattgtct	540
ttctgttaacc	acaacactct	cccacacttc	ttctgtgact	tggtccctct	gtcctaaactg	600
tcctgttcag	atacattgat	caatgagctt	gtgtgtgtta	ttgtgggttt	atcagttatc	660
atcttcccc	ttacactcag	cttcttttcc	tatgtctgca	tcacagagc	tgctctgaga	720
gtatcttcca	cacagggaac	gtggaaagcc	ttctccactt	gtggctctca	cctgacagtt	780
gtattactgt	tctacggaac	cattgtaggc	gtgtactttt	tccccctctc	cactcacct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gataaacccc	900
ttcatctaca	gcttgaggaa	taaggatatg	aaagggtgcc	tgagaaagct	catcaataga	960
aaaattttctt	ccctt					975

<210> 500

<211> 768

<212> DNA

<213> Unknown (H38g349 nucleotide)

<220>

<223> Synthetic construct

<400> 500

atgtactttt	tcctcagtc	tctatccttt	ttggatactt	gttatttcaa	tgtattttaca	60
cccaaaactgt	tagagatttt	ggttgtggaa	gacagaacta	tctccttcaa	aggatgcatg	120
gtacaatttt	tctttgggtg	tgcatattgta	atcacagaaa	tggtcatgtt	agcgggtgatg	180
gcttatgact	tgtttatggc	tgtttgtaac	ccccgtctct	acacagtggc	tatgtctcct	240
aagctctgtg	ctctcctggg	agctggaact	tacacatggg	gtggactctg	ttccctgaca	300

ctcacttatt	ctcttttggg	gttatcctac	tgtggatcta	acatcataaa	tcactttggc	360
tgtgagtact	ctgccattct	ttctctatcc	tgtctgatac	cctacttcaa	ccagatggcg	420
tgtttagtca	tttctatatt	cagtgaagct	tgtagcctcc	tggccatcct	tgcttcttat	480
gtcttcatag	ttgccactgt	catcaagatg	ctttctacgg	gtggacccca	aaaggccatc	540
tccacctgtg	cctcccacct	gaccaccgtc	tccattttcc	atgggggtcat	cctgctcctt	600
tactgtgtgc	ccaactccaa	aagctcatgg	ctccgggtca	aagtgggtac	tgtacttttt	660
acagtcataa	tccctatgct	gaatccccct	atctacagcc	ttaggaacaa	agatgtaaaa	720
gggaccgtca	ggaagttgat	aaactcccaa	tcaccttttc	actcaaaa		768

<210> 501

<211> 951

<212> DNA

<213> Unknown (H38g350 nucleotide)

<220>

<223> Synthetic construct

<400> 501

atggcagaga	gtggcaccac	ggtgacagaa	ttttttctga	gggggttccg	gttgaaggca	60
gagctgcaga	taggtctctt	ctttgtgttt	ctggtcattt	ttctcatcac	catggggggc	120
aacctgggca	tgattgtgct	aatttaattc	agactgacct	tcggctccag	actcccattg	180
acttcttctt	cagtcattct	tccttctctg	acatttgcta	ctcttctgtt	attgggtcctc	240
agttgcttga	gactttggga	ctgataagat	gatcatcacc	tatgagcgct	gtgccagcca	300
attcttcttt	ttcacactct	gtgctagcat	tgagtgtttc	cttttggctg	tgatggctta	360
tgaccggtag	gtggctgtgt	gtaacccctt	cctctatgcc	atagtcatga	caccaaagac	420
ccgcctggcg	ctgctggccg	gggcatattc	tggtgccata	gtcaattctg	tgatctgcac	480
tggtgcacc	ttctctatct	ccttctctaa	gtccaacccat	gtagacttct	ttttctgtga	540
cctcccagcc	ctgtggaagc	ttgcctgtag	tgaacccagg	ccacgggaat	gggtaactta	600
cctctcagct	ttctgggtca	tcacaaccag	catttctagt	attctttacat	cgtacttgtt	660
catcattcag	tctgttctga	agattcgtac	agcaggtgga	aagccaagac	cttctccacc	720
tgtgcttctc	acatgactgc	attgactctc	ttctttggaa	cactcatatt	catatacctg	780
aaaggcaaca	tgggcgaatc	ccttgaggaa	gacaagatcg	tgtcaatatt	ttacactgtg	840
gtcatcccca	tgctaaatcc	aatgatctac	agcctgagaa	acaaagacat	gaaagaggct	900
ctgaagaaa	ttttcaacag	gataagggtt	tcccaagcag	agtaactctt	g	951

<210> 502

<211> 939

<212> DNA

<213> Unknown (H38g351 nucleotide)

<220>

<223> Synthetic construct

<400> 502

atgctgctga	cagatagaaa	tacaagtggg	accacgttca	ccctcttggg	cttctcagat	60
taccagaac	tgcaagtccc	actcttcctg	gtttttctgg	ccatctacaa	tgctactgtg	120
ctagggaata	ttgggttgat	tgtgatcatc	aaaatcaacc	ccaaactgca	taccccatg	180
tactttttcc	tcagccaact	ctcctttgtg	gattttctgt	attcctccat	cattgctccc	240
aagatgttgg	tgaaccttgt	tgtcaaagac	agaaccattt	catttttagg	atgcgtagta	300
caattctttt	tcttctgtac	ctttgtgggtc	actgaatcct	ttttattagc	tgtgatggcc	360
tatgaccgct	tcgtggccat	ttgcaaccct	ctgctctaca	cagttgacat	gtcccagaaa	420
ctctgcgtgc	tgctgggtgt	gggatccctat	gcctggggag	tctcatgttc	cttggaaactg	480
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gagttctcct	cactactctc	cctttcttgc	tctgatactt	acatcaacca	gtggctgcta	600
ttctttcttg	ccacctttta	tgaaatcagc	acactactca	tcgttctcac	atcttatgcg	660
ttcattgttg	taaccatcct	caagatgcgt	tcagtcagtg	ggcgccgcaa	agccttctcc	720
acctgtgcct	cccacctgac	tgccatcacc	atcttccatg	gcaccatcct	cttcttttac	780
tgtgtgcccc	actccaaaaa	ctccaggcac	acagtcacaa	tgccctctgt	gttttacacc	840
gtggtgatcc	ccatgttgaa	tccccgtatc	tacagtccta	gaaataaaga	tgtcaaggat	900
acagtcaccg	agatactgga	caccaaagtc	ttctcttac			939

<210> 503
 <211> 932
 <212> DNA
 <213> Unknown (H38g352 nucleotide)

<220>
 <223> Synthetic construct

<400> 503
 atggctgaaa ggaattacac cgtagtgcag gagttcttcc ttactgcatt tactgaacat 60
 ctccagtggg ggggttcctct ctctctcata tttttgagtt tctatcttgc cactatgtta 120
 gggaacacag gcatgatcct cctgatccgt ggcgatcgtc ggctccacac cccgatgtac 180
 ttcttctctca gccacctttc cttgggtggac atctgctact cgtccgccat catccctcag 240
 atgctggctg tgctgtggga gcacggcaca accatctccc aggtctcgctg tgcagctcag 300
 ttcttctctct tcaccttctt tgcttccatc gactgctacc ttctggccat catgcctatg 360
 accgtacac ggccgtgtgc agcccctgct ttatgtcacc atcataaccg agaaggaccg 420
 ctgggcctag tcaactggggc ttacgttgct ggttttttca gtgcctttgt tgcacgggtca 480
 cagccttcac tctctcctt tgtggaaaca atgagatcaa cttcattttc tgtgacctcc 540
 ctctctatt aaaactctcc tgtggggaca gctacactca ggaagtgggtg attattgtgt 600
 ttgctctttt cgtcatgcct gcctgtatct tgggtgactt ggtatcctac ctgtttatca 660
 ttgtggccat cctgcagatc cactctgctg gagggcgggc caagaccttc tccacctgcg 720
 cctccacact cactgccgtc gctcttttct ttggcaccct catcttcatg tacctgcgag 780
 acaacacagg ccagtcctcc gagggagacc gagtgggtgtc tgtgctctac acggtgggtga 840
 cccaatgct gaatccctt atctatagcc tgagaaacaa ggaggtaaaa gagggcacta 900
 ggaaagccct gagcaaatca aagcctgcta ga 932

<210> 504
 <211> 762
 <212> DNA
 <213> Unknown (H38g353 nucleotide)

<220>
 <223> Synthetic construct

<400> 504
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 gtcaccatgc tgagtatatt ctggttcaat gtgagggaaa tcagctttaa tgcctgcttg 120
 tcccacatgt tctttattaa attcttcaact gtcatggaat cctcagtgcg gttggccatg 180
 gcttttgatc gttttgtggc cgtctctaata ccccttaggt atgccatgat ttaactgac 240
 tccagaatag ctcaaattgg agtggcaagt gtcacaggg ggctcctaata gctgacacca 300
 atggtagcac ttcttataag actttcctac tgccacagcc aagtactcca ccactcctac 360
 tgctaccacc ctgatgtgat gaagctctca tgcacagaca ccagaatcaa cagtgcagtt 420
 gggctgactg ccatgttctc tactgttggt gtagacttac ttctcatcct cctttcttat 480
 gttttgatca ttaggactgt ccttagcggt gcttcccag aagagaggaa ggaaaccttc 540
 agtacatgtg tctccacat tgtggctttt gctatatatt acattccatt gatcagctctg 600
 tccattgttc acagatttgg gaaacaagcc ccagcctatg tacatactat gattgctaac 660
 acctacctgc tgatctcccc tttgatgaac cctgtcatct acagtgtgaa aaccaaacag 720
 atacgtagag ctgtgataaa aattctccat tccaaagaaa ca 762

<210> 505
 <211> 565
 <212> DNA
 <213> Unknown (H38g354 nucleotide)

<220>
 <223> Synthetic construct

<400> 505
 atggactggg aaaattgctc ctcatctaact gatttttttc tcttgggaat taccaataac 60
 ccagagatga aagtgacctt atttgctgta ttcttggctg tttatatcat taatttctca 120
 gcaaactctg gaatgatagt ttaatacaga atggattacc aacttcacac accaatgtat 180

ttcttctca	gtcatctgtc	tttctgtgat	ctctgctatt	ctactgcaac	tgggcccag	240
atgctggtag	atctacttgc	caagaacaag	tcaataccct	tctatggctg	tgctctgcaa	300
ttcttggct	tctgtatctt	tgcagattct	gagtgtctac	tgctgtcagt	gatggccttt	360
gatcggtaga	aggccatcat	caacccccctg	ctctatacag	tcaacatgtc	tagcagagtg	420
tgctatctac	tcttgactgg	ggtttatctg	gtgggaatag	cagatgcttt	gat.acatatg	480
acactggcct	tccgcctatg	cttctgtggg	tctaattgaga	ttaatcattt	cttctgtgat	540
atccccctct	ctcttattac	tctct				565

<210> 506

<211> 978

<212> DNA

<213> Unknown (H38g355 nucleotide)

<220>

<223> Synthetic construct

<400> 506

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ctcagcactg	tgacagagtt	cattcttcta	gtcttcacag	atcaccctga	actggcagtt	120
ccactcttcc	tagtgtttct	cagtttctat	cttgtcactt	ttctggggaa	tggggggatg	180
atcattctaa	tccaagtga	tgcccaactc	cacacccccg	tgtacttctt	cctgagccac	240
cttgctttcc	tggatgcctg	ctgtgcctca	gtaatcacc	ctcagattct	ggccacactg	300
gccacagaca	agacagttat	ctcctatggc	tgccgtgctg	tgcagttctc	tttcttcacc	360
atatgtgcag	gcacagagtg	ttacctgctg	tcagtgatgg	cctatgaccg	ctttgttgcc	420
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gccagtgcct	tcatctgtgg	ggtgtcaggg	gccattctgc	ataccacgtg	caccttcacc	540
ctctccttct	gttgtgacaa	tcagatcaac	ttcttcttct	gtgacctccc	acccctgctg	600
aagctcgcct	gcagcagcat	gacacaaact	gagattgtca	ttctcctttg	tgcaaaatgc	660
atgttcctag	cgaatgcat	ggttatcctg	atctgctaca	tgctcattat	cagagccatt	720
ttgagggtag	agtcggcagg	tgggtaagcc	aagacctctc	ccacctgcac	ctcccatctc	780
accactgttg	tcctcttctt	tgggacactt	gccttcattg	accagagaag	taactccgcc	840
aaatcctcag	aggaagacaa	gatatgtctt	gtcttttaca	ctgtaatcat	ccctatgttg	900
aacccttgga	tctacagtct	gaggaacaaa	gatgtaaaag	ctgcatttgg	aaaactcggt	960
ggtaaattcc	aatttcca					978

<210> 507

<211> 983

<212> DNA

<213> Unknown (H38g356 nucleotide)

<220>

<223> Synthetic construct

<400> 507

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attggcatcc	cagggtctga	ggcgggtcat	ggctggctcg	ccatccccctt	ctcctccatg	120
tacactgtgg	ccctccctgg	gaactgcctg	atcctcctgg	ctgtgaagag	gaacccagc	180
ctgcaccagc	ccatgtgcta	cttctctgtc	atgctggcgc	tccccaaagc	gggcctcacc	240
ttgtccacac	tgcccatcac	cttggctgtg	ctctggtttg	accaccggct	catgggcttc	300
aatgcctgcc	tgggtccagat	gttcttctctg	cactcctctg	tgggtggagtc	ctcagtgtc	360
ctggccatat	cctttgacca	ctttgtggcc	atctccaacc	ccctgcacta	tgcagtgtc	420
ctcacaaata	gtgtcatcat	caggattggg	ctggccattg	tggctcaagt	taccttgtgc	480
ctcttctctg	gccatttccg	gttaagagtc	taaatttctg	ccctgggtgat	aacatcccat	540
cccactcggt	ctgtttccac	cctgatgtaa	tgaggcgggc	ctgtgcggac	atcacgatca	600
atatatgcta	tggggtctac	gtggttgttt	ctacaggggg	cttagactcg	ctgctcatct	660
ttctgtccta	taccttcac	ctgcacacag	tcatgggtct	ggctgtctcc	agggagcgca	720
tctgggccct	caacacctgc	gtttcccaca	ttccggctgt	ctttgtcttc	tttattccag	780
gtatcacctg	gtccatgac	caccattttg	ggaggcacct	gccccacatt	gtacatgtc	840
ttgttaccta	tgtgtacctg	gtgtgcctt	ctgtgtctca	ccccatcatt	tacagtatga	900
agtccaagcc	cctcagggag	gccatcctca	ggatgctgat	ggggagaagc	caaggctgat	960
gaaattacaa	aattattatg	ggt				983

<210> 508
 <211> 933
 <212> DNA
 <213> Unknown (H38g357 nucleotide)

<220>
 <223> Synthetic construct

<400> 508
 atgggcaagg aaaactgcac cactgtggct gagttcattc tccttggact atcagatgtc 60
 cctgagttga gagtctgcct cttcctgctg ttcccttctca tctatggagt cacgttggtta 120
 gccaacctgg gcatgattgc actgattcag gtcagctctc ggctccacac ccccatgtac 180
 tttttcctca gccacttgte ctctgtagat ttctgctact cctcaataat tgtgccaaaa 240
 atgttggcta atatctttaa caaggacaaa gccatctcct tcctaggggtg catgggtgcaa 300
 ttctacttgt tttgcacttg tgtggctact gaggtcttcc tgctggccgt gatggcctat 360
 gaccgctttg tggccatctg taaccctttg ctatacacag tcaccatgtc ttggaagggtg 420
 cgtgtggagc tggcttcttg ctgctacttc tgtgggacgg tgtgttctct gattcatttg 480
 tgcttagctc ttaggatccc cttctataga tctaagtga ttaaccactt tttctgtgat 540
 ctacctctcg tcttaagtct tgcttgcctc gatatcactg tgaatgagac actgctgttc 600
 ctgggtggcca ctttgaatga gagtgttacc atcatgatca tcctcacctc ctacctgcta 660
 attctcacca ccactcctgaa gatgggctct gcagagggga ggcacaaagc cttctccacc 720
 tgtgcttccc acctcacagc tatcactgtc ttccatggaa cagtcctttc catttattgc 780
 aggcccagtt caggcaatag tggagatgct gacaaagtgg ccaccgtgtt ctacacagtc 840
 gtgattccta tgctgaactc tgtgatctac agcctgagaa ataaagatgt gaaagaagct 900
 ctcagaaaag tgatgggctc caaaattcac tcc 933

<210> 509
 <211> 621
 <212> DNA
 <213> Unknown (H38g358 nucleotide)

<220>
 <223> Synthetic construct

<400> 509
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 cgcctttttt ttttttctca gtgttttaga cgcccagctg cacaacttga ttgccttaca 120
 aatgacctgc ttccaggatg cggaaattcc taatttcttc tgtgaccctt ctcaactccc 180
 ccatcttgca tgttgtgaca ccttcaccaa taacataatc atgtatttcc ctgctgtcat 240
 atttggtttt cttcccactc ctgggacctt ttctcttac tataaaattg tttcctccat 300
 tctgagtgtt tcatcatcac gtgggcagta taaggccttc tccacctgtg ggtctcactt 360
 gtcagtgtgt tgctgatttt acggaacggg cggttgagga tacttcagtt cagatgtgtc 420
 atcttccccg agaaaggctg cagtggcctc agtgatgtac acgggtgatca ccccatgctg 480
 aacccttcca tctacagcct gagaaacagg catattaaaa gtgtcctgcg gcggccgcac 540
 agcagcaccg tccaatctcc gtgtcttctt aactgttcca ttccctttgt agtgtgggtt 600
 aacaaaggca gcaaggtcaa a 621

<210> 510
 <211> 633
 <212> DNA
 <213> Unknown (H38g359 nucleotide)

<220>
 <223> Synthetic construct

<400> 510
 atttgactga aattgatctt tggaaatcct agatagtaat agattttcag atgtgtctat 60
 gattattttg tgggactgtc aacccttgct ttatgacacc atcacaactc tcaagatgtc 120
 tggcagaagc tgggtactgc atattgtaga gggtttgaca aatgtaatcc aatgtatata 180
 cttcacctgc tcactctcct tttgtgcctt catctatagg ttccactctc tgtgacctcc 240

attgctgctg	accctgaatt	gggtgatagc	ttectccagc	agctgctgat	ttttcacttt	300
gctctgtata	tgattctgac	cagactagtt	ttgatcctgt	tctctgactt	gttcatcagc	360
aaggccatct	aaacacctgc	aaatcaggtc	tctaggcaaa	gattcctcaa	cctttttcta	420
cctttgcctc	atgcagaact	gcagttcggg	tgattgttga	gactacagct	ttgatctatg	480
tgtgcagcag	taggcaagtc	ccttacaggg	gagagggccg	tgaccatgtt	ttagactgta	540
gtgaacacca	ggctgaccat	tccaatttta	tagcctgagg	aaaaaaaggc	aaaggaggcc	600
ctgaggaaag	gtcttaataa	agccaagttg	ttc			633

<210> 511

<211> 945

<212> DNA

<213> Unknown (H38g360 nucleotide)

<220>

<223> Synthetic construct

<400> 511

atgagttcct	gcaacttcac	acatgccacc	tttgtgctta	ttggtatccc	aggattagag	60
aaagccatt	tctgggttgg	cttccccctc	ctttccatgt	atgtagtggc	aatgtttgga	120
aactgcatcg	tggtcttcat	cgtaaggacg	gaacgcagcc	tgacagctcc	gatgtacctc	180
tttctctgca	tgcttgacgc	cattgacctg	gccttatcca	catccaccat	gcctaagatc	240
cttgcccttt	tctggtttga	ttcccagagag	attagctttg	aggcctgtct	taccagatg	300
ttctttattc	atgccctctc	agccattgaa	tccaccatcc	tgctggccat	ggcctttgac	360
cgttatgtgg	ccatctgccca	cccactgcgc	catgctgcag	tgctcaacaa	tacagtaaca	420
gcccagattg	gcatcgtggc	tgtgggtcgc	ggatccctct	tttttttccc	actgcctctg	480
ctgatcaagc	ggctggcctt	ctgccactcc	aatgtcctct	cgcactccta	ttgtgtccac	540
caggatgtaa	tgaagtgtgg	ctatgcagac	actttgcccc	atgtggtata	tggtcttact	600
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gtgtcacaca	ttggtgtggg	actgccttcc	tatgtgccac	ttattggcct	ctcagtggta	780
caccgctttg	gaaacagcct	tcatcccatc	gtgcgtgttg	tcattgggtga	catctacctg	840
ctgctgcctc	ctgtcatcaa	tcccatcatc	tatgggtgcc	aaaccaaaaca	gatcagaaca	900
cgggtgctgg	ctatgttcaa	gatcagctgt	gacaaggact	tgacg		945

<210> 512

<211> 834

<212> DNA

<213> Unknown (H38g361 nucleotide)

<220>

<223> Synthetic construct

<400> 512

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cgactgcatg	agcccatgta	cctcttcctg	gccatgcttt	ccactattga	cctagtccctc	120
tcctctatca	ccatgcccaa	gatggccagt	cttttcctga	tgggcatcca	ggagatcgag	180
ttcaacattt	gcctggccca	gatgttcctt	atccatgctc	tgtcagccgt	ggagtcagct	240
gtcctgctgg	ccatggcttt	tgaccgcttt	gtggccattt	gccacccatt	gcgccatgct	300
tctgtgctga	cagggtgtac	tgtggccaag	attggactat	ctgccctgac	caggggggttt	360
gtattcttct	tcccactgcc	cttcatcctc	aagtggttgt	cctactgcca	aacacatact	420
gtcacacact	ccttctgtct	gcaccaagat	attatgaagc	tgctcctgtac	tgacaccagg	480
gtcaatgtgg	tttatggact	cttcatcatc	ctctcagtca	tgggtgtgga	ctctctcttc	540
attggcttct	catatatcct	catcctgtgg	gctgttttgg	agctgtcctc	tccgagggca	600
gcactcaagg	ctttcaacac	ctgcatctcc	cacctctgtg	ctgttctggg	cttctatgta	660
cccctcattg	ggctctcggt	ggtgcatagg	ctgggtgggc	ccacctccct	cctccatgtg	720
gttatggcta	atacctactt	gctgctacca	cctgtagtca	acccccttgt	ctatggagcc	780
aagaccaaaag	agatctgttc	aagggtcctc	tgatatgttct	cacaagggtg	caag	834

<210> 513

<211> 957

<212> DNA

<213> Unknown (H38g362 nucleotid)

<220>

<223> Synthetic construct

<400> 513

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atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120
acagccctgt	taggaaacac	cctcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgctttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcc	240
gtggtagcca	agatgggtgag	catcttctgc	tcgggagaca	gctccatcag	ctttagtgtc	300
tgtttctactc	agatgttttt	tgtccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	ttgaccgcta	tgtagccatc	tgcaagcctc	tacactataa	gagaattctc	420
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tcctactgta	agcacatagc	tttggccagg	ttagcatgtg	ctgaccccg	gcccagcagt	600
ctctacagtc	tgattgggtc	ctctcttatg	gtgggctctg	atgtggcctt	cattgtctgc	660
tcctatatct	taattctcag	ggcagtattt	gatctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggcct	tgtactatct	acctgggatg	780
gcatccatct	atgcggcctg	gttggggcag	gatatagtgc	ccttgccacac	ccaagtgtctg	840
ctagctgacc	tgtacgtgat	catcccagcc	actttaaatc	ccatcatcta	tggcatgagg	900
accaaacaat	tgctggaggg	aatatggagt	tatctgatgc	acttcctctt	tgaccac	957

<210> 514

<211> 966

<212> DNA

<213> Unknown (H38g363 nucleotide)

<220>

<223> Synthetic construct

<400> 514

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agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcattcatct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	taccctataa	240
atgattgcag	actttctggt	tgagcacaag	actatttctt	ttgatgccca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgttatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tggtgtgtgc	tcgtctctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcc	ttttgtgggt	ctaataaggt	agatagtttt	tttctgtgac	540
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gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttgtctc	ctacactgta	660
atacttgta	cagttaggaa	tcgtctcctc	gtaagcatgg	tgaaggccca	ctccacattg	720
actgctcaca	tcactgtggt	cactttatct	tttggatcgt	gtattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	cctgctgtat	tctacacat	cttcacgtct	840
attttaaac	ctgtaatacta	catgctaaga	aacaaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatcagaa	gcttgggtcag	gtttctgtag	tcataagaaa	cgttcttttc	960
ctagaa						966

<210> 515

<211> 966

<212> DNA

<213> Unknown (H38g364 nucleotide)

<220>

<223> Synthetic construct

<400> 515

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atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120

atagccctgt	taggaaacac	catcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgctttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcg	240
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tgtttcactc	agatgttttt	tgtccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	ttgaccgcta	tgtagccatc	tgcaagcctc	tacactaaa	gagaattctc	420
aegcctcaag	tgatgctggg	aatgagtatg	gccatcacca	tcagagctat	catagccata	480
actccactga	gttggatggt	gagtcactta	cctttctgtg	gctccaatgt	ggttgtccac	540
tcctactgtg	agcacatagc	tttggccagg	ttagcatgtg	ctgaccccg	gcccagcagt	600
ctctacagtc	tgattgggtc	ctctcttatg	gtgggctctg	atgtggcctt	cattgctgcc	660
tcctatatct	taattctcaa	ggcagtattt	ggtctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggctt	tgtactatct	acctgggatg	780
gcattccatct	atgcggcctg	gttggggcag	gatgtagtgc	ccttgccacac	ccaagtcctg	840
ctagctgacc	tgtacgtgat	catcccagcc	accttaaatc	ccatcatcta	tggcatgagg	900
accaacaac	tgcgggagag	aatatggagt	tatctgatgc	atgtcctctt	tgaccattcc	960
aacctg						966

<210> 516

<211> 942

<212> DNA

<213> Unknown (H38g365 nucleotide)

<220>

<223> Synthetic construct

<400> 516

atggaggggt	tcaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattctt	ttctgtggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtccta	tccacctcac	accttcactc	tcgcatgtac	180
ttcctgctca	gcaacatgtc	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgtct	tgcgtaagac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ttgatctcca	tgtcttttga	360
caggtatatt	gccatattga	aacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttgttggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcctttgg	tgattccagt	agcttgtata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgatgtc	tcttataagt	tttctgtttt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcagggg	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcatt	ttattgttgt	gttaatgttc	tttgggccct	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttcctggg	agacaaaatt	ctctccggtt	tctataccat	cttcactccc	840
tttctgaatc	cacttatcta	tactttgaga	aaccaggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgctc	cg		942

<210> 517

<211> 952

<212> DNA

<213> Unknown (H38g366 nucleotide)

<220>

<223> Synthetic construct

<400> 517

atgctcactt	ttcataatgt	ctgctcagta	cccagctcct	tctggctcac	tggcatccca	60
gggctggagt	ccctacacgt	ctggctctcc	atcccccttg	gctccatgta	cctggtggct	120
gtggtgggga	atgtgaccat	cctggctgtg	gtaaagatag	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgcat	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tggaatctt	ctggttcggg	gcttgtgaca	ttggcctgga	cgccctgctt	300
ggccaaatgt	tccttatcca	ctgctttgac	actgttgagt	caggcatctt	ccttgccatt	360
gcttttgatc	gctacgtggc	ccatctgcaa	cccactacgt	catagcatgg	tgtccactta	420
tacagtgggt	ggctggttgg	ggcttgtttc	tctcctccgg	ggtgttctct	acattggacc	480
tctgcctctg	atgatccgcc	tgcggtgcc	cctttataaa	acctatgtta	tctccacttc	540
ctactgtgag	cacatggctg	tagttgcctt	gacatgtggc	gacagcaggg	tcaataatgt	600

ctatgggctg agcatcggtt ttctgggtgtt gatcctggac tcagtggcta ttgctgcac	660
ctatgtgatg attttcaggg cctgatggg gttagecact cctgaggcta ggcttaaaac	720
cctggggaca tgcgcttctc acctctgtgc catcctgac ttttatgttc ccattgctgt	780
ttcttccttg attcaccgat ttggtcagtg tgtgctcct ccagtcaca ctctgctggc	840
caacttctat ctctcattc ctccaatcct caatcccatt gtctatgctg ttgcaccaa	900
gcagatccga gagagccttc tccaaatacc aaggatagaa atgaagatta ga	952

<210> 518

<211> 301

<212> DNA

<213> Unknown (H38g367 nucleotide)

<220>

<223> Synthetic construct

<400> 518

cagatgctga cagattgggtg gggacctaat aggaccacaa gttacgtgaa ctcaccattc	60
aattccttgt ctctctgtag ttatgtgcca ctatataatt tctacaatta tttataatt	120
atatgccatc ctttgaataa tttgttaatc atgaacctat atctcctcct taatcttact	180
ttaatacttg agggataatt cattcatttt tggcatcatg tatactctca tcctaaaaat	240
tcgaaggatg aaaaaaaaaa accttcagat aattcccctc attggttget gccttgctga	300
a	301

<210> 519

<211> 506

<212> DNA

<213> Unknown (H38g368 nucleotide)

<220>

<223> Synthetic construct

<400> 519

aatagtgagt ccaagcattt cttactctta aaattgtgtt caatgtttgc agtcactttc	60
ctatccctga tattatcagg aaagggcctg caatttcctt tctacttctc tgagtcaact	120
gcaaagtctc agatgttttc acagttgaga caagagaaca agaagcacca atgaaaacca	180
cgggggttcta tggaggcatc atgggtgtgt gagtagaagc atgctactct agctgtatct	240
cactgggttc aaatcctgac tatacggcat atgggtgcatt aacagcccgc tgaccacaag	300
aatttctatg ctggtaaaaat aggtttataa taatgccagt caatctaaag atgctttaag	360
tgaagactat ttggtgtttt tcaaggactc aataatcatt aactgtgatc acgatctttc	420
ccttacctac tttcaataag taaataattt acatttatta aacaaaagaa atttaattct	480
gcttttctga aacaacacaa ttctat	506

<210> 520

<211> 837

<212> DNA

<213> Unknown (H38g369 nucleotide)

<220>

<223> Synthetic construct

<400> 520

ctccctcccc tgttttttag agtttttgta attttggttt gtttcactac tctttgttaa	60
gctatgcatt ctctttctaa ttattctact tgttaaattt ttattaaaaa caaaaatagc	120
aatgacatat ttacatatt tatctaatta taagctcaaa gcatgaaata gtattgactt	180
ccacatacat atgtttgtgt acgtgtatat tatgaataaa ttagttcatc tcaaatatga	240
aactttaaca tctttaccat ttttttgga tagtctagga ttttagacac ttcttaattt	300
tgttttacct tttatgtcac atattcttca ttaatagtta ttaatatgtt gtattttcta	360
gctgttcttg caaaaagtag ttttatttta tgtttcaaca gtctcagcgt caactgtgac	420
actttctgtg tttggctttc ttgttttgga attgtttatc ttgatgtgca tcccattgca	480
cattgttatg tttctcaaaa gattatttaa atgtttatgt tttttatgat cactcgtttt	540
ttgcttcacg catgcattat tgccttaaac attaaaaaat acttgttttg atgtgctttt	600

tatctttata	tgtgaaaaat	ctttgctggc	taatatgtct	tttgtcacaa	ttgtttcctc	660
cttaattctc	ttaacgaatt	aagagattat	ttcattttct	tctgtcattt	tatgtggtag	720
aatacatctg	aatctgtcct	cattttttct	acataggttt	ttcattttct	ttttctgctt	780
gaaattgcc	acatatatct	aaatggtgac	ctacttagta	ttatactgac	tttgga	837

<210> 521

<211> 461

<212> DNA

<213> Unknown (H38g370 nucleotide)

<220>

<223> Synthetic construct

<400> 521

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aacaagccaa	agcaagtcac	ccacccatt	gcttctggga	caaggatgta	cattcctcct	120
gggcgtgggg	gtgcgggtac	cgcaaggga	ataaattttt	cctgagctac	gatacactct	180
cccacaaaa	gtcatacacc	catttagata	acaacttttc	ttgagtagtt	cagatatcat	240
caatgatcca	catattgata	aacatgactc	gacactaata	acactgtgag	cattttacac	300
tattttctat	aaactccact	atgtccatt	tattctcaga	aattctctct	atgatatact	360
tcatgggcac	aaagaagaat	gagtgaagc	cacgcaaaaa	ggactgtgaa	agccactaaa	420
aagggtcgga	ataaatggga	caaatacatca	tactcttcta	t		461

<210> 522

<211> 554

<212> DNA

<213> Unknown (H38g371 nucleotide)

<220>

<223> Synthetic construct

<400> 522

cctgtccacc	cccgttcccc	ccaccaccct	ctctttcccc	cttacatcta	cccaaaaact	60
ttttccccac	catctttccg	caaaaccttc	tctccctcct	gttcaccacc	gtttttcccc	120
ctccacctac	cccacacatt	ttttccccac	cgtcttttcc	tcactgtctt	ttttgcaaca	180
ccttctcctg	ctcgccatcc	tcttttccct	ttggcactaa	ccaccctctt	tactcctcca	240
tctaccccaa	aactattttc	cccttccctac	cgtctccagcc	acactgcagt	ctccgtcgct	300
gccaccaacc	gcagcgaggc	gagctgtggg	gccgcagcca	cagcctccag	catgcagcgg	360
tggctagccc	ttgtcctggg	cctctaagcc	gggaacggag	cagccccgcg	cgagacacg	420
catgagccta	gaacggcctg	acaccccttc	agcaccattt	atatactgag	gttatgcata	480
tgaggttcct	ggactacatg	ttccaggatt	gggtaagaga	aaacgcagag	gcctactctg	540
attggacttt	gtta					554

<210> 523

<211> 424

<212> DNA

<213> Unknown (H38g372 nucleotide)

<220>

<223> Synthetic construct

<400> 523

tatatagaaa	tggacaacta	ttttctaaca	taactataac	gatattttact	atttttccat	60
tttataatct	ctactcaata	ttttgggtatt	aaaaaattca	tcctaacttc	tttgttggct	120
tattgttttt	gatgttcagc	attactaaat	ttttgactta	tgggtttgaaa	tggctgctca	180
ttcctgattg	ctgatcctgg	tatcaacatg	cctgatttaa	cccttaacaa	attctattct	240
tacaaaatag	ctgaagttgg	ttggagggtt	atttttacca	tttcttttat	ttgctgtccc	300
ttttgataaa	attattttcc	ttagttaaaa	aatgtattta	aataagtaaa	taatatctgt	360
gctagttggg	actcgggtgga	catttcagag	gtgtgtccat	actttatgta	ttttatcact	420
gttt						424

<210> 524
 <211> 246
 <212> DNA
 <213> Unknown (H38g373 nucleotide)

<220>

<223> Synthetic construct

<400> 524
 aatgtattta ggtaatttct tgactttctgc agggactctg atatacacag agcgtacctg 60
 tgtatactgt ccagtttagct cagattctca gttttgggca ttttctaagg gagggcaatg 120
 aacatcctga taggtttaac taaggtttta aaatgtccaa ttttatgtgt ggtttttaac 180
 cacacctgca tcctaattac gaccttggct gttatagctt ataggtttag gcaatctgga 240
 tatagt 246

<210> 525
 <211> 619
 <212> DNA
 <213> Unknown (H38g374 nucleotide)

<220>

<223> Synthetic construct

<400> 525
 gaaattatat tgattgggat ttctctcaaa ctaatctagt tgtattcacc attattaaaa 60
 ttaagtgaca ctcaattgga ctaagtagca ataaaaatat gagacttctt agtgattttt 120
 ttttatccca agccatttac tactgatggg ccttgatgtg tgtgcttgaa aacaaaacat 180
 atgcaagtgt tagactgggt tgaagatttg ggtgggtgaaa gttagctaata tagatgtcag 240
 tgctctatct agaagccaat cttggaaata tgtgataatg ccctttttaa atagctgaaa 300
 agaaattatt ttgtgtttgt ttctacttca ttcttgtttg gttgtatagc atttaagtga 360
 aaggagattt tttatcctta tactagtatt tgcatttacc atcttttaata gatggagaga 420
 aaagttagtt gtcttacttt gatatgtttg gcataggacc tatgacactt ttgatgtttt 480
 tggtcacagt tctgtcacta gaatgctagc aattagatat atgcaatgag taacctactt 540
 taatacaatg gtttgaagta ccacaggcag taactcctaa acaccaaata acagtgtttt 600
 aatttgaata atgttaaag 619

<210> 526
 <211> 939
 <212> DNA
 <213> Unknown (H38g375 nucleotide)

<220>

<223> Synthetic construct

<400> 526
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 gagaatgcac ttattgtctt cacaatatgg cttgctccaa gccttcatcg tcccatgtac 180
 tttttccttg gccatctctc tttcctggag ctatggtaca tcaatgtcac cattcctcgg 240
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 gatcgctacc tggccatctg tggacccctc ctttacccta gtctcatgcc ttccagtctg 420
 gccactcgcc ttgctgtctg ctcttggggc agtggcttct tcagctccat gatgaagctt 480
 ctttttattt cccaattgtc ctactgtgga cccaacatta tcaaccactt tttctgtgat 540
 atttccccac tactcaacct cactgtctt gacaaggagc aagcagagct agtagacttc 600
 cttctggccc tgggtgatgat tctactccct ctattggctg tggtttcata atacactgcc 660
 atcattgcag ccatacctgag gatccctacg tccaggggag gccacaaage cttttccact 720
 tgtgccgctc atctggcagt ggttgttata tactactcct ccactctctt cacctatgca 780
 cggtccccggg ccatgtacac cttcaaccac aacaagatta tctctgtgct ctacactatc 840
 attgtaccat tcttcaaccc agccatctac tgcctgagga acaaggaggt gaaggaggcc 900
 ttcaggaaga cagtgatggg cagatgtcac taccctagg 939

<210> 527
 <211> 965
 <212> DNA
 <213> Unknown (H38g376 nucleotide)

<220>
 <223> Synthetic construct

<400> 527
 cacacagagc cactgaatct cacagggtgtc tgagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcagccggc cctcgctttg ctctccctgt ccctgtccat gtatctgggc 120
 acgggtgctga ggaacctgct cagcatcctg gctgtcagct ctgactccca cctccacacc 180
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggttacac ctcggccacg 240
 gttcccaaga tgattgtgga cagcgagtcg catggcagag tcatctctca tgctggctgc 300
 ctgacacaga tgtctttctt ggctcctttt gcatgtatag aagacatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt tgccctctgc actaccagc catcgtgaat 420
 cctcacctct gtgtcttctt cgttttgggtg tcctttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggatttgtgt acaattcacc atcatcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaaactt gcctgttctg acagcgctcat caatagcata 600
 ttcataatatt ttgatagtag tatgtttggg tttcttccca tttcagggat ccttttgtct 660
 tactctaaaa ttgtccctct cgttctaaagg atgtcatcgt cagatgggaa gtataaaagcc 720
 ttctccacct gtggctctca cctagcagtt gtttgcgtgat ttgatggaac aggcattggc 780
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 tacgctgtgg tcacccccc gctgaacctt ttcattctaca gcctgagaaa caggcacaca 900
 caaagtgcc tgcggagggt gcgcacagaa cagttgaatc tcatgatctc ttgcatcctt 960
 tttct 965

<210> 528
 <211> 557
 <212> DNA
 <213> Unknown (H38g377 nucleotide)

<220>
 <223> Synthetic construct

<400> 528
 ccagtagccc agcatctgtt cttcttctctg aaagtgactg gccaccattg acctaaatca 60
 gaaacctatg atttgtccca gatttttctt tttcccttgc tcttcatatc tatcagtgat 120
 actaattcta aactaacctt aacgaactgc atctgtgccc ctctctcatc tctcctccct 180
 cactttcagt gcattgactg aggctacacc atgtgaatta ttaccatggc atgctaacag 240
 aattattgct tccaatggta ccatgccata attcatcctt catatgggtg ccaataaatt 300
 tttaaaatat ttatttggat ctgctacttc tcaggttaaa agcttcccag catgttgaag 360
 atggaatgca aacagctctg catgcatgcc ctttgcctcat gcagctccta ttgtccatcc 420
 cccactctta cccactcttg ctggataatt cctttttatt cttaagactt catccaagaa 480
 gcaagctctc atatttctt catatacttc tgtcatagcc ctttacatat gttaatcatc 540
 tgttaccttt tctcttg 557

<210> 529
 <211> 1007
 <212> DNA
 <213> Unknown (H38g378 nucleotide)

<220>
 <223> Synthetic construct

<400> 529
 tctagagacc cacagaatct aacagatgtc tctatattcc tcctcctaga agctcagagg 60
 atccagaacg gcagccggc ctcactgggc tgttcctgtc cacgtgcctg gtcattggcg 120
 tggggaacct gctcatcatc ctggccatca gccctgactc ccacctccac acccccatgt 180
 acttcttctt ctccaacctg tccttgccctg acatcagttt cacctccacc acagtcccca 240

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agatgactgt ggacatccaa tctcacagca gagtcacttc ctatgcaggc tgccctgactc 300
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gcctatgacc agtttgtagc caaatgtcac cctctatatc attcagccat catgaaccgc 420
tggttctgtg gctttctact tttgttgtct tttttttttc cctcagtctt ttagatgccc 480
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taatcctgta tttccctgat gccatatttg gttttcttcc catctcgggg acacttttct 660
cttacgataa aattgtttcc tccattctga ggggttccatc atcagggtggg aagtataaag 720
ccttctccac ctatgggtct cacctgtcag atgtttcctg attttatgga acaggcgttg 780
gagggtagct cagttcagat gtgtcatctt ccccgagaaa gactgcagtg gcctcagtga 840
tgtacgcagt ggtcaccccc atgatgaacc ccttcatcta cagtcggaga aacaggggata 900
tgaaaagtgt cctgcggcgg ccgcacggca gcacgttcta atctcaatac cttcttatct 960
gttccattcc ttttgcagtg tgggtcgaaa aaggctgcat gatgaaa 1007

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<210> 530

<211> 471

<212> DNA

<213> Unknown (H38g379 nucleotide)

<220>

<223> Synthetic construct

<400> 530

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gaaggtaggc acatttaggg gatgttcttg gcctttccgt ttggctgacc tatcccaaaa 120
cttttctctt gggctctctat cagagacatg gcagtaacct ggatggacca taggcacgag 180
tctgttagcc cattcctccc gaagctgcag cctttttcat cctgccatgt atctgagtta 240
tgacagtgcc ttgacacctt cactaaatca tatataactt gaatccgggg actcaagggt 300
ttcaaccate tttgttttct tctccattac tgtcactgtg ctagagccca agtctcctga 360
aatgcgccct ggagccttgc tcaaagatgt caacccaaca tgctgatcag gtactatatt 420
tgtctgaagc tggtagttca tgacaggctc tgacatgtgc tgagcttgct c 471

```

<210> 531

<211> 974

<212> DNA

<213> Unknown (H38g380 nucleotide)

<220>

<223> Synthetic construct

<400> 531

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atgaagatca accagacaat cctgaaggaa ttcattcttg ttggcttttc tgtgtaccca 60
catgtacaga catttctttt tgtggtcttc ttttgtctct accttctcac ccttgcaggt 120
aatctgacca tcatgggtct aacttgagtg gacaggtccc tccacacccc tatgtatctc 180
ttccttagtg cactctcctt ctctgagacc tgctatacac tgaccatcgt cccaagatg 240
ctggaagatc tactggccaa ggacagaagc atttcagtca cagggtttag cttacagatg 300
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ctggcagtta ttaggtgtgc ttgtatagac agtaaccaca cagaattcat tataacactg 600
atctcagtg ctggtttgct gggtagccct ctgctcatca tcttgactga tgtcttcatt 660
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gcctccacc taccgtggt tataatccac tttggttttg catctattgt ttatttgaag 780
ccagaagcct caggagatga cacactcata gcagtcctt atactgtcat tacccttctc 840
ctcagcccca tcatattcag cctgaggaat aaggacatga aaaatgcttt tagaagaatg 900
atgggaaca cagttgcctt gaaaaaataa tcttgggttg ttgctgcttg tttgaagaag 960
ggctcaatgt cccc

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<210> 532

<211> 939

<212> DNA

<213> Unknown (H38g381 nucleotide)

<220>

<223> Synthetic construct

<400> 532

atggggcaga	ccaacgtaac	ctcctggagg	gattttgtct	tcctgggctt	ctccagttct	60
ggggagttgc	agctccttct	ctttgccttg	ttcctctctc	tgtatctagt	cactctgacc	120
agcaatgtct	tcattatcat	agccatcagg	ctggatagcc	atctgcacac	ccccatgtac	180
ctcttccttt	ccttcctatc	cttctctgag	acctgctaca	ctttgggcat	catccctaga	240
atgctctctg	gcctggctgg	gggggaccag	gctatctcct	atgtgggctg	tgctgccag	300
atgttctttt	ctgcctcatg	ggcctgtact	aactgcttcc	ttctggctgc	catgggcttt	360
gacagatatg	tggccatctg	tgctccactc	cactatgcc	gccacatgaa	tcctaccctc	420
tgtgcccgag	tggtcattac	ttccttctctg	actggatacc	tctttggact	gggaatgaca	480
ctagttatct	tccacctctc	attctgcagc	tcccatgaaa	tccagcactt	tttttgtgac	540
acgccacctg	tgctgagcct	agcctgtgga	gatacaggcc	cgagtgcagc	gaggatcttt	600
atcctcagtc	ttttggctct	cttggctctc	ttcttcttca	tcaccatctc	ctacgcctac	660
atcttggcag	caatactgag	gatccctctc	gctgaggggc	agaagaaggc	cttctccact	720
tgtgcctcgc	accttacagt	ggtcattatt	cattatggct	gtgcttcctt	cgtgtacctg	780
aggcccaaa	ccagctactc	tcttgagaga	gatcagctta	ttgccatgac	ctatactgta	840
gtgaccccc	tccttaatcc	cattgtttat	agtctaagga	ctagggctat	acagacagct	900
ctgaggaatg	ctttcagagg	gagattgctg	ggtaaagga			939

<210> 533

<211> 866

<212> DNA

<213> Unknown (H38g382 nucleotide)

<220>

<223> Synthetic construct

<400> 533

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gtgttctttg	ccatcaaaact	ggatttctgc	ctgcacagct	ccttgatatt	cttcatcagt	120
gtcctctcct	tcctagagat	ctgggtatacc	accatcacca	tccccaagat	gttcttcaac	180
ctagccagtg	agcagaagac	cacctccctg	gatggttgcc	tattgcagat	gtatttcttt	240
tactccctcg	gcatcactga	ggtttgcttg	ctcaccacca	gggctatgga	cagatacctg	300
gccatctgta	atcacctttg	ctacccccaca	gtcacgacac	cttagctcta	cactcagggtg	360
attctaggtt	gttgcactctg	tggcttcttc	acgctgctcc	ctgagattgc	ttggatatcc	420
acactgccat	tttgtggctc	aaatcaaatc	cacaacattt	tctgtgacct	tgatcctatc	480
ctgaatctag	catgtgtaga	cactggccca	gttgttttaa	tcaagggttg	ggacattgta	540
catgctgtgg	agatcatcac	agctataatg	cttgtgacct	tggcttacgt	ccaaattatt	600
gcagtgatcc	taagaaactg	ctctgctgat	ggatgccaaa	aggcattttc	tacctatgct	660
ttccaccttg	ctattttctt	aatctttttt	ggaagtgtag	ccctgatgta	cctgctcttc	720
tctgccaagt	actccttttt	ctgggacaca	accatcagcc	taatgtttgc	agtgtgtgca	780
ccgacacaat	catctgtagt	ctgaggaata	aagagataaa	ggaagcaata	aaaaagcaca	840
tgtgccaatc	aatgatatgc	acacat				866

<210> 534

<211> 954

<212> DNA

<213> Unknown (H38g383 nucleotide)

<220>

<223> Synthetic construct

<400> 534

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ggaaacctgg	tcatcatcac	agtggctccg	ttgaatactc	acctccacac	tcccatgtat	180

acttttatca	gtgctctttc	tttcttgagg	atttggtata	ccacagccac	aatcccaaag	240
atgctgtcta	gcctgcttag	tgagaggagc	atttccttca	atggttgtct	cctgcagatg	300
tattttctcc	attccaccgg	catctgtgag	gtgtgtctct	tgacagttat	ggcctttgac	360
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gttttgtctc	ccttcttcaa	ccccattatc	tatagcctga	ggaataaaga	aataaaagaa	900
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<210> 535

<211> 386

<212> DNA

<213> Unknown (H38g384 nucleotide)

<220>

<223> Synthetic construct

<400> 535

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actgtcctga	aggteccatc	cacaaaggga	agggtgaaaag	ccttctccac	ctgtggttct	180
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tctctccact	cagctgagaa	agacactatg	gctactgtgt	tgtatacagt	agtgactccc	300
atgctaaacc	ctttatctac	agcctgagga	acaggctactt	gaaaggggct	ctgaaaaaag	360
tagttggcag	ggtgggtgtt	tctgtc				386

<210> 536

<211> 486

<212> DNA

<213> Unknown (H38g385 nucleotide)

<220>

<223> Synthetic construct

<400> 536

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gacgtgcaaa	gagatccctt	gtgtcatgtc	aggatgcaaa	gggattcctt	atgctgggtg	180
cctgacccag	atgtctttct	tcatctgtta	ggcatccaca	gcttctgct	gactgcaatg	240
gccaatgaac	actgtgtggc	catctgtcac	tctctgaact	ccatcaggtc	tgtgacacca	300
tagctctgtg	gcctcctggg	ggtggcctcc	tggaccttcg	cattcaggaa	tgccctgacc	360
cacccagtgt	tactgaccgg	cctctcactc	tgcacctacg	agtgggtcag	ccatgtcttc	420
tgcaacctca	gccagctgct	gaagttggcc	tgctcagacg	ccactctcaa	caatgtgacg	480
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<210> 537

<211> 980

<212> DNA

<213> Unknown (H38g386 nucleotide)

<220>

<223> Synthetic construct

<400> 537

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gtgctgggga acataaccat cctggcagtg gtaaggatgg agtacagcct gcatcagccc 180
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cccaactac tggccatctt ctggtttggt gccacaaca ttggtgttaa tgctgtttg 300
gccagatgt tcttcattca ttgctttgcc actggtgagt caggcatctt ccttgccatg 360
gcttttgatc actatgtggc catctgtgac ccactgcac atacctgtt gctcaccat 420
gctgtggtgg gtcgtttggg gctggctgcc ctctccggg gggtaatcta cattggacct 480
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atatccat ccataccat atccttttgg ccaacattta cctcctcatc ccacctatcc 900
tcaaccat agtctatgt gtcgcacaa agcagatccg agaggctctt ctccatatta 960
aggcaaggac tcaaacagg 980

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<210> 538

<211> 967

<212> DNA

<213> Unknown (H38g387 nucleotide)

<220>

<223> Synthetic construct

<400> 538

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gagttggcga gttcctcttg ctcagcatca ccagtgactc agagaagcag caggccctct 120
tctggctctt cctgtgtatg cacttagtca ctgaggctgg aaacacaccc atcatcctgg 180
gcatcggtcc caaccctgc ctgcacaccc ccactgactt cttcacccat ctctcctttg 240
tcaacatctg cttcatcacc aacctgatcc ccaagctcct ggtcaaccat gtggcaggaa 300
cagggatgat cacgatctct tctccccagt gcctgactca gatgtacttc ctcatctcct 360
ttgccaacgt ggacaccttt ctgctggcca tcatggcact ggaccactat gtggccatct 420
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ccctgttcta tggaaactgtc ctggggatct gcatatgacc cccagactcc ttctcagccc 840
aggacaccat agcaaccatc atgtacactg tggtagacct tatgctaaac cccttcatct 900
acagtctgat gaacaaggag gtccaggagg ccgtagaag gctcttcagt aggggctcac 960
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<210> 539

<211> 603

<212> DNA

<213> Unknown (H38g388 nucleotide)

<220>

<223> Synthetic construct

<400> 539

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cccctacgac actacataat gtgggcaacg cattgtcgca ttatgtctgc gcatgggaat 120
tgctttctcc attcgttgag ccagttggcc tttgccgtgc acttaccctt ctgtggtccc 180
aatgagttcg atagttttta ttgtgacctt cctagggtaa tcaaacttgc ctgtacagat 240
acctacaggc tagatattat ggtcattgct aacagtggtg tgctcactgt gtgttctttt 300
gttcttctaa tcatctcata cactatcacc ctaatgacca tccagcatcg cccttttagat 360
aagtcgtcca aagctctgtc cactttgact gctcacatta cagtagttct tttgttcttt 420
ggaccatgtg tctttattta tgctggcca ttcccatca agtcattaga taaattcctt 480
gctgtatttt attctgtgat caccctctc ttgaacccaa ttatatacac actgaggaac 540

```

aaagacatga agacggcaat aagacagctg agaaaatggg atgcacattc tagtgtaaag 600
 ttt 603

<210> 540

<211> 935

<212> DNA

<213> Unknown (H38g389 nucleotide)

<220>

<223> Synthetic construct

<400> 540

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gggctggagt	ccctacacgt	ctggctctcc	atcccccttg	gctccatgta	cctgggtggct	120
gtgggtggga	atgtgaccat	cctggctgtg	gtaaaagatag	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgcat	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tgggaatctt	ctggttcggt	gcttgtgaca	ttggcctgga	cgctgtcttg	300
ggccaaatgt	tccttatcca	ctgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgc	gctacgtggc	catctgcaac	ccactacgtc	atagcatggg	gctcacttat	420
acagtgggtg	gtcgtttggg	gcttgtttct	ctcctccggg	gtgttctcta	cattggacct	480
ctgcctctga	tgatccgcct	gctggtgccc	ctttataaaa	cccatgttat	ctcccaactcc	540
tactgtgagc	acatggctgt	agttgccttg	acatgtggcg	acagcaaggt	caataatgtc	600
tatgggatga	gcatcggctt	tctgggtgtg	atcatggaat	cagtggatag	tgatgcatca	660
taggtgagga	gtatcagggc	cgtgatgggg	ttagccaatc	atgaggatag	gattagagac	720
catggggaca	ggcgaatata	acatatgtgc	catcatgata	ttataggatc	ccagtgatgt	780
atattccatg	agatcaccga	gatggtcagt	gtgtgcatca	tccagtccac	aatatgatgg	840
ccaggatata	tatcatcagt	catccaagca	tcaagcccag	tgtataggat	gatcgcacca	900
agcagagccg	agagagctat	atccaaagag	caaga			935

<210> 541

<211> 945

<212> DNA

<213> Unknown (H38g390 nucleotide)

<220>

<223> Synthetic construct

<400> 541

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cacagtactg	ctgaccttgt	cctcttctcc	gtggttatgg	cggtcttcac	agtggccctc	120
tgtgggaatg	tcctcctcat	cttctctcat	tacatggacc	ctcaccttca	cacccccatg	180
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caaattggcc	tctttgtctg	tcttgtggga	tctgaggggc	tcttgtctggg	actcatggct	360
tatgaccgct	atgtggccat	tagccacca	cttctctatc	ccatcctcat	gaatcagagg	420
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cacattctag	ggactgtgct	gcaaatacac	tctgctcagg	cctggaaaaa	ggccctggcc	720
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gtccttactc	ccatgtctaa	ccccctcatt	tacagcttga	ggaacaggga	ggtgatgggg	900
gcactgagga	aggggctgga	ccgctgcagg	atcggcagcc	agcac		945

<210> 542

<211> 975

<212> DNA

<213> Unknown (H38g391 nucleotide)

<220>

<223> Synthetic construct

<400> 542

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cacagccaga	ctgaccttgt	cctcttctct	gcagttatgg	tggtcttcac	agtggccctc	120
tgtgggaatg	tcctctcat	cttctctc	tacctggacg	ctggacttca	cacccccatg	180
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aattggcttt	tttgtctctc	ttgtgggac	tgaggggctc	ttgctgggac	tcattggctta	360
tgaccgctac	gtggccgtta	gccaccact	tcactatccc	atcctcatga	atcagagggt	420
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tgcttctgtg	gtcttcatgc	ttctccttcc	cttctccatc	atcatggcct	cctatggctt	660
catcctaggg	gctgtgctcc	gaatacgtc	tgctcaggcc	tggaaaaaag	ccctggccac	720
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cttactccca	tgctgaaccc	cctcatttac	agcttgagga	atggggaggt	gatgggggca	900
ctgaggaagg	ggctggaccg	ctgcaggatt	ggcagccagc	actgaacccc	agagtctggt	960
gcctgctgtg	ccct					975

<210> 543

<211> 942

<212> DNA

<213> Unknown (H38g392 nucleotide)

<220>

<223> Synthetic construct

<400> 543

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ggcaacaccc	ttcttctctt	cttgatccgt	gtggactccc	ggctccacac	acccatgtac	180
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atattcttcc	tcacactgat	gggtgtggct	gagggcgtcc	tgttggctcc	catgtcttat	360
gaccgttatg	ttgctgtgtg	ccagccctg	cagtatcctg	tacttatgag	acgccaggta	420
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gtgccagccc	tactgaagct	ctcctgtgca	gatacctgtg	cctacgagat	ggcgtgtctc	600
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gtgttgctcg	ctgttctaag	catgcgtca	gaggaggcca	gacacaaggc	tgtaaccacc	720
tgctcctcgc	acatcacggc	agtggggctc	ttttatggtg	ccgccgtgtt	catgtacatg	780
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gtcaccccta	cactcaaccc	ccttatctac	agtctgagga	atccggaggt	gtggatggct	900
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<210> 544

<211> 350

<212> DNA

<213> Unknown (H38g393 nucleotide)

<220>

<223> Synthetic construct

<400> 544

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ctctatctat	atctttatcc	cttcaggcag	ttctacaact	ctcctctcag	aggcccgtca	120
caaagcattt	gggacatgtg	tctctcacat	agggtccatc	ttagccttct	acacaccttc	180
agtcattctt	tcagtcattg	accgtgtggc	ccgctgtgct	gcgccacacg	tccacattct	240
cctcgccaat	ttctatctgc	tcttcccacc	catggtcaat	cccatcatct	acggcggtta	300

gaccaagcag atccgtgaca gtcttgggag tattcccag aaaggatgtg

350

<210> 545

<211> 948

<212> DNA

<213> Unknown (H38g394 nucleotide)

<220>

<223> Synthetic construct

<400> 545

atgcctagtc	agaactatag	catcatatct	gaatttaacc	tctttggctt	ctcagccttc	60
ccccagcacc	tctgcccac	ctgttcctg	ctgtacctcc	tgatgttcct	gttcacattg	120
ctgggcaacc	ttctcatcat	ggccacaatc	tggattgaac	acagactcca	cacacccatg	180
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tacctcaagc	ccaagggcct	ccattctatg	tacagtgcag	ccttgatggc	caccacctat	840
actgtcttca	cccccttct	tagcccaatc	attttcagcc	taaggaaaca	ggagctgaag	900
aatgccataa	ataaaaactt	ttacagaaaa	ttctgtcctc	caagttcc		948

<210> 546

<211> 990

<212> DNA

<213> Unknown (H38g395 nucleotide)

<220>

<223> Synthetic construct

<400> 546

atgtgttctt	ttttcttctg	ccaaacaggt	aaacaggcaa	aaatatcaat	gggagaagaa	60
aaccaaacc	ttgtgtccaa	gtttatcttc	ctgggtcttt	cacaggactt	gcagacccag	120
atcctgctat	ttatcctttt	cctcatcatt	tatctgctga	ccgtgcttgg	aaaccagctc	180
atcatcattc	tcattcttct	ggattctcgc	cttcacactc	ccatgtattt	ttttcttaga	240
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cttctgggtg	gggtgtacaga	gtgtgcgctg	ctggcagtga	tgctctatga	ccggtatgtg	420
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ctgaagctgg	cttccataga	cacttacagc	acagaaatgg	ccatcttttc	aatgggctgtg	660
gtaatcctcc	tggccccctgt	ctccctgatt	cttgggtctt	attggaatat	tatctccact	720
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ttgaacccca	taatttatag	cttgaggaac	aaagatgtca	aaggggctct	caggaaacta	960
gttgggagaa	agtgtctctc	tcataggcag				990

<210> 547

<211> 676

<212> DNA

<213> Unknown (H38g396 nucleotide)

<220>

<223> Synthetic construct

<400> 547

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cggcacgctg	cgagggtaac	aagctatcag	gaatgcgggg	tccgtggcgg	gggagtgttg	120
tgggcgcggt	taggcgagtg	cctttagacg	cccagctgca	caacgtgatt	gcctacagaa	180
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cttgcattgt	tggcaccttc	accaataaca	taatcatgta	ttccctgct	gccatatttg	300
gttttcttcc	catctcgggg	acccttttct	cttacgataa	aattgttttc	tccattctga	360
gggtttcatc	atcagggtggg	aagcataagg	ccttctccac	caggggggtct	cacctgtcag	420
ttgtttgctg	atttttatgga	acaggcattg	gaggctacct	cagttcagat	gtgtcatctt	480
ccccgagaaa	ggctgcagtg	gcctcagtg	tgtacacggg	ggccatcccc	atgctgaacc	540
ccttcatcta	cagcctgaga	aacagggata	ttaaaagtgt	cctgcggcac	cgcacggcag	600
cacggtctca	tctcaatata	ttcttatctg	ttccattcct	tttgtagtgt	gggttaaaaa	660
aggcagcaag	gtcaaaa					676

<210> 548

<211> 992

<212> DNA

<213> Unknown (H38g397 nucleotide)

<220>

<223> Synthetic construct

<400> 548

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ttcccttgcc	ccagggaggg	acagatcctc	ctcgttgtgc	tcttcaactgt	tgtttacctc	120
ctgaccttca	tgggcaatgg	ttccatcaac	tgtgctgtgc	actgggtcag	agactccatg	180
cccccatgta	catcctgctc	gccaaacttct	ccttctcgga	gatctgttat	gtcacctcta	240
cagtccccaa	cgtgctggcc	aacttctctt	ctgacacaag	atcatctcgt	tctctggctg	300
cttctctcaa	ttctactttt	ttttctcctt	gggctctaca	gaatgctttt	tcctgggagc	360
tatggcattt	gacctatacc	ttgccatctg	ccggcctcta	cgctatccaa	ccattatgac	420
cagacgtctc	tgcaacattc	ttgtgggcag	ctgctgggta	cttgggtttct	tgtggttcct	480
gattcctata	agtgtcattt	ctcaaattgac	ctgtggatct	aggattattg	accacttccc	540
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tagctccacc	ttaagttctc	tacttctatt	tattcccttt	ctcttcatcg	tgggggtgcta	660
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tctgtggtea	ctcccttat	taatcctgtc	atatacagtc	tgaggaacaa	ggaaatgaaa	900
catgcaatga	ggaactacac	tgtaattgtt	tattttctag	aattcatagg	gctacaagag	960
atgtcaaaga	tgtattctat	ctctttaatt	tt			992

<210> 549

<211> 805

<212> DNA

<213> Unknown (H38g398 nucleotide)

<220>

<223> Synthetic construct

<400> 549

ttctcaagta	tatatgcttg	tatatatcag	atctctatct	caactatcta	tctaatactc	60
tatctatatt	taaattagta	gactggatta	tcaattgtta	tttgtattat	attttacagc	120
ctactcaact	tattctagca	gttcattttac	acttgtgaaa	tgaatcaatt	taaattagtaa	180
caaaatagga	acaatctgac	aacttttttag	ggatacttct	actcaggaat	atgtggcagg	240
agaaactgta	caatgtgatt	gataacaatc	ttcatttttga	aatattgcta	gcattggcttc	300
atcacaaatc	actctgtcat	ggacagtggg	cagcacttgg	ccatctgcca	cccactgcac	360
taccttatcc	tcatgactga	tgaaaataga	gatcgaatgt	ttatgggccc	gctgacagcc	420
tttccctaca	ccgatgccac	atctcagaac	atgcactatg	taaattttct	tattatcatt	480
ctcagtattt	tgtacatccc	tggaacatat	acgttgatcc	taagagctat	gcttcagctg	540

ctttcagcag	ctagccatca	aaatgccttt	tctatccgtg	ggtctcactt	aatagtgggtg	600
tctctgttct	gtgaaacat	atgatgatgt	gtgtgaatct	catatctgac	catttagtat	660
aaatgaagat	gacaaatcac	aatatcataa	tgatacctc	cataaagact	ctagttttaa	720
actttgtcaa	ttacacctta	ctcaatatga	acttaaaacc	tatcttcagt	tttttttta	780
tggautgagt	attagccaaa	gtca				805

<210> 550

<211> 933

<212> DNA

<213> Unknown (H38g399 nucleotide)

<220>

<223> Synthetic construct

<400> 550

atgaaaatct	tcaacagccc	cagcaactcc	agcaccttca	ctggcttcat	cctcctgggc	60
ttcccttgcc	ccaggagggg	gcagatccctc	ctctttgtgc	tcttcaactgt	tgtttacctc	120
ctgacctca	tgggcaatgg	ttccatcatc	tgtgctgtgc	actgggatca	gagactccac	180
gccccatgt	acatcctgct	cgccaacttc	tccttcttgg	agatatgtta	tgtaacctcc	240
acagtcacca	gcatgctggc	caacttcctc	tctgacacca	agatcatctc	gttctctggc	300
tgcttccctc	agttctactt	tttcttctcc	ttgggctcta	cagaatgctt	tttctggca	360
gttatggcat	ttgatcgata	ccttgccatc	tgtcggcctc	tacgtatcc	aaccattatg	420
accagacgtc	tctgtaccaa	tcttgtgggc	aattgctggg	tacttggttt	catctgggtc	480
ttgattccta	tctgtaacat	ctcccaaatg	tccttctgtg	gatctaggat	tattgaccac	540
ttcctatgtg	accagctcc	tcttctaact	ctcacttgca	aaaaaggccc	tgtgatagag	600
cttgtctttt	ctgtcttaag	tcctctgctt	gtctttatgc	tctttctctt	cattgtgggg	660
tcctatgctc	tggtcgtgag	agctgtgttg	agggctccct	cagcagctgg	gagaagaaag	720
gctttctcca	cctgtgggtc	tcacctggct	gtgggttcac	tggtctacgg	ctcagtactg	780
gtcatgtatg	ggagcccacc	atctaagaat	gaagctggaa	agcagaagac	tgtgactctg	840
ttttattctg	ttgttaccct	actgcttaac	cctgtgatat	atagtcttag	gaacaaagat	900
atgagaaaag	ctctgaagaa	attttgggga	aca			933

<210> 551

<211> 977

<212> DNA

<213> Unknown (H38g400 nucleotide)

<220>

<223> Synthetic construct

<400> 551

acagccctgg	aattcacaaa	caattcagag	acaagcacta	tgacggaatt	tgttctcctt	60
ggctttcctg	gttgctcagga	gatgcaaagt	ttcctcttct	ccctgttctt	tgtgatctat	120
gtatttacca	taataggaaa	tgggaccatt	gtctgtgctg	tgagattgga	caaacggctt	180
cataccccaa	tgtatattct	cctaggggaa	tttgctttcc	ttgaaatccg	gtaagttact	240
tccactgtac	ccaacatgct	agtcaacttc	ctctcagaga	caaaaaccat	ctcttttgtt	300
ggctgtttcc	tccagttcta	cttttttact	tcctttggta	caatagaagc	atacttccctc	360
tgcatcatgg	catatgatcg	gtacettgct	atctgcccgc	cattgcacta	cccaaccatc	420
atgacccccc	aactctgcta	catattgatg	tctttttgct	gggtgtttgg	attcctcagt	480
tactctgtct	ccactgtgca	actgtctcaa	ctgcctttct	gtgggcccaa	catcatcaat	540
cactttttgt	gtgacatgga	cccactgatg	gctctgtcct	gtgcctcagc	tcctatcaact	600
gagattatct	tctatatcct	gagctccctc	attatcatte	tcactcttct	gtacatctgt	660
ggctcctata	tgctttactg	atagctgtat	taaaagtcct	ttcagcagct	ggccagcaga	720
aggccttttc	cacctgtgga	tctcatctga	cagtgggtgtg	tttattcttt	ggggccctac	780
tggcaatgta	tgtgagcccc	acaactgata	acccagctgc	aatttagaag	attataaact	840
tggtctattc	tgtgttgacc	cccttcttaa	acccctgat	ttacagctta	cgaacaaaag	900
agatgaaggc	tgctgtgaag	aaagtctcta	ggatagaatg	agaataaagt	catctacatg	960
agaccaagca	aaccatt					977

<210> 552

<211> 945

<212> DNA

<213> Unknown (H38g401 nucleotide)

<220>

<223> Synthetic construct

<400> 552

atggagagcg	gaaaccaatc	aacagtgact	gaatttatct	tcaactggatt	ccctcagctt	60
caggatggta	gtctcctgta	cttctttcct	ttacttttca	tctatacttt	tattatcatt	120
gataacttat	taatcttctc	tgctgtaagg	ctggacaccc	atctccacaa	ccccatgtat	180
aattttatca	gtatattttc	ctttctggag	atctgggtaca	ccacagccac	cattcccaag	240
atgctctcca	acctcatcag	tgaaaagaag	gccatctcaa	tgactggctg	catcttgca	300
atgtatttct	tccactcact	tgaaaactca	gaggggatct	tgctgaccac	catggccatt	360
gacagatcag	ttgccatctg	caaccctctt	cgctatcaaa	tgatcatgac	ccccgggctc	420
tgtgctcaac	tctctgcagg	ttcctgcctc	ttcgggtttcc	ttatcctgct	tcccagagatt	480
gtgatgattt	ccacactgcc	tttctgtggg	cccaaccaa	tccatcagat	cttctgtgac	540
ttgggtccctg	tgctaagcct	ggcctgtaca	gacacgtcca	tgattctgat	tgaggatgtg	600
attcatgctg	tgaccatcat	cattaccttc	ctaactcattg	ccctgtccta	tgtaagaatt	660
gtcactgtga	tattgaggat	tccctcttct	gaagggaggc	aaaaggcttt	ttctacctgt	720
gcaggccacc	tcatgggtctt	cctgatattc	tttggcagtg	tatcactcat	gtacttgctg	780
ttcagcgaca	cttatccacc	agttttggag	acagccattg	cactgatgtt	tactgtactt	840
gtccattctt	tcaatcccat	catttatagc	ctgagaaaca	aggacatgaa	caatgcgatt	900
aaaaaactgt	tctgtcttca	aaaagtgttg	aacaagcctg	gaggt		945

<210> 553

<211> 921

<212> DNA

<213> Unknown (H38g402 nucleotide)

<220>

<223> Synthetic construct

<400> 553

atgcattttg	tgactgagtt	tgctctcctg	ggtttccatg	gtcaaaggga	gatgcagagc	60
tgcttcttct	cattcatcct	ggttctctat	ctcctgacac	tgctagggaa	tggagctatt	120
gtctgtgcag	tgaaattgga	caggcggctc	cacacacca	tgtagatcct	tctgggaaac	180
tttgcccttc	tagagatctg	gtacatttcc	tccactgtcc	caaacatgct	agtcaatata	240
ctctctgaga	ttaaaaccat	ctccttctct	ggttgcttcc	tgcaattcta	tttctttttt	300
tcaactgggt	caacagagtg	tttcttttta	tcagttatgg	cttatgatcg	gtacctggcc	360
atctgtcgtc	cattacacta	cccctccatc	atgactggga	agttctgtat	aattctggtc	420
tgtgtatgct	gggtaggcgg	atttctctgc	tatccagtcc	ctattgttct	tatctcccaa	480
cttcccttct	gtgggcccac	catcattgac	cacttggtgt	gtgaccagg	cccattgttt	540
gcactggcct	gcattctctg	tccttccact	gagcttatct	gttacacctt	caactcgatg	600
attatctttg	ggccttctct	ctccatcttg	ggactcttaca	ctctgggtcat	cagagctgtg	660
ctttgtattc	cctctgggtg	tggtcgaact	aaagctttct	ccacatgtgg	gtcccaccta	720
atgggtgggt	ctctatttcta	tggaaccctt	atgggtgatg	atgtgagccc	aacatcaggg	780
aaccacagcag	gaatgcagaa	gatcatcact	ctgggtatata	cagcaatgac	tccattctta	840
aatcccttta	tctatagtct	tcgaaacaaa	gacatgaaag	atgctctaaa	gagagtcctg	900
gggttaacag	ttagccaaaa	c				921

<210> 554

<211> 768

<212> DNA

<213> Unknown (H38g403 nucleotide)

<220>

<223> Synthetic construct

<400> 554

atgtataatt	ttatcagcat	tttctcattt	ctggagatct	ggtacacaa	tgccacaatt	60
cccaagatgc	tctccatcct	catcagcagg	cagaggacca	tctccatggg	tggctgcctc	120

ttgcagatgt	actttctcca	ttcactggga	aattcagagg	ggattttgtt	gaccaccatg	180
gccattgata	ggtacgttgc	catctgtaac	cctctccgct	acccaacccat	catgaccccc	240
gggctctgtg	ttcagctctc	tgtgggggtcc	tgcattctttg	gctttcttgt	gttgctccca	300
gagattgcat	ggatttccac	actgcccttc	tgtggaccca	accaaatacca	ccagatcttc	360
tgtgattttg	aacctgtgct	gcgcttggtc	tgtacagaca	cgtccatgat	tctgattgag	420
gatgtgatcc	atgctgtggc	cattgtattc	tctgtcctga	ttattgccct	ttcttatatc	480
agaatcatca	ctgtaatcct	gaggattccc	tctgttgaag	gccgccagaa	ggccttttct	540
acctgtgccc	cccattcttag	tgtctttctg	atgttctatg	gcagtgtatc	cctcatgtac	600
ctgcgtttct	ctgccacttt	cccaccgatt	ttggacacag	ctgttgcaact	gatgtttgca	660
gttcttgctc	cctttttcaa	ccctatcatc	tatagcttta	gaaataagga	catgaagatt	720
gcaattaaaa	agctttttctg	ccctcagaag	atggttaatt	tatctgta		768

<210> 555

<211> 960

<212> DNA

<213> Unknown (H38g404 nucleotide)

<220>

<223> Synthetic construct

<400> 555

agtctgggaa	gcatgaataa	ctcacagata	tctactgtga	cgagtttgt	gttggtgggg	60
tttctgggtc	cctggaaaat	tcagatcatc	ttttctctca	tgattttgtt	ggtctacatc	120
ttcactctga	ctgggaatat	ggccatcatc	tgtgcagtga	ggtggggacca	tcgactccat	180
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acagtcccca	acatgctggt	aaattttttc	tccaaaacta	agaccatatc	attctctgga	300
tgtttcaact	agttccactt	cttctttttc	ctgggcacaa	ctgaatgctt	cttcctctgt	360
gtcatggcct	atgatcggtg	cctggccatc	tgccacccac	tgcactatcc	ctccattatg	420
actgggcagc	tctgtggcat	cttgggtgct	ctttgttggc	tcattgggtt	ccttggacat	480
tcaatttcca	ttttcttcat	ttttcaacta	cctttctgtg	gtcccaacat	cattgatcat	540
tttctgtgtg	atgtagacce	actgatggca	ttgtcctctg	cccctactca	catcataggg	600
catgtgttcc	attctgtgag	ctctcttttc	atcaacctca	ccatgggtgt	catccttggg	660
tcctatacct	tggtgctcag	aactgtgctt	taggttcctt	cttcagctgg	atggcaaaaag	720
gccatctcta	cctgtgggtc	acacttggtt	gttgtgtctc	tgttctatgg	agccataatg	780
ctgatgtatg	tgagtccac	acctggcaac	tcagtgtgta	tgcataagct	catcacactg	840
atatattctg	tggtaacacc	tgtcttaaac	ccctcatct	acagcctacg	caacaaggac	900
atgaaatatg	ccctccatca	tgtcttctgt	ggaatgagaa	ttatccagag	atcatgaata	960

<210> 556

<211> 957

<212> DNA

<213> Unknown (H38g405 nucleotide)

<220>

<223> Synthetic construct

<400> 556

atggatccag	agaatcagac	aatggtgact	gagttttatt	tctctgattt	tcctcaatct	60
aagaatggca	gcctcttatt	cttcattcct	atgctcttta	tttatatatt	cattcttgtt	120
ggaaatttca	tgattttctt	tgctgtccaa	ccggaccccc	atctccataa	tcctatgtac	180
agttttatca	gtgtcttctc	cttcctggag	atttgggtaca	ccaccgtgac	tatccccaag	240
atgctctcca	accttctcag	tgaacagaaa	accatctctt	tcatagggtg	cctcctgcag	300
atgtacttct	tccactcact	cggggtcaca	gaagccctag	tcctcacagt	gatggccatt	360
gacaggtgtg	tagccatctg	caaccccctt	cgctatgcaa	tcactatgtc	cccttgactg	420
tgcatccagc	tctccactgg	ctcttgcat	tttggtctcc	tcattgttact	gccagagatt	480
gtgtgcattt	ccactcttcc	attctgtggc	gccaaccaa	ttcatcaact	cttttgtgac	540
tttgaacctg	tgtgtcagtt	agcctgcaca	gatacgtaca	taattctggt	tgaagatgtg	600
atccgtgcta	tttccattct	gacctctgtc	tctgtctaca	cccttttcta	tttaagaatc	660
atcacgggtga	tcctgaggat	tcctctgtgt	gagagtcgtc	agaaggcttt	cttcacatgt	720
gcagcccaca	ttgctatttt	cttgcgtgtt	tttggcagtg	tgctactcat	gtatctgcgc	780
ttctctgtca	cattcccacc	attactggac	aaggccattg	cactgatgtt	tgctgtcctt	840

gccctacttt tcaacccagt aatctatagt ctgaggaaca aagatatgaa aaacgccacc 900
aagaaaatcc tctgttctca aaagatgttc aatgcctctg ggagctaata gagttca 957

<210> 557

<211> 951

<212> DNA

<213> Unknown (H38g406 nucleotide)

<220>

<223> Synthetic construct

<400> 557

atgacacagt	tgacggccag	tgggaatcag	acaatgggtga	ctgagttcct	cttctctatg	60
ttcccgcagt	cgcacagagg	tggcctctta	ttctttatct	ccttgcttct	catctacgga	120
tttatcctaa	ctggaaacct	aataatgttc	attgtcatcc	aggtgggcat	ggccctgcac	180
acccctttgt	atttctttat	cagtgtcctc	tccttcctgg	agatctgcta	taccacaacc	240
accatcccca	agatgtctgc	ctgcctaata	agtgagcaga	agagcatttc	cgtggctggc	300
tgcctcctgc	agatgtactt	tttccactca	cttggtatca	cagaaagctg	tgtcctgaca	360
gcaatggcca	ttgacaggta	catagctatc	tgcaatccac	tccgttacct	aaccatcatg	420
attcccaaac	tttgtatcca	gctgacagtt	ggatcctgct	tttgtggctt	cctccttggtg	480
cttctcgaga	ttgcatggat	ttccaccttg	cctttctgtg	gctccaacca	gatccaccag	540
atattctgtg	atttcacacc	tgtgctgagc	ttggcctgca	cagatacatt	cctagtgggtc	600
attgtggatg	ccatccatgc	agcggaaatt	gtagcctcct	tcctgggtcat	tgctctatcc	660
tacatccgga	ttattatagt	gattctggga	atgcactcag	ctgaagggtca	tcacaaggcc	720
ttttccacct	gtgctgctca	ccttgctgtg	ttcttgctat	tttttggcag	tgtggctgtc	780
atgtatttga	gattctcagc	cacctactca	gtgttttggg	acacagcaat	tgctgtcact	840
tttgttatcc	ttgctccctt	tttcaacccc	atcatctata	gcctgaaaaa	caaggacatg	900
aaagaggcta	ttggaaggct	tttccactat	cagaagaggg	ctggttgggc	t	951

<210> 558

<211> 831

<212> DNA

<213> Unknown (H38g407 nucleotide)

<220>

<223> Synthetic construct

<400> 558

atggctctaa	ttggaaacct	atccatgatt	cttctcatct	tcttggacac	ccatctccac	60
acacccatgt	atttccctact	tagtcagctc	tccttcattg	acctaaatta	catctccacc	120
attgttctta	agatggcatc	tgattttctg	tctggtaaca	agtctatctc	cttcaactggg	180
tgtgggattc	agagtttctt	cttctcggca	ttaggaggtg	cagaagcact	acttttggca	240
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tgtgtctaca	ctgtatatgt	actccatatt	ccttattgcc	aatccagggc	catcaatcat	420
ttcttctgtg	atgtcccagc	aatgggtgact	ctggcctgca	tggaacacctg	ggctctatgag	480
ggcacagtgt	ttttgagcac	caccatcttt	ctcgtgtttc	ccttcattgc	tatttcatgt	540
tcctatggcc	gggttctcct	tgctgtctac	cacatgaaat	ctgcagaagg	gaggaagaaa	600
gcctacctga	cctgcagcac	ccacctcact	gtagtaactt	tctactatgc	accttttgtc	660
tacacttacc	tacgtccaag	atccctgcga	tctccaacag	aggacaaggt	tctggctgtc	720
ttctacacca	tcctcaccct	aatgctcaac	cccatcatct	atagcctgag	gaacaaggag	780
gtgatggggg	ccctgacacg	agtgagtcag	agaatctgct	ctgtgaaaat	g	831

<210> 559

<211> 725

<212> DNA

<213> Unknown (H38g408 nucleotide)

<220>

<223> Synthetic construct

<400> 559

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atctttttct	tttttggttc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccaggctact	180
gcctactggc	caacatttat	cttcttgatc	tgggtcttct	cctacagttc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcattgatac	agatattttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgtgtctcat	aaccatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagatac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatcctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
taggg						725

<210> 560

<211> 936

<212> DNA

<213> Unknown (H38g409 nucleotide)

<220>

<223> Synthetic construct

<400> 560

atggacacag	ggaactggag	ccaggtagca	gaattcatca	tcttgggctt	ccccatctc	60
cagggtgtcc	agatttatct	cttcctcttg	ttgcttctca	tttacctcat	gactgtgttg	120
ggaaacctgc	tgatattcct	ggtggctctc	ctggactccc	ggcttcacac	acccatgtac	180
cactttgtca	gcattctctc	cttctcagag	cttggctata	cagctgccac	catccctaag	240
atgctggcaa	acttggtcag	tgagaaaaag	accatttcat	tctctgggtg	tctcctgcag	300
atctatttct	ttcactccct	tggagcgact	gagtgctatc	tcctgacagc	tatggcctac	360
gataggatatt	tagccatctg	ccggccccctc	cactacccaa	ccctcatgac	cccaacactt	420
tgtgcagaga	ttgccattgg	ctgttgggtg	ggaggcttgg	ctggggccagt	agttgaaatt	480
tccttgattt	cagcctctcc	attctgtggc	cccaatcgca	ttcagcacgt	cttttgtgac	540
ttccctcctg	tgtgtagttt	ggcttgcact	gatacgtcta	caaattgtcct	agtagatttt	600
gttataaatt	cctgcaagat	cctagccacc	ttcctgctga	tcctctgctc	ctatgtgcag	660
atcatctgca	cagtgtcag	aattccctca	gctgccggca	agaggaaggc	catctccacg	720
tgtgcctccc	acctcactgt	ggttctcctc	ttctatggga	gcaccccttc	catgtatgtg	780
cggctgaaga	agagctactc	actggactat	gaccaggccc	tggcagtggt	ctactcagtg	840
ctcacaccct	tcctcaaccc	cttcatctac	agcttgacaa	acaaggagat	caaggaggct	900
gtgaggaggc	agctaaagag	aattgggata	ttggca			936

<210> 561

<211> 635

<212> DNA

<213> Unknown (H38g410 nucleotide)

<220>

<223> Synthetic construct

<400> 561

gaattccttt	tttataatta	caatcaaaca	tcaactgatt	tcattcttatt	ggggctgttc	60
ccacaatcaa	gaattggcct	tttcgtattc	acctcattt	ttctcatttt	cctaattggct	120
ctaattggaa	atctatccat	gattcttctc	atcttttttg	acatccatct	ccacacacct	180
atgtatttcc	tacttagtca	gctctccctc	attgacctaa	attacatctc	caccattgtt	240
ccaaagatgg	tttatgattt	tctgtatgga	aacaagtcta	tctccttcac	tggatgtggg	300
attcagagtt	tcttcttctt	gacttttagca	gttgacagaag	ggctgctcct	gacatcaattg	360
gcctatgata	gttatgtggc	catttggctt	cctctccact	atcccatccg	tataagcaaa	420
agagtgtgtg	tgatgatgat	aacaggatct	tggatgataa	gctctatcaa	ctcttgtgct	480
cacacagtat	atgcactctg	tatcccatat	tgcaagtcca	gagccatcaa	tcattttttc	540
tgtgagggat	cctctgagag	gtacctggga	gcattgcaagc	ttggcgctgg	gccgcgggtg	600
aaacggcggtg	actggtaaaa	ccctgggctg	gccca			635

<210> 562
 <211> 789
 <212> DNA
 <213> Unknown (H38g411 nucleotide)

<220>
 <223> Synthetic construct

<400> 562
 atgttgggga attactctag cgccactgaa ttttttctct taggcttccc tggctcccaa 60
 gaagtatgcc gtatcctatt tgcgaccttc ttcctcttgt atgcagtgc agtgatggga 120
 aacgtgggtca tcatcatcac tgtctgtgtt gataaatgtc tgcagtcccc catttatttt 180
 ttcttgggcc acctctgtgt cctggagatc ctgatcacat ccaccgctgt cccttttatg 240
 ctctgggggt tgetgtcttc aagcaccag atcatgtctt tgacagcctg tgetgcacag 300
 ctatatttat acctttcttt gggtagcttg gagttggcat taatgggagt gatggctgtg 360
 gaccgttatg tggctgtgtg taaccctttg aggtacaaca tcattatgaa cagcagcacc 420
 ttcatattggg tgataattgt gtcattgggt ttgggggttc tttctgaaat ctggccagtt 480
 tatgccactt ttcagcttac tttctgcaaa tcaagtgtgt tagatcattt ttattgtgac 540
 cgaggacaat tgetcaaggat atcctgtgag gacactcttt tcagagagtt tattcttttt 600
 ctaatggctg ttttcattat cattggttct ttgatcccta cgattgtctc ctacacctac 660
 atcatctcca ccaacctcaa gattccgtca gcctctggct ggaggaaatc cttttccacc 720
 tgtgcctccc acttcaccta tgttgtgatt ggctatggca gctgcttgtt tctctacgtg 780
 aaacccaag 789

<210> 563
 <211> 951
 <212> DNA
 <213> Unknown (H38g412 nucleotide)

<220>
 <223> Synthetic construct

<400> 563
 atggatcaat acaaccattc aagcctggct gaatttgtgt tccttggctt tgccagtgtg 60
 ggctatgtca ggggctggct ttttgtcctg ctgctattgg catacctgtt caccatctgt 120
 ggtaacatgc tcatcttctc agtcatccga ctggatgcag ctctgcacac acctatgtac 180
 cactttgtca gtgttctttc cttcttggag ttgtgggtata cagctaccac tatccctaag 240
 atgttgtcta atattctcag tgagaagaaa accatttctt ttgcaggatg cctccttcag 300
 acctacttct tccactcctt gggagcgtct gaatgctacc ttcttacagc catggcctat 360
 gatagatacc tggccatttg tcggccccct cactacccta taattatgac caccacactc 420
 tgtgccaaga tggctgctgc ttgttggact tgtggcttcc tgtgtcccat ttctgaggtc 480
 atccttgcct cccagctccc attttgtgct tacaatgaaa tccaacacat tttctgtgac 540
 tttccacctt tgetgagctt ggctgcaag gacacatctg ctaacattct ggtggacttt 600
 gccattaatg ctttcataat tcttatcact ttcttcttta tcatgatttc ttatgcaagg 660
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 tgtgcctcac atcttgetgt ggtcctcatc ttctttggga gcatcatctt catgtatgtg 780
 cggctaaaga agagctattc cctgacctt gaccgaacac ttgctatagt ttactccgta 840
 ctaacaccaa tggtaatcc aattatctac agtcttcgta acaaggaaat cattaaagct 900
 atcaagagga ccatcttcca gaaggagat aaagctagtc ttgctcatct t 951

<210> 564
 <211> 945
 <212> DNA
 <213> Unknown (H38g413 nucleotide)

<220>
 <223> Synthetic construct

<400> 564
 atgcaggggc taaaccacac ctccgtgtct gaattcatcc tcgttggctt ctctgccttc 60

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ccccacctcc agctgatgct cttcctgctg ttcctgctga tgtacctgtt cagcgtgctg      120
ggcaacctgc tcatcatggc cactgtctgg agcgagcgca gcctccacat gcccatgtac      180
ctcttcctgt gtgccctctc catcaccgag atcctctaca ccgtggccat catcccgcgc      240
atgctggccg acctgctgtc caccacagcg tccatcgccct tctggccctg tgccagtcag      300
atgttcttct ccttcagctt cggcttcacc cactccttcc tgcctactgt catgggctac      360
gaccgctacg tggccatctg ccaccccctg cgttacaacg tgctcatgag cctgcggggc      420
tgcacctgcc ggggtgggctg ctccctgggct ggtggccttg tcatggggat ggtggtgacc      480
tcggccattt tccacctcgc cttctgtgga cacaaggaga tccaccattt cttctgccac      540
gtgccacctc tgttgaagtt ggcctgtgga gatgatgtgc tgggtggtggc caaaggcgtg      600
ggcttggtgt gtatcacggc cctgctgggc tgttttctcc tcatcctcct ctcctatgcc      660
ttcatcgctg ccgccatctt gaagatccct tctgctgaag gtcggaacaa ggccttctcc      720
acctgtgcct ctcacctcac tgtggtggtc gtgcactatg gctttgcctc cgtcatttac      780
ctgaagccca aaggccccca gtctccggaa ggagacacct tgatgggcat cacctacacg      840
gtcctcacac ccttcctcag ccccatcate ttcagcctca ggaacaagga gctgaaggtc      900
gccatgaaga agacttgctt caccaaactc tttccacaga actgc                      945

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<210> 565

<211> 958

<212> DNA

<213> Unknown (H38g414 nucleotide)

<220>

<223> Synthetic construct

<400> 565

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cacacagagc caccgcatct cacaggtgtc tgagaattcc tcctcctggg actctcagag      60
gatccagaac tgcagcctgt cctcgctggg ctgtcccat ccatgtatct ggtcacagtg      120
ctgaggaacc tgctcgatct cctggctgtc agctctgact cccacctcca caccctcatg      180
tacttcttcc tctccaaccc gtgctgggct gacatcggtt tcacttcggc cagggttccc      240
aagatgactg tggacatgca gtcacatata agagtcattt cttatgcgag ctgcctgaca      300
cggatgtctt tcttggtcct ttttgcattg atagaagaca tgctcctgac tgtgatggcc      360
taggactgct ttgtagccat ctgtcgccct ctgcactacg cagtcactgt gaatcctcac      420
ctctgtgtct tcttagtttt ggtgtccttt ttccttagcc tgttggtatt ccagctgcac      480
agttagattg ttacaattca ccttcttcaa gaatgtggaa atctctcatt ttgtctgtga      540
gccatctcaa cttctcaacc ttgcctgttc tgacagcgct atcaatagca tattcatgta      600
tttcaatagg actatgtttg gtttcttccc catttcaggg atccttttgt cttactataa      660
aattgttccc tccattctaa ggatttcate gtcagatggg aagtataaag cttctccac      720
ctgtggctct caccctggcag ttgtttgctt attttatgga acaggcattg gcatgtacct      780
gacttcagct gtggcaccac cccccaggaa tgggtgtggt gcgtcagtga tgtacgctgt      840
ggtcaccccc atgctgaacc ctttcatcta cagcctgaga aacaggggaca ttcaaagcgc      900
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<210> 566

<211> 470

<212> DNA

<213> Unknown (H38g415 nucleotide)

<220>

<223> Synthetic construct

<400> 566

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gtctccccac tgtgggaatg tgtgtcatga cagcggctct cccacttctt atgctctgga      60
gactcagttt tctgtctggt tcacagtgtg ggctgctgca cactacttct ttcacagagt      120
ttgcggcttc tttcagtttt cctgttaagt tctgtgctg cttcttgga aaaaagtcac      180
agcatgaatc tctacacacc attttgtctt tctaagtggg agaatcacgt taacaatgcc      240
ttcaacctgc catcatggaa aaaaagtaaa agtgtggtca ccatgttcta agggccccgc      300
atgatcacgt acttgaggct tgactcctag tataacctac agtgggaaaa cagttggtgc      360
tgttctacag cattgtctct gccttcataa aacccatcat ctccagcctc aggaacaagg      420
atgtaaaagg ggcttcttgg aaagtactta gagtcaaagg gacagctcaa      470

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<210> 567

<211> 862
 <212> DNA
 <213> Unknown (H38g416 nucleotide)

<220>
 <223> Synthetic construct

<400> 567
 atggaaaatt acaatcaaac atcaactgat ttcattcttat tggggctgtt tccaccatca 60
 agaattgacc ttttcttctt cattctcttt gttctcattt tcctgatggc tctaattgga 120
 aacctatcca tgattcttct catcttcttg gacacccatc tccacacacc catgtatttc 180
 ctgcttagtc agctctccct cattgaccta aattacatct ctacgattgt tcctaagatg 240
 gcttctgatt ttctgtatgg aaacaagtct atctccttca ttgggtgtgg gattcagagt 300
 ttcttcttca tgacttttgc aggtgcagaa gcgctgtccc tgacatcaat ggcctatgat 360
 cgttatgtgg ccatttgcct tcctctccac tatcccatcc gtatgagcaa aagaatgtat 420
 gtgctgatga taacaggatc ttggatgata ggctccatca actcttgtgc tcacacagta 480
 tatgcattcc gtatcccata ttgcaagtcc agagccatca atcatttttt ctgtgatgtt 540
 ccagctatgt tgacattagc ctgtacagac acctgggtct atgagtacac agtgtttttg 600
 agcagcacca tctttcttgt gtttcccttc actggcattg cgtgttccca tggctgggtt 660
 ctcttctgtg tctaccgat gcaactctgca gaaggaggaa aaaggcctat tcgacctgca 720
 gcacccacct cactgtagta actttctact atgcaccctt acgttatacc tatctatgtc 780
 caagatccct gtttatttct gacagaggac aagggttggg gggggggggg acaccatcct 840
 cacctcaatg ctcaacccca tc 862

<210> 568
 <211> 930
 <212> DNA
 <213> Unknown (H38g417 nucleotide)

<220>
 <223> Synthetic construct

<400> 568
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 cctcagatgg agatcatctt ctctgtggc ttcctcatag ttacctggt taatgtagtg 120
 gggaatatgg gtatgattat cctgattaca acagacactc agcttcacac acccatgtat 180
 tttttcctct gcaacctctc ctttggtgac ctgggctact cctcagccat tgccccagg 240
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 tttgcttttt ttgtaggttt tgtggatgct gagtgctatg tcctggcagc catggcctat 360
 ggctcgttttg tggccatttg tgcacccctc cactatagca ccttcatgtc caagcaggtc 420
 tgcttggctc tcatgctggg ctcttacctg gctgggtctag tgagtttagt agccacact 480
 accctcacct tcagcctgag ttactgtggt tccaatatca tcaatcattt cttctgcgaa 540
 atccccacac tcttggccct ctcttgctca gacacctaca tcagtggatg cttgtcttc 600
 agtctgtgtg gcttcattga attcagcacc atcctcatca tcttcatctc ctataccttt 660
 atccttgttg caatcatcag aatgcgttca gctgaaggcc gccttaaggc tttctccacc 720
 tgcgggtctc accttactgg catcaccctc ttctatggca cagtcatgtt tatgtacctg 780
 aggccaacat ccagctactc cctggaccaa gacaagtggg cctctgtgtt ctacacggtt 840
 atcatcccca tgttaaatac cttgatctac agtttgcgga acaaggatgt gaaagctgct 900
 ttcaaaaagc taattggaaa aaaatctcaa 930

<210> 569
 <211> 1005
 <212> DNA
 <213> Unknown (H38g418 nucleotide)

<220>
 <223> Synthetic construct

<400> 569
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 atccagaacg gcagctgggc cttgctgggc tgttctgtc catgtgcctg gtcacgggtg 120

tggggaacct	gctcatcatc	ctggccgtca	gtcctgactc	ccacctccac	acccccatgt	180
acttcttcct	ctccaaccta	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgattgt	ggacatccga	tctcacagca	gagtcacctc	ctatgcaggc	tgcctgactc	300
agacgtctct	ctttgccatt	tttgaggca	tggaagagag	acatgctcct	gagtgtgatg	360
gcctatgacc	agttttagc	catctgtcac	cctctatata	attcagccgt	catgaacctt	420
tgtttctgtg	gctttctagt	tttggtgact	tttttttttc	tcagtctttt	agacgcccag	480
ctgcacaact	tgattgcctt	acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	540
ttctgtgacc	cttctccact	cccccatctt	gcatgttggt	acaccttcac	caataacata	600
atcatgtatt	tccttgcctg	catatttggg	tttcttccca	tctcggggac	ccttttctct	660
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ttctccacct	gtgggtctca	cctgtcgggt	gtttgtgat	tttatggaa	aggcattgga	780
gggtacctca	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcggtggc	ctcagtgatg	840
tacacggtgg	tcaccccat	gtgaacccc	ttcatctaca	gcctgagaaa	cagggatatt	900
aaaagtgtcc	tgcggtggct	gcacggcagc	tctgtcta	ctcaacatct	tcttatctgt	960
tgcattcctt	ttgtagtggt	ggttaaaaaa	ggcagcaggg	tcaaaa		1005

<210> 570

<211> 907

<212> DNA

<213> Unknown (H38g419 nucleotide)

<220>

<223> Synthetic construct

<400> 570

atggatcacg	tcagtcataa	ctggactcag	agttttatcc	ttgctgggtt	caccaccact	60
gggaccctac	aacctcttgc	cttcttgggg	accctatgca	tctatctcct	cacacttgca	120
gggaacattc	tcatcattgt	cctgggtacag	ttagattctg	gactgttcac	gccccgtac	180
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ctatgtcttt	cattccttag	ggatgactga	gtgctacctg	ctgggtgtca	tggcactgga	360
tagctacett	atcatctgcc	accactcca	ctaccacgca	ctcatgagca	gacagggtaca	420
gttacgacta	gctggggcca	gttgggtggc	tggcttctca	gctgcacttg	tgccagccac	480
cctcactgcc	actctgcctt	tctgcttgaa	agagggtggc	cattactttt	gtgacttgge	540
accactaatg	cggttggcat	gtgtggacac	aagctggcat	gctaggggcc	atggcacagt	600
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ctcccacgta	actgtgggtg	cactattcta	tgtctctgcc	ttcacagtat	atgtgggctc	780
acctgggagt	cgacctgaga	gcacagacaa	gcttgttgcc	ttgggttatg	cccttattac	840
ccctttcttc	aatcctatca	tctatagcct	tcgcaacaag	gaggtgaaga	aggctttaag	900
gagagtc						907

<210> 571

<211> 1006

<212> DNA

<213> Unknown (H38g420 nucleotide)

<220>

<223> Synthetic construct

<400> 571

ccaacgaaga	gagagaacca	cacagtgata	agggagtgtt	ttttccaggg	tttctccagc	60
tttcatgaac	acaagcttac	cctctttgtg	gtattttctta	ccttgtgtct	tttaaccttg	120
gctggcaatg	tcataattgt	gacaattatc	agcattgatc	gtcaccttca	cacccccatg	180
tacttctttg	ttagtatgct	ttccacttca	gagactgtct	acacattagt	cattgtacca	240
cggatgctct	ccagtctctt	aagtctaagc	caacctatct	ctttgggtgg	ctgtgccacc	300
cagatgtttt	ttttattacc	ttggccatca	acaactgctt	tctgctcaca	gcaatggggt	360
atgatcgcta	tgtggccatc	tgtaaccctt	tgaggtacat	gatcatcatg	aacaagaaaag	420
tgtgtgtcca	gctgggtatg	gggtcctgca	gtgttgggct	gcttgtggcc	atagttcaga	480
tttcatctgt	gttcaggctg	cctttttgtg	ataaacaggt	ggcccatatt	ttctgtgata	540
tccacccagt	tatgaaactt	tcctgtgttg	ataccactct	acatgaccta	attaattttg	600

ttgttagttc	cctgggttatt	gtggtgcccgc	tgggttttgg	cttcattctcc	tacatcctca	660
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gtgcctccca	cctcactgtg	gttatcatcc	actatggctg	tgccctccatt	gcctacctca	780
agcccaagtc	agagaacacc	agggatcagg	accagcta	ttcagtgaca	tacaccgtct	840
ttactccact	acttaactct	gttgtgtaca	ctttgaggaa	caaggaggtc	aagaatgccc	900
ttcaccgtgc	tattggc1aa	aaaccttttg	cctagaatct	tcattcagttt	gacatatagt	960
cagtcatagt	ctgggtattt	ttttaagctc	gagaaaattg	aatcct		1006

<210> 572

<211> 945

<212> DNA

<213> Unknown (H38g421 nucleotide)

<220>

<223> Synthetic construct

<400> 572

atgtccataa	ccaaagcctg	gaacagctca	tcagtgacca	tgttcatcct	cctgggattc	60
acagaccatc	cagaactcca	ggccctcctc	tttgtgacct	tcctgggcat	ctatcttacc	120
accctggcct	ggaacctggc	cctcattttt	ctgatcagag	gtgacaccca	tctgcacaca	180
cccattgact	tcttcctaag	caacttatct	ttcattgaca	tctgtctact	ttctgctgtg	240
gtccccaata	tgctcactga	cttcttctgg	gagcagaaga	ccatatcatt	tgtgggctgt	300
gctgctcagt	tttttttctt	tgctggcatg	ggtctgtctg	agtgcctcct	cctgactgct	360
atggcatacg	accgatatgc	agccatctcc	agcccccttc	tctacccca	tatcatgacc	420
cagggcctct	gtacacgcat	ggtgggttgg	gcatatgttg	gtggcttcc	gagctccctg	480
atccaggcca	gtcccatatt	taggcttcac	ttttgaggac	ccaacatcat	caaccacttc	540
ttctgcgacc	tcccaccagt	cctgggtctg	tcttgctctg	acaccttcc	cagtcaagtg	600
gtgaatttcc	tcgtgggtgg	cactgtcgga	ggaacatcgt	tcctccaact	ccttatctcc	660
tatggttaca	tagtctctgc	ggtcctgaag	atcccttcag	cagagggccg	atggaaagcc	720
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gtgtacttgc	gacccagctc	cagctacttg	ctaggcaggg	acaaggtgg	gtctgttttc	840
tattcattgg	tgatcccat	gctgaaccct	ctcatttaca	gtttgaggaa	caaagagatc	900
aaggatgccc	tgtggaaggt	gttggaaggt	aagaaagtgt	tttct		945

<210> 573

<211> 949

<212> DNA

<213> Unknown (H38g422 nucleotide)

<220>

<223> Synthetic construct

<400> 573

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gggttgctct	ctgaaccaa	gatacagctt	attcttttta	ttatgttctt	gttctattta	120
tcaacggtgg	ctggaaatgt	tataatcatc	actattatct	agatggaacc	tctcctccaa	180
acccccatgt	acttcttcc	cactaattta	tcctttctgg	acatttgcta	cacatccacc	240
aatgtccccc	aatgctgtc	caacatggcg	gggaaaaaga	acaccatctc	attctccagc	300
tgcgctactc	agatgtactt	ctccctctcc	tttggaatga	ttgtgtcctc	cctgggtgtca	360
tggtttatga	cagatatgta	gccatttgtc	atcctcttca	ttataccttc	attatggacc	420
aaaacacctg	cattcaactg	gcagttattt	cctgggtccag	tagcttccctg	agttccatgg	480
ttatcaatgt	tctcacgttg	agtttgccct	actgtggggc	taataatcctg	aatacatttt	540
tctgtgaggt	actttctgtc	ctgaggttgg	cctgcaccaa	cacctcattc	acagagctgg	600
ttgtttttat	cttcagtatc	atcattgtct	tcattccctt	cctcctcatt	gttgtttcct	660
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tatccacctg	tacctcccat	ttgacagtgg	taaccttatt	tatgggactg	ccatcttcat	780
ggacatgaga	ccacagtcga	ggtcctcctg	ggctggcggc	aagatcattg	cggttttcta	840
cacgggtggc	acacccatgc	ttaaccctt	gatttacagc	ctgaggaacc	aagatgtgaa	900
aggagctcga	aggagagcta	ttgcaaagca	gaggatgtga	cagctgtta		949

<210> 574

<211> 1022

<212> DNA

<213> Unknown (H38g423 nucleotide)

<220>

<223> Synthetic construct

<400> 574

atgccaaagc	taaattccac	ttttgtgact	gagttcctct	ttgaagggtt	ctccagcttc	60
aggcggcagc	acaaacttgt	cttctttgtt	gtcttcctaa	ctttgtacct	gctgactctc	120
tctggcaatg	tgattatcat	gaccattatt	cgccctggacc	atcatcttca	caccccatg	180
tacttcttcc	tgtgcatgct	atccatctct	gagacctgct	acactgtggc	catcattccc	240
catatgcttt	ctggtctctt	gaatcctcat	cagccccattg	ccacccaaag	ctgtgccact	300
cagctcttct	tctatctcac	ctttggcatc	aacaactgct	tcctgctcac	agtcatggga	360
tatgaccgct	atgtggccat	ctgcaacccc	ctaagggtatt	cagtcacat	gggtaagagg	420
gcctgtatcc	aactggcctc	tggatcactg	gggattggcc	ttggcatggc	cattgtccaa	480
gtaacatctg	tgtttggcct	gccattctgt	gatgcctttg	tcattctcca	cttcttctgt	540
gatgtgagac	acctgctgaa	gctggcctgc	acagacacca	ctgtcaatga	gataatcaac	600
tttgttgtca	gcgtctgtgt	ccttggttcta	cctatggggc	tggctcttat	ctcctatgtc	660
ctcatcatct	ccaccattct	taagattgcc	tcagctgaag	gtcagaagaa	ggcctttgcc	720
acctgcgcct	cccacctcac	agtggctcatc	atccactatg	gctgtgcctc	catcatctac	780
ctgaagccta	agtcccagag	ttccctggga	caggacagac	tcattctcagt	gacctacact	840
catcactccc	ctactgaacc	ctgtttgtgta	cagcctgaag	aacaaggagg	tcaaagatgc	900
tctgcacaga	gccgtggggc	aaaaaactct	gtctccttaa	tgaagagagg	ttgtgaaggc	960
ttttcctttg	cgtttataaa	tatgtactaa	tttttaatgc	tctttcaata	atgcccttat	1020
gt						1022

<210> 575

<211> 938

<212> DNA

<213> Unknown (H38g424 nucleotide)

<220>

<223> Synthetic construct

<400> 575

atggatattg	gcctgagtat	agccaatagc	tcagggtttc	aactgtctga	gttcattctg	60
atagggttcc	caggcattca	tgagtggcag	cactggctct	ccctgccctt	agctcttggg	120
gccaatctcc	tcatacata	caccattcaa	catgagacca	tgctacatga	acccatgtac	180
catttgctgg	gcatattagc	agtgggtggc	attggcctgg	ccaccaccat	catgcccagg	240
atcctggcca	tcttctgggt	tgatgccaa	gccatcagcc	tccttgagt	ttttgtctag	300
atctatgcca	tccactcttt	catgtgcatg	gagtcaggca	tcttcctctg	catggcagtg	360
gatagatata	tggccatttg	ttatcccctt	cagtacactt	ccatagttac	tgaagctttt	420
gtcatcaaag	ccacactgtc	agtagtgctc	aggaatggcc	tggtgaccat	cccagtgcca	480
gtattggctg	cccagcgaca	ctactgctcc	aggaatgaga	ttgatcagtg	cctctgctct	540
aacttggggg	tcacaagtct	ggcctgtgat	gacaccacta	ttaacagggt	ttaccagctg	600
gccttggctc	gggttgtggt	tgggagtgc	atgggtctgg	tctttgcttc	ctattctttg	660
attattcact	cagtgtgtaa	gctgaactct	gctaaagcaa	catctaaggc	cctgaatacc	720
tgcagctccc	accttatect	cattctcttt	ttctacacag	ctattattgt	agtatctgtc	780
accacctggc	aggaagaagg	gctccccgca	tcctgtttct	cctcaatgtg	ctgcatattg	840
tcaccccttc	agcccttaac	cccatagtat	atgcccttag	gacctaggag	ctgagagcgg	900
gcttccagaa	gctgcttggt	ttgggcgagt	atgtgtcc			938

<210> 576

<211> 945

<212> DNA

<213> Unknown (H38g425 nucleotide)

<220>

<223> Synthetic construct

<400> 576

atgtttctccc	caaaccacac	catagtgaca	gaattcattc	tcttgggact	gacagacgac	60
ccagtgtctag	agaagatcct	gtttggggta	ttccttgcca	tctacctaat	cacactggca	120
ggcaacctgt	gcatgatcct	gctgatcagg	accaattccc	acctgcaaac	acccatgtat	180
ttcttctctg	gccacctctc	ctttgtagac	atttgctatt	cttccaatgt	tactccaaat	240
atgctgcaca	atttcctctc	agaacagaag	acctctcct	acgctggatg	cttcacacag	300
tgtcttctct	tcatcgccct	ggtgatcac	gagttttaca	tccttgcttc	aatggcattg	360
gacgctatg	tagccatttg	cagccctttg	cattacagtt	ccaggatgtc	caagaacatc	420
tgtgtctgtc	tggtcactat	cccttacatg	tatgggtttc	ttagtgggtt	ctctcagtc	480
ctgctaacct	ttcacttata	cttctgtggc	tcccttgaaa	tcaatcattt	ctactgcgct	540
gacctctctc	ttatcatgct	ggcctgctct	gacacccgtg	tcaaaaagat	ggcaatgttt	600
gtagtgtcag	gctttaatct	ctcaagctct	ctcttcatca	ttcttctgtc	ctatcttttc	660
atthttgagc	cgactctcag	gatccgttct	gctgaaggca	ggcacaaaagc	cttttctacg	720
tgtgcttccc	acctgacaat	agtcactttg	ttttatggaa	ccctcttctg	catgtacgta	780
aggcctccat	cagagaagtc	tgtagaggag	tccaaaataa	ctgcagtctt	ttatactttt	840
ttgagcccaa	tgctgaaccc	attgatctat	agcctacgga	acacagatgt	aatccttgcc	900
atgcaacaaa	tgattagggg	aaaatccttt	cataaaattg	cagtt		945

<210> 577

<211> 771

<212> DNA

<213> Unknown (H38g426 nucleotide)

<220>

<223> Synthetic construct

<400> 577

atgtttctac	tggtggccat	cctggcagcc	acagacctgg	gcttagccac	atctatagcc	60
ccagggttgc	tggctgtgct	gtggcttggg	ccccgatctg	tgccatatgc	tgtgtgcctg	120
gtccagatgt	tctttgtaca	tgcactgact	gccatggaat	cagggtgtgct	tttggccatg	180
gcctgtgata	gtgctgcggc	aataggcggt	ccactgcact	accctgtcct	ggtcacaaa	240
gcctgtgtgg	gttatgcagc	cttggccctg	gcactgaaag	ctgtggctat	tgttgtacct	300
ttcccactgc	tgggtggcaaa	gtttgagcac	ttccaagcca	agaccatagg	ccatacctat	360
tgtgcacaca	tggcagtggt	agaactgggt	gtgggtaaca	cacaggccac	caacttatat	420
ggtctggcac	tttactggc	catctcaggt	atggatatc	tgggtatcac	tggctcctat	480
ggactcattg	cccatgctgt	gctgcagcta	ctaccgggg	aggcccatgc	caaggccttt	540
ggtacatgta	gttctcacat	ctgtgtcatt	ctggccttct	acatacctgg	tctcttctcc	600
tacctgcac	accgctttgg	tcatacact	gtcccaaagc	ctgtgcacat	ccttctctcc	660
aacatctact	tgtgtgtgcc	acctgccttc	aacccctca	tctatggggc	ccgcaccaag	720
cagatcagag	accgactcct	ggaaaccttc	acattcagaa	aaagcccggt	g	771

<210> 578

<211> 1074

<212> DNA

<213> Unknown (H38g427 nucleotide)

<220>

<223> Synthetic construct

<400> 578

gtgagcatga	gcttcttaat	aagaagtgt	tcaacactac	acactccaat	gtgcttgttc	60
ctcagtcate	tctcctttgt	agatctctat	tatgccacca	atgccactcc	tccgatgctg	120
gttaactttt	tttttccaag	agaaaaaccg	tttcttttat	tgggttgctt	atccaatttc	180
accttttcat	tgcactgggt	atcacagatt	atcatatgct	cacagtgatg	gtgtatgacc	240
actacatggc	catctgcaag	cctttgttat	atggaagcaa	aatgtccagg	tgtgtctgcc	300
tctgtctcac	tgtgtctccc	tatatattat	gctctgcaaa	tggcttggt	caggctatcc	360
tgatgctttg	tctgttcttc	tgtgaaccca	atgagatcaa	ccactttttt	ttttttggag	420
aaaatgcatt	atatgcacat	ttaattccac	tataaatttt	tgaatggacg	gttggagagg	480
aagggagaaa	tacatatata	cggagagaat	accaccaga	aagtatatata	aatgggagaa	540
aggaacctgt	tgatccaagt	ttccatattc	ttattatggc	atataagggt	atgattattt	600
tctcagtatg	aagcatctcc	cagggctgac	tctgatgtaa	aattggagat	caaccacttt	660

tattatgcag	aaccacccct	cttagtcctc	gcctgcttgg	atacttatgt	caaagaaact	720
gccatgttca	tggtggtc	ttccaacctc	atctgccctc	tcactatcat	ctttatttcc	780
tacactttca	tcttcacaga	cattctgcac	atctgcactg	ctgaggggag	gtacaatgcc	840
ttctccacct	gggggtccct	tgtgactgcc	gtcactgtct	ttcaagggaac	gctgtttcac	900
atgtgcctga	ggcccccttc	tgaggcatct	gtagaacagg	ggaaaattgt	agctgctttt	960
tatatctttg	tgagtcctac	gttaaaccce	ttgatctacc	gtctgaggaa	taaaaatggt	1020
aaaagaacaa	taagggaagt	tatccaaaag	aaactgtttg	ctaagtaagg	taga	1074

<210> 579

<211> 937

<212> DNA

<213> Unknown (H38g428 nucleotide)

<220>

<223> Synthetic construct

<400> 579

atgtttggtg	ctaattctcac	caccttccat	cccactctat	tcattctcct	tggcatccca	60
ggactggagc	aataccacat	ctggctttcc	attcctttct	accttatgta	catcactgca	120
gtcttgggaa	atggagccct	catcctagtt	gtcctcagtg	aacacaccct	ccatgtcttc	180
ctatccatgc	tggttggcac	tgatatcctg	ctatccacca	ccactgtgcc	taaggccttg	240
gcgatcttct	gggtccacgc	tgaggagata	gcctttgatg	cctgcattac	tcagatgttt	300
ttcattcatg	ttgcctttgt	ggctgagtca	ggaatcctgc	tggccatggc	atttgacagt	360
tatgtagcca	tttgactccc	cttgagatac	actaccatct	taacttctat	ggtaaattgga	420
aaaatgaccc	tgacaatctg	gggacaaaag	attgggacaa	tttttctcgt	catattcctg	480
ctgaagaggc	tgccatactg	tcagaccaat	atcatccccc	actcatactg	tgagcacatt	540
gggttggccc	aattggcctg	tgctgacata	actgtcaata	tctgggatgg	cttttcagtg	600
ccaatggcat	cggtttttgt	agatgttgca	ttcattgggt	tttccctacac	tttgatcttc	660
caggctgtgt	ttagacttcc	ttcccaggag	tcccagcaca	aagctcttaa	cacctgtggt	720
tctacattgg	agttgttctc	ctcttcttca	tcccatcatt	ttttactttc	ctgacccacc	780
gctttggcaa	gaatatcccc	catcatgtcc	acatacttct	ggcaaattct	tacttgcttg	840
ttcccccatg	cttaacccca	ttatctacgg	agagaagacc	aagcaaataca	gggacagtat	900
ggctcatatg	ttatctgtgg	tggggaagtc	ttgagac			937

<210> 580

<211> 941

<212> DNA

<213> Unknown (H38g429 nucleotide)

<220>

<223> Synthetic construct

<400> 580

atgaagatga	agatagatcc	caaatgcaat	ggcacggagg	taactgaatt	tattctgttg	60
ggactgacta	gccagccaga	gctgcagcct	atgctctttg	tggtattcct	cctgattttac	120
ctcatcaccc	tgactgggaa	atttgggatg	attttcctaa	tcagattcac	tcctcagctc	180
caaaccacac	tgtatttttt	ccttactcat	ttagcatgtg	tggaattttt	ttactccact	240
aatgtctctc	cacagagctt	gttaatttct	tatctgagaa	gaagaccatt	tcctacgctg	300
ggtgtctggc	ccagtgtttt	gtctttgtga	ctctgtcctt	tactgagtat	tacatgcttg	360
gtgccatggc	ctatgactgc	tacatggcaa	tctgcaatcc	cctacattac	agcagcaaaa	420
tgtccagagc	agtttgcac	tgccgtgtga	ctttccccta	cttctggggg	tctatgggtg	480
gcacgatgca	agtaatactg	acctctcggt	tgctcttttt	tggaaccaac	accatcaacc	540
atttctactg	tactgaccca	ccccctctaa	tgttgacatc	ttctgacact	tacataaaac	600
aaactgcctt	gtttgtgtca	gcagggatta	acctcacagt	ttccctgctc	atcatttctca	660
tctctacat	tttcattttc	atcaccatta	tgaggatccg	ttccagtga	gggcagctca	720
aagccttctc	cactgttggc	tcccactga	cagctgtcac	tatgttctat	gggtccctat	780
tctgcatgta	cctgagacca	acaaatgagc	tgctgtttga	gcaagggaaa	atgggagtgg	840
tgttttgtat	ttttgtgagt	cccatgctga	acctgtttat	ctaccgctg	agaaacaagg	900
atgtgaaaca	ggccttgaaa	agagtgttta	tgagaaacct	t		941

<210> 581

<211> 958
 <212> DNA
 <213> Unknown (H38g430 nucleotide)

<220>
 <223> Synthetic construct

<400> 581

atgagtccttc	tattctgaga	ctaagatatg	agaaacttta	caccactgtc	tggaatttatt	60
atcctgggat	tcacggatca	cccagaatta	cagtgtcttc	tttttgtgtt	gtttcttctc	120
atctatatgt	tcaccgttgt	tggaatctt	ggcatgattc	tattaatcaa	gattgactca	180
catctccata	ctccaatgta	cttttccctc	agtaacttgt	gccttgttga	cttctgttat	240
tcttctgtca	ttgcccctaa	tatgctgata	aatttctggg	tggaagaacc	agtcatttca	300
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ctgttggctg	tcattggccta	tgactgttat	gtggccatct	gcaagcctct	gctttataca	420
gtcctgatgt	cacccacact	cagtgccctc	ctggtgttag	ccacatatct	tttgggcttt	480
gtaaatgctg	ccattcacac	tggtctcacc	ttccagctgt	cattctgcca	ctccaatatc	540
attaactatt	ttttttgtga	tattccaccc	ctcctgaaac	tcttgttctg	atacacacat	600
caatgaggtt	gtcatttttg	cctttgccag	ttttaatgaa	ttgagctgtc	tcctactgat	660
tcttgtttcc	tgtctctaca	tccttgtctg	catcttgaag	atccactctg	cagaagggag	720
gcacaaggcc	ttctccacct	gtgcttccca	cttggcgggtg	gtcactatct	tctttgggac	780
aatcctgttc	atgtatctct	gcgtcccagc	tccagctact	caatggatca	agacaaagtg	840
gtgtctgtct	tacacagtag	tcatccccat	gttgaatcct	ttcatctata	gtttgagaaa	900
caaggaagtc	aaagcttctt	taagtaaaat	gtttaaaaca	gtctcttata	tctctact	958

<210> 582
 <211> 897
 <212> DNA
 <213> Unknown (H38g431 nucleotide)

<220>
 <223> Synthetic construct

<400> 582

atgggattac	caggcattca	tgagtggcag	cactggctct	ccctgcccct	gactctgtct	60
tacctcttag	ctcttgggtg	caacctcctc	atcataatca	ccattcaaca	tgagaccgtg	120
ctacatgaac	ccatgtacca	tttgtggggc	atattagcag	tggtggacat	tggcctggcc	180
accaccatca	tgcccaagat	cctggccatc	ttctggtttg	atgccaaagg	cattagcctc	240
cccattgtgt	ttgtctcagat	ctatgccatc	cactgcttct	tctgcataga	gtcaggcatc	300
tttctctgca	tggcagtaga	cagatacata	gccatctgtc	gccctcttca	gtacccctcc	360
atagtacta	aagcttttgt	cttcaaagcc	acagggttca	tcattgtctc	gaatggcctg	420
ttgaccatcc	cagtgcctat	actggctgcc	cagagacact	actgttccag	gaatgaaatc	480
gagcactgcc	tctgtcttaa	cttgggggtt	atcagcctgg	cttgtgatga	catcactgtg	540
aacaaatttt	accaactgat	gctagcatgg	gtcttgggtg	ggagtgatat	ggctctggta	600
ttttcttcct	atgctgtaat	ccttcaactc	gtgctgaggc	tgaactcagc	agaagcaatg	660
tccaaggctc	tgagcacttg	tagctcccat	ctcatcctca	tcctcttcca	cacaggatc	720
attgtgctgt	ctgtcacaca	ccttgcagag	aaaaagattc	cccttattcc	tgtgttccct	780
aatgtgctgc	acaatgtcat	ccccctgca	ctcaaccccc	tggcctgtgc	actcaggatg	840
cacaaactca	gactgggctt	tcagagactg	cttggactgg	gtcaggacgt	gtccaag	897

<210> 583
 <211> 951
 <212> DNA
 <213> Unknown (H38g432 nucleotide)

<220>
 <223> Synthetic construct

<400> 583

atgatgagac	ttatgaaaga	ggttcgaggc	agaaatcaaa	cagaagtaac	agaatttctc	60
ctcttaggac	tttccgacaa	tccagatcta	caaggagtcc	tctttgcatt	gtttctgttg	120

atctatatgg	caaacatggt	gggcaatttg	gggatgattg	tattgattaa	gattgatctc	180
tgtctccaca	ccccatgta	tttctttctc	agtagcctct	ctttttaga	tgctctttac	240
tcttcttccg	tcactcccaa	gatgctgggt	aacctcatgg	ctgagaataa	ggccatttct	300
tttcatggat	gtgctgcca	gttctacttc	tttggctcct	tcttggggac	tgagtgttc	360
ctgttgccca	tgatggcata	tgaccgctat	gcagccattt	ggaacccct	gctctacca	420
gttctcgtgt	ctgggagaat	ttgctttttg	ctaatagcta	cctccttctt	agcaggttgt	480
ggaaatgcag	ccatacatc	agggatgact	tttaggttgt	ccttttgtgg	ttctaataag	540
atcaaccatt	tctactgtga	caccccgcca	ctgctcaaac	tctcttgctc	tgataccac	600
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gtcctcattt	cctacctgtg	tatcttcatt	gccgtcttga	agatgccttc	gttagagggc	720
aggcacaag	ccttctccac	ctgtgcctct	tacctcatgg	ctgtcaccat	attctttgga	780
acaatcctct	tcatgtactt	gcgccctaca	tctagctact	caatggagca	agacaagggt	840
gtctctgtct	tttatacagt	aataatccct	gtgctaaatc	ccctcatcta	tagtttaaaa	900
aataaggatg	taaaaaaggc	cctaaagaag	atcttatgga	aacacatctt	g	951

<210> 584

<211> 951

<212> DNA

<213> Unknown (H38g433 nucleotide)

<220>

<223> Synthetic construct

<400> 584

atgagtcaca	ccaatgttac	catcttccat	cctgcagttt	ttgtccttcc	tggcatccct	60
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gtcctgggaa	acagcatcct	gatagtgggt	attgtcatgg	aacgtaacct	tcatgtgccc	180
atgtatttct	tctctcaat	gctggccgtc	atggacatcc	tgctgtctac	caccactgtg	240
cccaaggccc	tagccatctt	ttggcttcaa	gcacataaca	ttgcttttga	tgctgtgtgc	300
acccaaggct	tctttgtcca	tatgatgttt	gtgggggagt	cagctatcct	gttagccatg	360
gcctttgatc	gctttgtggc	cattttgtgc	ccactgagat	atacaacagt	gctaacatgg	420
cctgttgtgg	ggaggattgc	tctggccgtc	atcacccgaa	gcttctgcac	catcttccca	480
gtcatattct	tgctgaagcg	gctgcccttc	tgccataacca	acattgttcc	tcactcctac	540
tgtgagcata	ttggagtggc	tcgtttagcc	tgtgtgtgaca	tcactgttaa	catttggtat	600
ggcttctcag	tgccatttgt	catggtcata	ttggatgtta	tctcatcgc	tgtgtcttac	660
tcactgatcc	tccgagcagt	gtttcgtttg	ccctcccagg	atgctcggca	caaggccctc	720
agcacttgtg	gctcccacct	ctgtgtcatc	cttatgtttt	atgttccatc	cttctttacc	780
ttattgaccc	atcatttttg	gcgtaatat	cctcaacatg	tccatatctt	gctggccaat	840
ctttatgtgg	cagtgccacc	aatgctgaac	cccatgtgtc	atgggtgtgaa	gactaagcag	900
atacgtgagg	gtgtagccca	ccggttcttt	gacatcaaga	cttgggtgctg	t	951

<210> 585

<211> 915

<212> DNA

<213> Unknown (H38g434 nucleotide)

<220>

<223> Synthetic construct

<400> 585

atgcagagga	gcaatcatc	agtgactgag	tttatactgc	tgggcttcac	cacagaccca	60
ggaatgcagc	tgggcctctt	cgtgggtgtc	ctgggcgtgt	actctctcac	tgtggtagga	120
aatagcacc	tcatcgtgtt	gatctgtaat	gactcctgcc	tccacacacc	catgtatttt	180
gtcgtctgga	atctgtcgtt	tctggatctc	tggtattctt	ctgtctacac	cccaaagatc	240
ctagtacct	gcattctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttcttctctg	cagggtctggc	ctatagttag	tgctacctgc	tggctgccgt	ggcttatgac	360
cgctacgtgg	ccatctccaa	gccctgctt	tatgcccagg	ccatgtccat	aaagctgtgt	420
gcattgctgg	tagcagtctc	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
aaaacgtttt	cctttaactt	ctgccgtgaa	aacatcattg	atgacttttt	ctgtgatttg	540
cttcccttgg	tggagctggc	ctgtggcgag	aaggcggtct	ataaaattat	gatgtacttc	600
ctgctggcct	ccaatgtcat	ctgccccgca	gtgctcatcc	tggcctccta	cctctttatc	660

atcaccagtg	tcttgaggat	ctctctctcc	aagggctacc	tcaaagcctt	ctccacatgc	720
tcctcccacc	tgacctctgt	cacttttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	tgaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	tccca					915

<210> 586

<211> 942

<212> DNA

<213> Unknown (H38g435 nucleotide)

<220>

<223> Synthetic construct

<400> 586

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ctgctaggca	actgtaccct	tctcttcatt	atccgggctg	atgcagccct	ccatgaaccc	180
atgtacctct	ttctggccat	gttggcaacc	attgacttgg	ttctttcttc	tacaacgctg	240
cccaaaatgc	ttgccatatt	ctggttcagg	gatcaggaga	tcaacttctt	tgctgtctg	300
gtccagatgt	tcttcttca	ctccttctcc	atcatggagt	cagcagtgtc	gctggccatg	360
gcctttgacc	gctatgtggc	catctgcaag	ccattgcact	acacgacggg	cctgactggg	420
tcctcatca	ccaagattgg	catggctgct	gtggcccggt	ctgtgacact	aatgactcca	480
ctccccctcc	tgctcagacg	cttccactac	tgccgaggcc	cagtgattgc	ccattgctac	540
tgtgaacaca	tggctgtggt	aaggctggcg	tgtggggaca	ctagcttcaa	caatatctat	600
ggcattgctg	tggccatgtt	tagtgtggtg	ttggacctgc	tctttgttat	cctgtcttat	660
gtcttcatcc	ttcaggcagt	tctccagctt	gcctctcagg	aggcccgcta	caaggcattt	720
gggacatgtg	tgtctcacat	aggtgccatc	ctgtccacct	acactccagt	agtcactctc	780
tcagtcatgc	accgtgtagc	ccgccatgct	gccccctggt	tccacatact	ccttgctatt	840
ttctatctcc	ttttcccacc	catgggtcaat	cctatcatat	atggagtcaa	gaccaagcag	900
attcgtgagt	atgtgctcag	tctattccag	agaaagaaca	tg		942

<210> 587

<211> 937

<212> DNA

<213> Unknown (H38g436 nucleotide)

<220>

<223> Synthetic construct

<400> 587

atgttaaaga	aaaaccatac	agccgtgact	gagtttgttc	tcctgggact	gacagatcgg	60
gctgagctgc	agtcccttct	ttttgtggta	tttctagtca	tctaccttat	cacagtaatc	120
ggcaatgtga	gcatgatctt	gttaatcaga	agtgactcga	cactacacac	tccaatgtac	180
ttcttctca	gtcacctctc	ctttgtagat	ctctgttata	ccaccaatgt	tactcctcag	240
atgctgggta	actttttatc	caagagaaaa	accatttctc	tcacgggctg	ctttatccaa	300
tttcactttt	tcattgcaat	gggtgattaca	gattattata	tgctcacagt	gatggcttat	360
gaccgctaca	tggccatctg	caagcccttg	ttatatggaa	gcaaaatgac	cagggtgtgc	420
tgccctctgtc	tcgctgtctg	tccttatatt	tatggctttg	caaatgggtc	aagcacagac	480
caccctgatg	cttcgtctgt	ccttctgtgg	acccaatgac	atcaaccact	tttactgtgc	540
ggacccaccc	ctcttagtcc	tcgctgtctc	agatacttat	gtcaaagaga	ccgccaatgt	600
gggtggtggct	ggttccaacc	tcatttgctc	tctcaccgtc	atcctcattt	cctacacttt	660
catcttcaat	gccattctgc	gtatccacac	tgctgagggg	aggcgcaagg	ccttctccac	720
ctgcgggtct	catgtgaccg	ctgtcactgt	cttctatggg	acactgttct	gcatgtacct	780
gaggccccct	tctgagacat	ctatacaaca	ggggaaaatt	gtagctgttt	tttatatctt	840
tgtgagtcgg	atgttaaacc	cattgatcta	cagcctgagg	aataaagacg	ttaaaagaag	900
tataaggaaa	gttattcaaa	agaaactggt	tgctaag			937

<210> 588

<211> 942

<212> DNA

<213> Unknown (H38g437 nucleotid)

<220>

<223> Synthetic construct

<400> 588

atgtcagcct	ccaatatcac	cttaacacat	ccaactgcct	tcttggttgg	ggggattcca	60
ggcctggaac	acctgcacat	ctggatctcc	atccctttct	gcttagcata	tacactggcc	120
ctgcttgga	actgcactct	ccttctcatc	atccaggctg	atgcagccct	ccatgaaccc	180
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cccaaaatgc	ttgccatatt	ctggttcagg	gacggggaga	taaacttctt	tgctgtctg	300
gcccagatgt	tcttcttca	ctccttctcc	atcatggagt	cagcagtgtg	gctggccatg	360
gcctttgacc	gctatgtggc	tatctgcaag	ccactgcact	acaccaaggt	cctgactggg	420
tcctctcatc	ccaagattgg	catggctgct	gtggcccggg	ctgtgacact	aatgactcca	480
ctccccttcc	tgctgagatg	tttccactac	tgccgaggcc	cagtgategc	tcactgtctac	540
tgtgaacaca	tggtgtgggt	gaggctggcg	tgtggggaca	ctagcttcaa	caatatctat	600
ggcatcgctg	tgcccatgtt	tattgtgggt	ttggacctgc	tccttgttat	cctgtcttat	660
atctttattc	ttcaggcagt	tctactgctt	gcctctcagg	aggcccgtta	caaggcattt	720
gggacatgtg	tctctcatat	aggtgccatc	ttagccttct	acacaactgt	ggtcactctt	780
tcagtcatgc	accgtgtagc	cgcctatgct	gcccctcatg	tcacatcctt	ccttgccaat	840
ttctatctgc	tcttcccacc	catggtcaat	cccataatct	atggtgtcaa	gaccaagcaa	900
atccgtgaga	gcattcttgg	agtattccca	agaaaggata	tg		942

<210> 589

<211> 936

<212> DNA

<213> Unknown (H38g438 nucleotide)

<220>

<223> Synthetic construct

<400> 589

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ggcctggagc	acctgcacat	ctggatctcc	atccctttct	cagcatatac	actggccctg	120
cttggaaact	gcaccttctt	tctcatcatc	caggctgatg	cagccctcca	tgagcccata	180
tacctcttcc	tgcccatgtt	ggcagccatc	gacctggctc	tttctctctc	agcattgccc	240
aaaatgcttg	ccatattctg	gttcagggat	cgggagatca	acttttttgc	ctgtctgggc	300
cagatgttct	tccttcactc	cttctccatc	atggagttag	cagtgtgtgt	ggccatggcc	360
tttgaccgct	atgtggccat	ctgcaagcca	ctgcactaca	ccacggctct	gactgggtcc	420
ctcatcacca	agattggcat	ggctgtctgt	gcccgggctg	tgacactaat	gactccactc	480
cccttctctg	tgagatgttt	ccactactgc	cgaggcccg	tgattgccc	ctgtactgtt	540
gaacacatgg	ctgtggtcag	gctggctgtg	ggaacactag	cttcaacaat	atctatggca	600
ttgctgtggc	catgtttatt	ggagtgttgg	atctattctt	tatcatccta	tcttatatct	660
ttatccttca	ggcagttcta	caactctcct	ctcaggaggc	ccgctacaaa	gcatttggga	720
catgtgtctc	tcacataggt	gccatcttag	ccttctacac	accttcagtc	atctcttcag	780
tcatgcaccg	tgtggcccg	tgtgctgcgc	cacacgtcca	cattctctct	gccaatttct	840
atctgtctct	cccacccatg	gtcaatccca	tcattctacg	cgtaagacc	aagcagatcc	900
gtgacagtct	tgaggagtatt	cccagagaa	gatgtg			936

<210> 590

<211> 955

<212> DNA

<213> Unknown (H38g439 nucleotide)

<220>

<223> Synthetic construct

<400> 590

atgacaaccc	acaactccac	tggtagcagc	cactcactct	tcattctgct	gagcattcct	60
ggcttagaag	accagcacac	atggatgtct	ctccccttct	ttatttcccta	ccttggttgc	120
ttccttgggg	acagcctcat	catcttcatc	atcatcactg	aatgcagcct	ccacgaaccc	180

atgtaccttt	tcctctgcat	gctggetgtg	gctgacctta	tcctgtctac	taccactgtg	240
cccaaggccc	tagccatatt	ttggttctat	gctggagcaa	tatcccttgg	tggctgtgtt	300
acccaaatct	tctttatcca	tgctaccttc	atcgaggaat	caggaattct	gttggcgatg	360
gcacttgacc	gctatgtggc	catctgtgat	ccactgcact	ataccacagt	gctcagtcgt	420
gcaaaaatca	caaagattgg	cttggetgtg	gtcctgagaa	gcttctgtgt	gatcatgccca	480
gatgtgtttc	tggtaaagcg	gctgcctttc	tgccatagca	atctgctgcc	acatacctac	540
tgtgagcaca	tggtctgtgc	caagtttgct	tgtgctgata	ttcatgtcaa	tgtttggtat	600
ggcttgtctg	tccttctcta	tactgtagtg	ctagatgcct	tgcttatctt	agtgtcctaa	660
agcttcaccc	tgtatacagg	cttcacacct	ccctcccaaa	ggagctcggc	aaaaggctct	720
gggcacatgt	ggctcccacc	tcagagtcac	ttccatgttc	tacttgcttg	gtattttttac	780
cataattacc	cagcggtttg	ggcaccatgt	tcctctccat	acacacattc	tgctgggtaa	840
tgtctgggtg	ttggctcctc	ccatgctgaa	ccccatcatt	tatgggatca	acaccaggca	900
gattcaagag	tgtgtgtctc	gtcttttgtc	ctcacagagg	aatgatgtct	agatt	955

<210> 591

<211> 939

<212> DNA

<213> Unknown (H38g440 nucleotide)

<220>

<223> Synthetic construct

<400> 591

atgaattggg	taaatgacag	catcatacag	gagttttatc	tgctggggtt	ctcagatcga	60
ccttggtctg	agtttccact	ccttgtggtc	ttcttgattt	cttacactgt	gaccatcttt	120
ggcaatctga	ccattattct	agtgtcacgc	ctggacacca	aacttcatac	ccccatgtat	180
ttttttctta	ccaatctatc	actcctggat	ctttgtttaca	ccacatgtac	agtcccacaa	240
atgctagtaa	atztatgcag	catcaggaaa	gtaatcagtt	atcgtggctg	tgtagcccag	300
cttttcatat	ttctggcctt	gggggctact	gaatatcttc	tcctggccgt	catgtccttt	360
gataggtttg	tagctatttg	tggcctctc	cattactcag	ttatcatgca	ccagagactc	420
tgctccagt	tggcagctgc	atcctgggtt	actggtttta	gtaactcagt	gtggttgtct	480
accctgactc	tccagctgcc	actctgtgac	ccctatgtga	tagatcactt	tctctgtgaa	540
gtccctgcac	tgctcaagtt	atcttgtgtt	gagacaacag	caaatgaggc	tgaactattc	600
cttgtcagtg	agctcttcca	tctaataccc	ctgacactca	tccttatatc	atatgctttt	660
attgtccgag	cagtattgag	gatacagtc	gctgaaggtc	gacaaaaagc	atttgggaca	720
tgtggttccc	atctaattgt	ggtgtctctt	ttttatagta	cagccgtctc	tgtgtacctg	780
caaccacctt	cgcccagctc	caaggaccaa	ggaaagatgg	tttctctctt	ctatggaatc	840
attgcaccca	tgctgaatcc	ccttatatat	acacttagga	acaaggaggt	aaagggaaggc	900
tttaaaaggt	tggttgcaag	agtcttctta	atcaagaaa			939

<210> 592

<211> 997

<212> DNA

<213> Unknown (H38g441 nucleotide)

<220>

<223> Synthetic construct

<400> 592

atggaaaaat	ccaatgtcag	ctcagtgat	ggttttatct	tggtggggtt	ctctgatcgt	60
cccaagctgg	agatgggtgt	ctttacagta	aattttatct	tgtattcagt	ggctgtgctg	120
ggaaattcaa	ccataatcct	tgtgtgtata	ttagactctc	aacttcatac	cccaatgtac	180
ttctttctgg	caaatctttc	ctttctagat	ctctgcttca	gtactagttg	catcccacaa	240
atgctggtaa	acctctgggg	ccctgacaag	actattagct	gtgctggctg	tgttgtccag	300
cttttctctt	tcctttctgt	caggggaatt	gagtgcaccc	ttctggctgt	catggcctat	360
gacagctatg	ctgcagctct	caaaccgttg	cgctatctgg	tcattatgca	cctccagctg	420
tgtctaggac	tgatggctgc	agcctggggg	agtggactgg	tcaatgccgt	tgcatgttca	480
ccactaacaa	tgaccctctc	cagaagtggc	cgccgcccag	ttaaccattt	cctctgtgaa	540
agccagcagt	gatcaagatg	gcttgtttgg	atgttctgtg	agtggaaatg	ctggcttttg	600
cttttgccgt	tctcattgtc	ctactgcccc	tcactcttat	tcttgtctcc	tacggcttca	660
ttgctgcagc	tgtgctaagc	atcaagtcag	ctgccaggca	atggaaggcc	ttccatacct	720

gtagctctca cctcacagt	gtctccctgt tttatgggag	catcatctat atgtatatgc	780
agccaggaaa cagttcttcc	caagaccaag gcaagtttct	cactctcttc tacaacctgg	840
tgactcctat gttgaatctg	ctcatctata ctttaaggaa	taaggagggtg aaaggagcac	900
tgaagaagggt tttggggagg	caataatgaa ctggagaaat	atgataagtt gtgaagtctt	960
aggcaaaata tctttttccaa	atacatttat tttgtgc		997

<210> 593

<211> 950

<212> DNA

<213> Unknown (H38g442 nucleotide)

<220>

<223> Synthetic construct

<400> 593

caagtagttc atacaggctt	ttctccctag ctatacgtct	tcaccctgct gggaaatggg	60
gcacccctggg gctcatctgg	ctggactcca gactgcacac	ccccatgtac ttctttctct	120
cacacccctggc catcattgat	atttcgtatg cttccaacaa	tgtccccaag atgctgacaa	180
accttggtctt gaacaagaga	aaaacaatct cctttgtccc	atgcacaatg cagacctttt	240
tatacatggc ttttgctcac	actgagtgtc tcatcttggg	aatgatgtcc tacgatcggg	300
acatggctgt ctgccacct	ctgcaatatt ctgtcatcat	gagatgggga gtgtgcacag	360
tcctggctgt cacttcttgg	gcatgtgggt ccttctggcc	ctgggtccatg tggttctcat	420
cctgaggctg cccttctgtg	ggccccatga aatcaaccac	ttcttctgtg aaatcctgtc	480
tgtcctcaag ttggcctgtg	ctgacacctg gctcaaccag	gtgggtcatct ttgcttcttc	540
agtgttcate ctggtggggg	cgctctgcct ggtgctgggc	tcctactcgc gcacccctggc	600
ggccatcctt aggaatcagt	ctggggaggg gcgcagaaag	ggcttctcca cctgctactc	660
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gtcccgccat cctgaggagc	agcagaaagt tctttccctg	ttttacagcc ttttcaatcc	780
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gtgcactgag gaaggagagg	ctgacgtgag acatctcaaa	gggaaccatg gggaggggagc	900
cttgcctcct gcaaaatata	gaagttggct ttttttttgg	tcttctgcta	950

<210> 594

<211> 711

<212> DNA

<213> Unknown (H38g443 nucleotide)

<220>

<223> Synthetic construct

<400> 594

cagatgctga cagattgggtg	gggacctaat aggaccacaa	gttacgtgaa ctcaccattc	60
aattccttgt ctctctgtag	ttatgtgcc aatatataatt	tctacaatta ttttataatt	120
atatgccatc ctttgtaata	tttgtaaatc atgaacctat	atctcctcct taatcttact	180
ttaatacttg agtgataatt	cattcatttt tgtcatcatg	tatactctca tcctaaaatt	240
cccaaggatg gaaaaaaaaa	aaccttcagg ataattccct	ccatgtgttg ctatgctatgc	300
tgaaaacagt ttttctagat	gctacaattg aagaaatgtc	tgtatttgtg ttaatacaat	360
gtaaatgtcc taatatgcct	tatcagtaat tttacctgct	atggctacat tgaggtgcac	420
taagaatgaa tactagtaat	taaattagaa gcaagctgag	aaatcagtat catcatcatc	480
atcatagggtg tcatttccatt	atagattcaa tcttctatgg	aatcattgtg taaatgctct	540
tgaagatggg aacaactcct	ccaagacca agaaatgatt	ctttatcttg ttttactacta	600
tactaactcc aagtctcaaa	cttctagttt atctgttaag	aataaagata taaaggatat	660
ttcaaggaga atactaagat	tggcagggaa tcttcaaaaa	tgaaaggaaa c	711

<210> 595

<211> 765

<212> DNA

<213> Unknown (H38g444 nucleotide)

<220>

<223> Synthetic construct

<400> 595

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cctaagatgg	catctgattt	tctgcatgga	aacaagtcta	tctccttcac	tgggtgtggg	120
attcatagtt	tcttcttcc	gacttttagcc	gttgtagaag	cgctactcct	gatatcaatg	180
gcctatgttc	gttgcatgac	tatttgcttt	cctctccact	atctcatgcg	catgagcaaa	240
agagtgtgtg	tctgatgat	aacaggatct	tggatcatag	gctcgatcaa	tgcttgtgct	300
cacactgtat	atatactcca	tattccttat	tgcccatcta	gggttatcaa	tcatttcttc	360
tgtgatgtcc	cagcaatggg	gactctggcc	tgcattggaca	cctgggtcta	tgagggcaca	420
gtgcttttga	gcgccaccat	ctttctcgtg	tttcccttca	ttgctatttc	atgttcctat	480
ggacgggttc	tccttgtctg	ctaccacatg	aaatctgcag	aagggaagaa	gaaggcctac	540
ctgacctgca	gcacccacct	cactgtagt	actttctact	atgcaccctt	tgcttacacc	600
tatctacgcc	caagatccct	gcgatctccg	acagaggaca	aggttctggc	tgtcttctac	660
accatcctca	ctccaatgct	caaccccatc	atctacagcc	tgagaaacaa	ggaggtgatg	720
ggggccctga	cacgagtgat	tcagaaaatc	ttttcagtga	aaata		765

<210> 596

<211> 960

<212> DNA

<213> Unknown (H38g445 nucleotide)

<220>

<223> Synthetic construct

<400> 596

ctgtcatgac	caaccagagc	tgcccagaaa	cagttcatct	tactgggttt	ctcaggcaga	60
cccaggctgg	agcatgtcct	ctttgtgttt	gtcctcatct	tctaccttgt	gaccttagtg	120
ggcaacatca	tcattatctt	gatctccac	ctggaccctt	gcctccacat	gcccattgtac	180
ttcttctcca	ctaacttgtc	tttctagat	ctctgcttca	ccaccagttc	tatccccag	240
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ctcttcatgt	tcctgggcct	gggtggcaag	agtgtattct	cttggcagcc	gtggcctatg	360
accgcttcat	tgcaatctgc	aagccccttc	actattctgt	cattatgcac	cctcagctgt	420
gctggaagtt	ggtgtctgtg	gcccgggggt	gttggactcc	tcagttctct	agttatgtct	480
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accttatcgg	tagtaattgt	cctgatgcct	ttgtgtctta	tcctcatctc	ttatagctac	660
attgccctag	cagtgtctgag	aatcaagtca	gccgcaggaa	gaaggaaggc	cttcaatatg	720
tgccgggtccc	acctcaccgt	ggtctccttg	ttttatggga	atattatcta	tatgtatatg	780
caaccatgaa	ataattcttc	tcaggaccaa	gggaagttcc	ttaccctttt	ctacaactta	840
atgaccccca	tgttaaaccc	tgatcatctat	acactgagaa	acaaggatgt	aaaagggtgca	900
ctgaagaggc	ttgtgtctag	aaaacacagt	gacagtgtact	gctcttgaga	ctgcttcttt	960

<210> 597

<211> 377

<212> DNA

<213> Unknown (H38g446 nucleotide)

<220>

<223> Synthetic construct

<400> 597

atggaaaatt	acaatcaaac	atcaactgct	ttcatcttgt	tgggattgtc	gccaccacca	60
aaaattggcc	atttcatctt	cattctcatt	aatttcggtt	tcctaattggc	tctaattgga	120
aacctatcca	tgattcttct	catcttcttg	gacatccatc	tcacacacc	catgtatttc	180
ctacttagtc	agctctccct	cattgacct	aattatattt	ccaccattgt	tcctaagatg	240
gtttatgatt	tttcatgtat	ggaaacaagt	ctatctcctt	cactgggtgt	gggattcaga	300
gtttcttctt	cctgacttta	gcagggtgcag	aagcgctgct	cctgacatca	atggcctatg	360
atcggtatgt	ggctatt					377

<210> 598

<211> 979

<212> DNA

<213> Unknown (H38g447 nucleotide)

<220>

<223> Synthetic construct

<400> 598

atggaaaagag	ctaacgacag	caccttctct	ggattcatcc	tcctgggctt	ctccaacagg	60
cctcagctgg	aaacagctct	ctttgtgggc	atcttgatca	tctactttct	gagctttctg	120
ggcaatggca	ccattatact	tttatccatt	gtagatcctc	gcctccatac	ccctatgtat	180
ttcttctct	ccaatctctc	ttttatggat	ctttgtttga	ccacttgtag	tgtccctcag	240
acactgggtca	actttaaggg	gaaggacaag	accatcacct	atgggtggctg	cgtgaccag	300
ctattcattg	ccttgggact	cgggggggag	ggagtgtgtc	ttattgtctg	ccatggccta	360
tgaccgctat	gcagccgtct	gccgccact	ccactacatg	gtgagcatgc	atccccaact	420
ttgcttgtag	ttggttgtaa	ccacttggct	cacagggttt	ggcaattctg	tgatacagac	480
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ggtgactcct	ctactgaatc	ccctaattta	cactctgagg	aacaaggaag	tcaaaggggc	900
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<210> 599

<211> 936

<212> DNA

<213> Unknown (H38g448 nucleotide)

<220>

<223> Synthetic construct

<400> 599

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aacctgtcca	tgattcttct	catcttcttg	gacacccatc	tccacacacc	catgtatttc	180
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cgttacattg	ctatttgctt	tcctctccac	tatctcatcc	gcatgagcaa	aagagtgtgt	420
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tatgtactcc	atattcctta	ttgccgatcc	agggccatca	atcatttctt	ctgtgatgtc	540
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agcaccacc	tcactgtagt	aactttctac	tatgcacctt	ttgtctacac	ttatctacgt	780
ccaagatccc	tgcgatctcc	aacagaggac	aaggttcttg	ctgtcttcta	caccatcctc	840
acccaatgc	tcaaccccat	catctatagc	ctgaggaaca	aggaggtgat	gggggccctg	900
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<210> 600

<211> 936

<212> DNA

<213> Unknown (H38g449 nucleotide)

<220>

<223> Synthetic construct

<400> 600

atgcccaatt	caaccaccgt	gatggaattt	ctctcatga	ggttttctga	tgtgtggaca	60
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<210> 601

<211> 931

<212> DNA

<213> Unknown (H38g450 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(931)

<223> n = A,T,C or G

<400> 601

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cctgcaatct ccaacagagg acaaggttct ggctgtgttc tacaccatcc tcacctcaat 840
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<210> 602

<211> 577

<212> DNA

<213> Unknown (H38g451 nucleotide)

<220>

<223> Synthetic construct

<400> 602

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agacacacag agccacggaa tctcacaggt gtctgagaat tcctcctcct gggactctca 60
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tatctgggtc tggttctgag gaacctgctc agcatcctgg ctgtcagctc tgactccccc 180
ctccataccc ccatgtactt cttcctctcc aacctgtgct gggctgacat cgggttcaat 240
tcggccacgg ttcccaaggt gactgtggac atgcagtcgc atagcagagt catctctcat 300
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cctgactgtg atggcctatg acggctttgt agccatctgt ctcctctctgc actaccaggt	420
catcatgaat cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt	480
ggattcccag ctgcacgggt ggattgtgtg acaattcacc atcatgaaga atgtggaaat	540
ctctcatttt gtaagtgaacc cctctcaact tctcaac	577

<210> 603

<211> 952

<212> DNA

<213> Unknown (H38g452 nucleotide)

<220>

<223> Synthetic construct

<400> 603

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acgctgtgtc ctgttgggtg ctgtgtcatg ggtgatcact attttacatg ccctagtga	480
tacctccta gtgaccaggc tttccttctg tgggtccaaat attatccctc acttcttctg	540
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ttacattgca ttggccatcc tgagaattga ttccccaagg ggtaagcaaa gggccttctc	720
cagctgcact tcccacctct ctgtagtctc tctgttctat agcacagcta tcggtgtcta	780
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ggtggtgact cccatgttga accccttcat ctacagcctg aggaacaggg atatgaaggg	900
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<210> 604

<211> 754

<212> DNA

<213> Unknown (H38g453 nucleotide)

<220>

<223> Synthetic construct

<400> 604

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catttgagaa gaaacgcagc tttttctatt gagttcttat gctataagta aaggatgcaa	180
gacattaatt agacaaaata aggtaaaatt ttgtattcgc ttagagagtt taagaggcta	240
ttagccacta gtctctatag tgcctaagta aatcgattct gcttaataaa ctgctacctg	300
gcttagtaag taaacaaatt gaaacttatt ttaggaaaga aatatatatt cttatatcta	360
catcagattc tcttatgtag aaacactaga ggggtgaatga ggagttaatg taagcagcat	420
catatttttg ctcattectt tctctatgat ttctgtctt tctgtccaaa ttctgtgagg	480
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catgattgca gttgtaacat actgggactc attcattttc acatatgtat atgagactta	600
aatcatccac atttcaggcc aggttaagtt tctagaaata ttctatgctt tccttgact	660
tacactcaat cctgtcgtct acagcgttgg cactgacagt gttctggtgg caatgaaaaa	720
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<210> 605

<211> 939

<212> DNA

<213> Unknown (H38g454 nucleotide)

<220>

<223> Synthetic construct

<400> 605

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cgagagctgg	agtttttctt	gtttgtgggc	ttctttgtctg	tgtatgtagc	aacagtccctg	120
ggaaatgcac	tcatttgtgt	cactattacc	tgtgagtccc	gcctacacac	tcctatgtac	180
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ttcctgggtg	atctttttatc	agacaggaaa	accatctcct	acaatgactg	catggcacag	300
atctttttct	tcacttttgc	tggtggggca	gatatttttt	tcctctctgt	gatggcctat	360
gacagatacc	ttgcaatcgc	caagcccctg	cactatgtga	ccatgatgag	gaaagagggtg	420
tgggtggcct	tggtgggtgc	ttcttgggtg	agtgggtggt	tgcattcaat	catccaggta	480
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atgctgaacc	ccatcatcta	ttccctgaga	aatcaagaga	tgaagtcagc	catgcagagg	900
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<210> 606

<211> 927

<212> DNA

<213> Unknown (H38g455 nucleotide)

<220>

<223> Synthetic construct

<400> 606

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acaggaacc	tgctcatcat	cctggccatt	cgcttcaacc	cccattctca	gacccctatg	180
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cagatgtatt	ttctctatgc	cttggggcaac	agtgcagact	gccttctggc	agtcatggcc	360
tttgaccgt	atgtggccgt	ctgtgacct	ttccactatg	tcaccaccat	gagccaccac	420
cactgtgtcc	tgctgggtgc	cttctcctgc	tcatttcctc	acctccactc	actcctgcac	480
acacttctgc	tgaatcgtct	caccttctgt	gactccaatg	ttatccacca	ctttctctgt	540
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ttacagcccc	catccacctc	cgctgtcaag	gaccacgtgg	caacaattgt	ttacacagtt	840
ttgtcatcca	tgctcaatcc	ttttatctac	agcctgagaa	acaaagacct	gaaacagggc	900
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<210> 607

<211> 939

<212> DNA

<213> Unknown (H38g456 nucleotide)

<220>

<223> Synthetic construct

<400> 607

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ccttcaaatt	caccatctgt	tattgacagg	ctgctttctg	tgatctacac	tgtgatgcct	840
ccagtattta	accctgtaac	ctacagcctg	cggaacaatg	acatgaaatg	tgctctgata	900
aggttgctgc	agaaaacata	tggtcaggag	gcttacttc			939

<210> 608

<211> 972

<212> DNA

<213> Unknown (H38g457 nucleotide)

<220>

<223> Synthetic construct

<400> 608

atggctgtag	gaaggaacaa	cacaattgtg	acaaaattca	ttctcctggg	actttcagac	60
catcctcaaa	tgaagatttt	ccttttcatg	ttatttctgg	ggctctacct	cctgacgttg	120
gcctggaact	taagcctcat	tgccctcatt	aagatggact	ctcacctgca	catgccccatg	180
tacttcttcc	tcagtaacct	gtccttccctg	gacatctgct	atgtgtcctc	caccgcccct	240
aagatgctgt	ctgacatcat	cacagagcag	aaaaccattt	cctttgttgg	ctgtgccact	300
cagtactttg	tcttctgtgg	gatggggctg	actgaatgct	ttctcctggc	agctatggcc	360
tatgaccggt	atgctgcaat	ctgcaacccc	ttgctttaca	cagtccctcat	atcccataca	420
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gccatgagga	aagccatgga	aagggacccc	gggatttctc	acggtggacc	attcattttt	960
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<210> 609

<211> 942

<212> DNA

<213> Unknown (H38g458 nucleotide)

<220>

<223> Synthetic construct

<400> 609

atgaccaatc	agacacagat	gatggaattc	ttgcttgtga	gatttactga	gaattgggtg	60
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ttagtcatca	ttctcctcat	gattctggac	catcgtctcc	acatggcaat	gtactttttc	180
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ccaaccttga	accctgttat	ctactgtctg	aagaacaagg	acattaaatc	cgctctgagt	900

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942

<210> 610

<211> 921

<212> DNA

<213> Unknown (H38g459 nucleotide)

<220>

<223> Synthetic construct

<400> 610

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ctcatcatca	ttgccaaaat	ctataacaac	accttgcata	cgcccatgta	tgttttctct	180
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accatgctaa	catcagaaaa	taccatttca	tatgcaggct	gcattgtcca	gctcttcttg	300
ttcacatggg	ctctggggag	tgagatgggt	ctcttcacca	ccatggccta	tgaccgctat	360
gtggccattt	gtttccctct	tcattacagt	actgttatga	accaccatat	gtgtgtagcc	420
ttgtcagca	tggatcatgg	tattgcagtc	accaatttct	gggtgcacac	agctcttctc	480
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acattaaacc	cgatgggtga	cagcttccag	aatagggaga	tgcaggcagg	aattaggaag	900
gtgtttgcac	ttctgaaaca	c				921

<210> 611

<211> 810

<212> DNA

<213> Unknown (H38g460 nucleotide)

<220>

<223> Synthetic construct

<400> 611

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gaaaaagagc	tgcagctcat	cctctttcca	gtcttcctgg	tgatctacct	tgtgaccctg	120
atttggaaca	tgggtcttat	catcctcctc	agaatagact	ctcatctgaa	cacacccatg	180
tacttttttc	tcagtttctt	ctcatttaca	gacatctgct	attcttctac	catcagccca	240
aggatgcttt	cagacttctt	aaaagataag	aagacaattt	ccttccttgc	ctgtgccact	300
cagtattttc	ttggggcctg	gatgagctct	gctgagtgct	gcctcttggt	catcatggcc	360
tgtgacagat	atgtggccat	tggcagcccc	ctgcagtact	cagcaatcat	ggtccctagt	420
atctgttggg	agatggtagc	tggagtctgt	gggggtggat	tccttagtag	cttagttcat	480
acagtccctt	gctttaatct	ctactactgt	gggccaaata	tcattcaaca	tttcttctgt	540
aacacacttc	agattatttc	cttgtcttgc	tccaaccctt	ttatcagcca	aatgattctt	600
tttctggaag	ctatttttgt	tgggttgggc	tctttgcttg	ttatcctttt	gtcttatggg	660
ttcattgtag	cttcataact	gaaaatatca	tcaaccaa	gttggtgcaa	ggccttcaat	720
acctgtgect	cccacctggc	agctgtggct	ctcttctatg	gcacagccct	ttctgtgtac	780
atgcattccta	gctctagcca	ctccatgaag				810

<210> 612

<211> 988

<212> DNA

<213> Unknown (H38g461 nucleotide)

<220>

<223> Synthetic construct

<400> 612

tactccaaag	aaattataga	ataatgtact	tccaatgata	ttataaaatg	tggttagcat	60
aataagatta	ctttttttac	tgttttatcct	tttagagttc	acagaagatt	tggtgttaca	120
gcaagtgtc	tttttcatct	ttctcatcat	ttatgtcatc	agcctctcag	gcaacatcat	180
tctgaattct	ctcatctgtg	ctgattcttg	gccctacaca	cccatgtatt	tcttacttgg	240
aaaccgggtc	cttctggatc	tctgggtattc	ctctgtccac	atccccgata	tccctgtgac	300
ttgcatttct	gatgacaaaa	ccatctcctt	tccctggctgc	cttgctcagt	tcttctctgc	360
tgtgttggtc	taaaatgagt	gctatatgat	ggcttccatg	gcttatgacc	gctacatggc	420
aatctccaag	cccctgcttt	attccccggc	cacattccca	gagttatgtg	ccagtcttgt	480
tgaggcttca	caccttggcg	gctttgtaaa	ctcaaccatc	atcaccagtg	agacacctac	540
cttgagcttc	tgtggcagca	atatcattga	tgatttcttc	tgtgatctgc	ccccacttgt	600
aaagtgggtg	tgtgatgtga	aggagcgcta	ccaggctgtg	ctgcatttta	tgcttgccctc	660
caatcatcac	tcccactgca	cttattcttg	cgtccatctc	ttcatcattg	cagccatctc	720
gaagatccgt	tccattaaag	gccgcctcca	ggtcttctcc	acttgtgggt	ctccccgtac	780
ggctctcacc	ttgtactatg	gtgcaatctt	ctttattttac	tcccaaccaa	gaactagcta	840
tgcccttaaaa	atggataaat	tggggtcagt	gttctatact	gtgggtgatc	caatgctaaa	900
ccccttgatc	tatagcttaa	gaaataagga	tgtcaaagat	gccttgaaga	aaatgttaga	960
tagacttcag	tttcttaaag	aaaaatat				988

<210> 613

<211> 1049

<212> DNA

<213> Unknown (H38g462 nucleotide)

<220>

<223> Synthetic construct

<400> 613

atggagcaga	gcaattattc	cgtgtatgcc	gactttatcc	ttctgggttt	gttcagcaac	60
gcccgtttcc	cctgggttct	ttgccctcat	tctcctggtc	tttgtgacct	ccatagccag	120
caacgtggtc	aagatcattc	tcattccacat	agactcccgc	ctccacaccc	ccatgtactt	180
cctgtctcagc	cagctctccc	tcaggggacat	cttggtatatt	tccaccattg	tgcccaaaat	240
gctgggtcgac	caggtgatga	gccagagagc	catttccctt	gcaggatgca	ctgccccaca	300
cttctctctac	ttgaccttag	cagggggctga	gttcttctct	ctaggactca	tgtcctgtga	360
tcgtacgta	gccatctgca	acctctctga	ctatcctgac	ctcatgagcc	gcaagatctg	420
ctgggttgatt	tggcgggcag	cctggctggg	agggctctac	aatgggttct	tgctcacccc	480
cgtcaccacg	cagttccctt	tctgtgcctc	tggggagatc	aaccacttct	tctgcgaggt	540
gcctgccctt	ctgaagctct	cctgcacgga	cacatcagcc	tatgagacag	ccatgtatgt	600
ctgctgtatt	atgatgtctc	tcattccctt	ctctgtgatc	tggggctctt	acacaagaat	660
tctcattact	gtttatagga	tgagcgaggc	agaggggagg	cgaaaggctg	tggccacctg	720
ctcctcacac	atgggtggtg	tcagcctctt	ctatggggct	gccatgtaca	catacgtgct	780
gcctcattct	taccacaccc	ctgagcagga	caaagctgta	tctgccttct	acaccactct	840
cactcccatg	ctcaatccac	tcattttagc	cttaggtgaac	aaggatgtca	cggggggcct	900
acagaagggt	gttggggaggt	gtgtgtcctc	aggaaaggta	accactttct	aaacaaattg	960
catatgtctg	tagagacttg	aaatgaagga	tacaagactt	tatcattgcc	cttgagttta	1020
aatattctct	gcctggaaac	aagtgacct				1049

<210> 614

<211> 957

<212> DNA

<213> Unknown (H38g463 nucleotide)

<220>

<223> Synthetic construct

<400> 614

atgggtgttc	acaatttggt	cacggtgact	cagtttatcc	ttatagggtc	ctcttacttc	60
tccaatgagc	actaccttct	ttttgtggcc	cttgccatta	tctgtcaggt	gttcttgggtg	120
cgaagtggag	acattctctt	ggccattggg	actgtgatta	agttgcacac	tactcatgta	180
ttattttttg	gcaaattgtg	ccatcttaga	catattgtgt	tcattcagcta	ctatacctaa	240
gatgcctaag	attctctaga	ctgaggatca	cagcatttct	tttgtttaggt	gagctttgca	300
gccctatttc	ctagtggcct	gggctgggaa	gaaagcttct	tactgtttac	ggcttatgac	360

tggtgtgtgg	tcacatgttt	ctccctttgt	tacatcctga	tcataaaca	attggctctg	420
tccagctggg	ttatgggacc	tgagcagctg	ggtttctaaa	tttctctctc	ctccacgtag	480
tgtctaccct	ctgcctgtct	ttctgcaagc	ctgatcgagt	taaccagtat	tactgtgata	540
tctcaccgat	gggggccctg	ttgtgccagt	ccatgcacct	ggcaaacaatg	cttgttttag	600
tggaatcagt	tatcttgggg	atcagtgtct	ttctggctgc	ctttaacttt	tacatatata	660
tcactctccac	tatcctaaag	atccagtgtg	tagagtggag	tgcaaagtgc	ttctctacat	720
gcacttccca	cctccttacg	gtctgtttgt	tctatggcat	attgacattt	acctacattt	780
actcctttctc	cagtcaacac	tcacatgtct	aaggcaagcc	cagatctagc	cacagacagg	840
ctcatctcta	tgctatacag	agttattacc	ctgatgttta	acttcatcac	tgacaacctg	900
agaaacacag	aggtaaaagg	agcctcagaa	aggttttatg	tcattgaaca	tgttttat	957

<210> 615

<211> 840

<212> DNA

<213> Unknown (H38g464 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(840)

<223> n = A,T,C or G

<400> 615

atgtacctga	ccacgggtgct	ggggaacctg	ctcatcatgc	tgctcatcca	gctggactct	60
caccttcaca	ccccatgta	cttcttctc	agccacttgg	ctctcactta	tttttctttt	120
tcactgttca	ctgtccctaa	gatgctgatg	gacatgcgga	ctaagtacaa	atcgatcctc	180
tatgaggaat	gcattttctca	gatgtatttt	tttatatttt	ttactgacct	ggacagcttc	240
cttattacat	caatggcata	tgaccgatat	gttgccatat	gtcaccctct	ccactacact	300
gtcatcatga	gggaagagct	ctgtgtcttc	ttagtggtctg	tatcttggat	tctgtcttgt	360
gccagctccc	tctctcacac	ccttctcctg	acccgggtgt	ctttctgtgc	tgcgaaacacc	420
atcccccatg	tcttctgtga	ccttgctgcc	ctgctcaagc	tgctctgctc	agatatcttc	480
ctcaatgagc	tggatcatgtt	cacagtaggg	gtggtgggtca	ttaccctgcc	attcatgtgt	540
atcctgggtat	catatggcta	cattggggcc	accatcctga	gggtcccttc	aaccaaaggg	600
atccacaaaag	cattgtccac	atgtggctcc	catctctctg	tgggtgtctct	ctattatggg	660
tcaatatttg	gccagtacct	tttcccgact	gtaagcagtt	ctattgacaa	ggatgtcatt	720
gtggctctca	tgtacacggg	ggtcacaccc	atgttgaaac	cctttatcta	cngcattngg	780
aacaggggaca	tgaaagaggc	ccttgggaaa	ctcttcagta	gagcaacatt	tttctcttgg	840

<210> 616

<211> 909

<212> DNA

<213> Unknown (H38g465 nucleotide)

<220>

<223> Synthetic construct

<400> 616

atgaattcat	caagtgactg	aagacaacca	gtgatggacg	gggtgaatga	tagctccttg	60
cagggttttg	ttctgatggg	catatcagac	catccccagc	tggagatgat	cttttttata	120
gccatcctct	tctctatttt	gctgacccta	cttgggaaact	caaccatcat	cttgctttcc	180
cgcctggagg	cccgggtcca	tacacccatg	tacttcttcc	tcagcaacct	ctcctccttg	240
gaccttgctt	tcgctactag	ttcagtcccc	caaagtctga	tcaatttatg	gggaccaggc	300
aagaccatca	gctatgggtg	ctgcataacc	cagctctatg	tcttcccttg	gctggggggc	360
accgagtga	tctgtctggg	ggtgatggca	tttgaccgct	acgtggcagt	gtgccggccc	420
ctccgctaca	cgcctatcat	gaacccccag	ctctgctggc	tgctggctgt	gattgcctgc	480
ctgggtggct	tgggcaactc	tgtgatccag	tcaacattca	ctctgcagct	cccattgtgt	540
gggcaccgga	gggtggaggg	attcctctgc	gagggtgctg	ccatgatcaa	actggcctgt	600
ggcgacacaa	gtctgaacca	ggctgtgctc	aatggtgtct	gcaccttctt	cactgcagtc	660
ccactaagca	tcctcgtgat	ctcctactgc	ctcattgctc	aggcagtgct	gaaaatccgc	720
tctgcagagg	ggaggcgaaa	ggcgttcaat	acgtgcctct	cccatctgct	ggtgggtgtc	780

ctctttctatg gctcagccag ctatgggtat ctgcttccgg ccaagaacag caaacaggac	840
cagggcaagt tcatttccct gttctactcg ttggtcacac ccatggtgaa tccccctc	900
tacacgctg	903

<210> 617

<211> 926

<212> DNA

<213> Unknown (H38g466 nucleotide)

<220>

<223> Synthetic construct

<400> 617

atgcagagga gcaatcacac agtgactgag ttcattcctgc tgggcttcac cacagatcca	60
gggatgcaac tgggcctctt tgggtgttc ctgggtgtgt actgtctgac tgggtagga	120
agtagcacc tcactgtgt gatctgtaaat gactccacc tacacacacc catgtatttt	180
gtcattggaa atctgtcatt tctggatctc tgggtattctt ctgtctacac ccaaagatc	240
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ttctctgcca ggcctggccta tagtgagtgc tacctactgg ctgccatggc ttatgaccac	360
tacgtggcca tctccaagcc cctgctttat gctcagacca tgccaaggag attgtgcatc	420
tgtttgggtt tatattccta tactgggggt tttgtcaatg caataatatt aaccagcaac	480
acattcacat tggatttttg tggtgacaat gtcattgatg actttttctg tgatgtccca	540
cccctcgtga agctggcatg cagtgtgaga gctaccaggc tgtgctgcac ttccttctgg	600
cctccaatgt catctccctt actgtgctca tcttgcctc ttacctctcc atcatcacca	660
ccatcctgag gatccactct acccagggcc gcatcaaagt cttctccaca tgctcctccc	720
acctgatctc cgttacctta tactatggct ccattctcta caactactcc cggccaagtt	780
ccagctactc cctcaagagg gacaaaatgg tttctacctt ttatactatg ctgttcccca	840
tgttgaatcc catgatctac agtctgagga ataaagacat gaaagacgct ctgaaaaaat	900
tcttcaagtc agcataatcc aaagtc	926

<210> 618

<211> 936

<212> DNA

<213> Unknown (H38g467 nucleotide)

<220>

<223> Synthetic construct

<400> 618

atggacgggg tgaatgatag ctcttgcag ggctttgttc tgatgagcat atcggaacat	60
ccccagctgg agatgatctt ttttatagcc atcctcttct cctatttgct gaccctactt	120
gggaactcaa ccatcatctt gctttccgc ctggaggccc ggctccatac acccatgtac	180
ttcttctca gcaacctctc ctcttggac ctgtcttctg ctactagtgc agtccccaa	240
atgctgatca atttatgggg accaggcaag accatcagct atgggtggctg cataaccag	300
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gaccgctacg tggcagtgtg ccggccctc cgctacaccg ccatcatgaa cccccagctc	420
tgctggctgc tggctgtgat tgcctggtg ggtggcttgg gcaactctgt gatccagtca	480
acattcactc tgcagctccc attgtgtggg caccggaggg tggagggatt cctctgcgag	540
gtgcctgcca tgatcaaact ggctgtggc gacacgagtc tcaaccaggc tgtgtcaat	600
ggtgtctgca ccttcttcac tgcagtccca ctaagcatca tctgtatctc ctactgcctc	660
attgctcagg cagtgtgaa aatccactct gcagagggga ggcgaaaggc gttcaatacg	720
tgcctctccc atctgtcgtt ggtgttcctc ttctatggct cagccagcta tgggtatctg	780
cttccggcca agaacagcaa acaggaccag ggcaagttca tttccctgtt ctactcgttg	840
gtcacacca tggatgaatc cctcatctac acgtgcgga acatggaagt gaagggcgca	900
ctgaggaggt tgctggggaa aggaagagaa gttggc	936

<210> 619

<211> 247

<212> DNA

<213> Unknown (H38g468 nucleotide)

<220>

<223> Synthetic construct

<400> 619

ggtgagagggc	ttaagaact	caacacatgt	gtgtcacata	tctatgcagt	gctgatcttc	60
tatgtgcta	tggtagtgt	gtccatgggt	catcgatttg	ggaggcatgc	tcctgaatat	120
gtgcacaagt	catgtctct	ttgtacctcc	aatgctctac	ccaattatct	attccatcaa	180
gactaaggag	attcgagga	gactacacaa	gatgttattg	ggagctaagt	tctgatcaag	240
gaaaact						247

<210> 620

<211> 936

<212> DNA

<213> Unknown (H38g469 nucleotide)

<220>

<223> Synthetic construct

<400> 620

atggaagtgg	gaaattgcac	catcctgact	gaattcatct	tgttggggtt	ctcagcagat	60
tcccagtggc	agccgattct	atgttgagtg	tttctgatgc	tctatttgat	aaccttggtca	120
ggaacatga	ccttggttat	cttaatccga	actgattccc	acttgcatac	acctatgtac	180
tttttcattg	gcaatctgtc	ttttttggat	ttctgggtata	cctctgtgta	tacccccaaa	240
atcctggcca	gttgtgtctc	agaagataag	cgcatttcct	tggctggatg	tggggctcag	300
ctgttttttt	cctgtgttgt	agcctacact	gaatgctatc	tcctggcagc	catggcatat	360
gaccgcatg	cagcaatttg	taaccatttg	ctttattcag	gtaccatgtc	caccgcccctc	420
tgtactgggc	ttgttgctgg	ctcctacata	ggaggatttt	tgaatgcat	agcccatact	480
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gcaccaccat	tggtaaaaat	gtcctgtaca	aacaccagg	tctacgaaaa	agtccctgctt	600
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aggcctagtt	ccacctactc	cctagagagg	gacaaagtag	ctgctctggt	ctacaccgtg	840
atcaaccac	tgctcaaccc	tctcatctat	agcctgagaa	acaaagatat	caaagaggcc	900
ttcaggaaa	caacacagac	tatacaacca	caaaca			936

<210> 621

<211> 954

<212> DNA

<213> Unknown (H38g470 nucleotide)

<220>

<223> Synthetic construct

<400> 621

atgcctactg	taaaccacag	tggcactagc	cacacagtct	tccacttgct	gggcattccct	60
ggcctacagg	accagcacat	gtggatttct	atcccatctc	tcatttctta	tgtcaccgcc	120
cttcttggga	acagcctgct	catcttcatt	atcctcacia	agcgcagcct	ccatgaaccc	180
atgtacctct	tcctctgcat	gctggctgga	gcagacattg	tcctctccac	gtgcaccatt	240
cctcaggcct	tagctatctt	ctggttccgt	gctggggaca	tctccctgga	tcgttgcatc	300
actcagctct	tcttcataca	ttccaccttc	atctctgagt	cagggatctt	gctgggtgatg	360
gcctttgacc	actatattgc	catatgctac	ccactgaggt	acaccaccat	tcttacaaat	420
gctctgatca	agaaaaattg	tgtgactgtc	tctctgagaa	gttatggtag	aattttccct	480
atcatatttc	ttttaaaaag	attgactttc	tgccagaata	atattattcc	acacaccttt	540
tgtgaacaca	ttggcctagc	caaatatgca	tgtaatgaca	ttcgaataaa	catttggtat	600
gggttttcca	ttctaattgc	gacggtgggc	ttagatgttg	tactaatttt	tatttcctat	660
atgctgatcc	tccatgctgt	cttccacatg	ccttctccag	atgcttgcca	caaagctctc	720
aacacatttg	gctcccattg	ctgcatcctc	atcctctttt	atgggtctgg	catcttcaca	780
atccttacc	agaggtttgg	acgccacatt	ccaccttgta	tccacatccc	gttggctaatt	840
gtctgcattc	tggtccacc	tatgctgaat	ccattatttt	atgggatcaa	aaccaagcaa	900
atccaggaac	aggtggttca	gtttttgttt	ataaaacaga	aaataacttt	ggtt	954

<210> 622
 <211> 942
 <212> DNA
 <213> Unknown (H38g471 nucleotide)

<220>
 <223> Synthetic construct

<400> 622
 atggaggctg ccaatgagtc ttcagagggga atctcattcg ttttattggg actgacaaca 60
 agtcctggac agcagcggcc tctctttgtg ctgttcttgc tcttgatatgt ggccagcctc 120
 ctgggtaatg gactcattgt ggctgccatc caggccagtc cagcccttca tgcacccatg 180
 tacttctctg tggcccacct gtcttttgtc gacctctgtt tcgctccgt cactgtgccc 240
 aagatgttgg ccaacttggt ggcccatgac cactccatct cgctggctgg ctgcctgacc 300
 caaatgtact tcttctttgc cctgggggta actgatagct gtcttctggc ggccatggcc 360
 tatgactgct acgtggccat ccggcacccc ctcccctatg ccacgaggat gtcccggggc 420
 atgtgcgcag ccttggtggg aatggcatgg ctggtgtccc acgtccactc cctcctgtat 480
 atcctgctca tggctcgctt gtcttctgtt gcttcccacc aagtgcacca cttcttctgt 540
 gaccaccagc ctctcttaag gctctctgtc tctgacaccc accacatcca gctgctcatc 600
 ttcaccgagg gcgcgcagc ggtggtcact ccttctctgc tcatcctcgc ctctatggg 660
 gccatcgag ctgacctgct ccagctgccc tcagcctctg ggaggctccg ggctgtgtcc 720
 acctgtggct cccacctggc tgtggtgagc ctcttctatg ggacagtcac tgcagtctac 780
 ttccaggcca catcccgagc cgaggcagag tggggccgtg tggccactgt catgtacact 840
 gtagtcaccc ccattgctgaa ccccatcacc tacagcctct ggaatcgaga tgtacagggg 900
 gcactccgag ccttctcat tgggcgaagg atctcagcta gt 942

<210> 623
 <211> 946
 <212> DNA
 <213> Unknown (H38g472 nucleotide)

<220>
 <223> Synthetic construct

<400> 623
 atctctatgt tctcctgcaa caccagcact tctggtcagt ctaccttct cctcactggg 60
 tttccaggcc tgggaagcctc tcatcattgg gtttccatcc ccatcaacct cttctgtgtg 120
 gtttccatcc tgggtaataa tatcatctc ttccctgatcc acacagatcc agccttacat 180
 gaacctatgt atatcttct gtccatgttg gcagcctctg atctgggct ctgtgcctct 240
 accttcccca ctatggtgag tctcttctgg ctgggagctc gtgagctgcc ctttgatctc 300
 tgtgcagcac agatgttctt catccatacc ttcacctatg tggagtccgg tgtactgctg 360
 gccatggcct tcgatcgctt tattgccatc cgggaccctc tgcattatgc cataatcatt 420
 acctgtcag tcacagccga ggtgggaact gccattctgg tgagggtgt tctgtctaac 480
 ctcccgggac ctatctctct gcagcagctg ctctttccca agatcagcgc tctctgtcac 540
 tgctactgcc tgcactgtga ccttgtgggg ttggcctgct cagacacca gatcaatagc 600
 ctggttggcc tggtttccat cctcttctca ctgtgccttg actccttct catcatgctt 660
 tcatatgccc tgatectatg aactgtgctg ggcattgcat caactgggga gcggtcaag 720
 gcactcaaca cgtgtgtctc acacctctgc attgttctca tcttttattt gcccaaagg 780
 gctgtctgtc ttgcaccgag taaagaagca tgactaccct gctctggcag tgcctatggc 840
 caacctacac ttcttggctc cacccttcat gaacccatt gtgtattgca tcaagtctag 900
 gcagatccgt cagagcctcc taaagcactt ccagcagaag aggatt 946

<210> 624
 <211> 960
 <212> DNA
 <213> Unknown (H38g473 nucleotide)

<220>
 <223> Synthetic construct

<400> 624

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gatccagaac	tgcagcccgt	cctcgctggg	ttgtcccggg	ccatgtatct	ggatcatggtg	120
ctgaggaacc	tgtcatcat	cctgggtgtc	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcacctcggc	catgggtccc	240
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aaaattgtcc	cctctattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	accccccagg	agtgggtgtg	tggcgtcagt	gatgtacgct	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tatagcctga	gaaacagaga	cattcaaagc	900
gccctctgga	ggctgcgcag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

<210> 625

<211> 985

<212> DNA

<213> Unknown (H38g474 nucleotide)

<220>

<223> Synthetic construct

<400> 625

atgaaactca	taaaccatac	catcagaacc	caacctcctt	tctgctcatg	ggaattccag	60
gcccgaggc	atcccacttt	tggattgctt	ttcccttctg	ctccatgtat	gccctggcag	120
tgctgggaaa	catgggtggtg	ctgctagtgg	tacattcaga	gcctgtattg	caccagccca	180
tgtacctgtt	cctctgcatg	ctatccacca	ttgacctggg	cctctgcacc	tccactgtgc	240
ccaagctcct	tgcacttttt	tgggcaaagg	atgctgagat	caactttggg	gcctgtgctg	300
cccagatggt	ctttatccat	ggcttctcag	ctgtagaatc	tgggtatactg	ctagcaatgg	360
cctttgaccg	ctacttagcc	atttgctggc	ctctgcacta	tgggtcattg	ctctccccag	420
agtctgtagg	caagctgggg	gctgcagcgt	gcttcgtggg	ttgggactca	tgacccact	480
cacctgtctt	ctggcaagac	tgagctactg	cagtcagatg	gtggccact	cctactgtga	540
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cactgctgcc	acactgggtg	tgggcaactga	ctccatctgt	attgctgtct	cctatgcact	660
catcctccga	gctgtgttag	gtctttcttc	caaggaggca	agggctaaga	cctttggcac	720
ttgtggctcc	cacctgggtg	tcatacttct	cttctacaca	ccaggactct	tctccttcta	780
cacacagcgg	tttggccagc	acgtgccccg	gcacatccac	atccttctag	ctgacctcta	840
cctggttgtg	ccacccatgc	tcaaccccat	catctatggc	atgaagacca	acagatctg	900
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<210> 626

<211> 989

<212> DNA

<213> Unknown (H38g475 nucleotide)

<220>

<223> Synthetic construct

<400> 626

cacacagagc	cacggcatct	cacaggtgtg	tgagaattcc	tcctcgtggg	actctcagag	60
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ataaggaacg	tgtcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tttttttctt	ctccaacgtg	tgggtgggctg	acatcagttt	cacgtcggcc	ggggttccca	240
agatgacctg	ggacatgcag	tcgcatagca	gagtcactta	ttatgcgggc	tgcatagtc	300
ggatgtcttt	tttgcctctt	ttagcatgta	tagaagacat	gctcgtgtgt	gtgatggcat	360
aggagtgtct	tgtagccatg	tgtcgccctg	tgcaatacac	agttattgta	aatcctcac	420

tgtgtgtttt	cagagttggg	gtgtcctttc	tccagagcgt	gttgatttcc	caggtgcaca	480
gatagagtgt	gtcacaattc	acttttttca	agaatgtgga	aatctctcat	tttgtgtgtg	540
agccatctca	atttctccac	tttgcggtgt	gtgacagttt	catcaagagc	atattcatgt	600
atttcgatag	taatatgttt	ggttttcttc	ccatcacagg	gatctttttg	tcttaataata	660
aaagtgtccc	ctccattata	aggatttcat	cgtcagatgg	aaagtataaa	gctttctcca	720
cgtgtggctc	tcacgtggca	gttggtttgt	tattatatgg	aacaggcatt	gggggtgtaca	780
tgacttcagg	tgtggcacca	ccccccagca	atgggtgtgg	ggcatcagtg	aagtacgcgg	840
tggtcacccc	catgctgacc	cctttctatc	acagcgtgag	aaacagggac	attcaaagcc	900
ccctgtggag	tgtgtgcagc	agcacagtta	aatcttttga	tgtgtcccat	cttttttgtg	960
tgtgggtaag	aaagggcacc	cacattaaa				989

<210> 627

<211> 512

<212> DNA

<213> Unknown (H38g476 nucleotide)

<220>

<223> Synthetic construct

<400> 627

cacacacagc	cacggggtct	cacacgtgtg	tgagaattcc	tcctcctggg	actctcacag	60
gatccacaac	tgcagctgtg	ctctctgggc	tgtccctgtg	catgtgtctg	ggcacacagc	120
tggggaacct	gctgcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tactcttttc	tctccaacct	gtgctggggc	tgacatcagt	ttcacctcca	ccacggggcc	240
caagttgatt	gtggacatcc	actcttacac	cagagacatc	tcctatgcac	gctgtctgac	300
tcacacacct	ctctttgcca	tttttggagg	cgtgggaaag	agacatgctc	ctgagagtga	360
tgggctatga	cgcggttgta	gacatctgtg	accctctata	tcattcacac	gccatgaacc	420
cctgtgtctg	tggctctcta	gatttgtggt	ctcttttttt	tctcacactt	ttatacaccc	480
acctgcacaa	ctcgattgcc	ttacacatga	cc			512

<210> 628

<211> 967

<212> DNA

<213> Unknown (H38g477 nucleotide)

<220>

<223> Synthetic construct

<400> 628

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagttca	60
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ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	ccaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	taccctaaa	240
atgattgcag	acttttctgg	tgagcacaa	actatttctt	ttgatgcccg	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatggtgc	tcctagtctc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgttgtgc	tcttcctcat	ttcctgggtt	gtgggcttca	tcataaccac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagatagttt	ttttctgtga	540
ccttcctcta	gtgaccaagt	tagcctgcat	agacacttat	gttgtcagcc	tactaatagt	600
tgcagatagt	ggctttcttt	ctctgagttc	ctttctcctc	ttggttgtct	cctacactgt	660
aatacttggt	acagtttaga	atagctcctc	tgtaagcatg	gtgaaggcct	gctccacatt	720
gactgctcac	atcactgtgg	tcactttatt	ctttggaccg	tgtattttca	tctatgtgtg	780
gcccttcagc	agttactcag	ttgacaaagt	ccttgctgta	ttctacacca	tcttcacgtc	840
tatttttaaac	cctgtaatct	acatgctaag	aaacaaagaa	gtgaaggcag	ctatgtcaaaa	900
actgaagagt	cggtatcaga	agcttgggtca	ggtttctgta	gtcataagaa	acgttctttt	960
cctagaa						967

<210> 629

<211> 942

<212> DNA

<213> Unknown (H38g478 nucleotide)

<220>

<223> Synthetic construct

<400> 629

atggaggggg	ttaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattctt	ttttgtgggt	ttttctgtct	tctattaaat	gaccatgttg	120
ggcaactgcc	tgattttact	cactgtccta	tccacctcac	accttcactc	tcgcacgtac	180
ttcctgtcga	gcaacctgtc	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgtct	tgcgtaagac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgtctg	ctgatctcca	tgtcttttga	360
caggatatatt	gccatatgta	aacctctccg	ctattcaaca	attatgagcc	aaagagtgtg	420
tggttgagctt	gtggcagttt	cttggtggag	agtgggcttt	ctacatacaa	tgagccaatt	480
agttttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcctttgg	tcattccagt	agcttgata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgactgc	tcttacaagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ctatcaggga	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcacatt	ttattgttgt	gttaatgttc	tttgggccct	gtattttcat	ttatgtgtgg	780
ccttccacaa	acttctgtgt	agacaaaatt	ctctctgttt	tctataccat	cttcaactccc	840
tttctgaatc	cacttatcta	tacttttgaga	aaccaggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgtct	cg		942

<210> 630

<211> 595

<212> DNA

<213> Unknown (H38g479 nucleotide)

<220>

<223> Synthetic construct

<400> 630

atgaaccctgt	gtttgtgtgg	cttttagagtt	gtgggtgtctt	tttttttttca	cagtcttttta	60
ggcgacacagg	tgcacaactt	gagcgccctca	caaatgacgt	gtttcgagta	tgtggaaatt	120
cataatttct	tgtgtgccct	ttctcaactc	ccccatcgtg	catgggtgtga	cactttcccc	180
aataacataa	togtgtattt	tccgtgtgcc	atatttggtt	ttcttcccat	cgcgggggacc	240
cctttttctct	taatatgaaa	gtgtttcctc	cattgagagg	gtttcatcat	aagggtggaga	300
gtataaggct	ttccccacgt	gtgggtctca	cctctcagtc	gtttgctgat	tatatggcac	360
aggcgttgga	gggcacctca	gttcagatgt	gtcatcttcc	ccgagaaagt	ctgcggtggc	420
ctcagtgatg	tacactgtgg	tcacccccat	gctgaaccct	ttcatctaca	gcatgagaaa	480
cagggatact	aaaagtgtcc	tgcggcgggc	gcacggcagc	acggtgtaat	tttgatatct	540
tcttatctgt	cccatctctt	ttgtagtgtg	ggttaaaaaa	ggcagaaagg	tcaaa	595

<210> 631

<211> 942

<212> DNA

<213> Unknown (H38g480 nucleotide)

<220>

<223> Synthetic construct

<400> 631

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attgtaggta	acctcagcat	tctcactctg	gtgttttggg	agcctgctct	gcatcagccc	180
atgtactact	tcctctctat	gtcgcctctc	aatgatctgg	gagtgtcctt	ttctacactt	240
cccactgtga	tttctacttt	ctgcttcaac	tacaaccatg	ttgcgtttaa	tgtttgcttg	300
gtccagatgt	tcttcattcca	cactttctcc	ttcatggagt	caggcatact	gctggccatg	360
agcttggatc	gctttgtggc	tatttgttat	ccattacgct	atgtcactgt	gctcactcac	420
aaccgtatat	tggctatggg	tctgggcata	cttaccaaga	gtttcaccac	tctcttccct	480
ttcccttttg	tgggtgaaacg	actgcccttc	tgcaaaggca	atgttttgca	tcactcctac	540
tgtctccatc	cagatctcat	gaaagtagca	tgtggagaca	tccatgttaa	caacatttat	600

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gggctcttgg tgatcatttt tacctatggt atggactcaa ctttcatcct gctttcctac 660
gcattgatcc tgagagccat gctggtcate atateccagg aacagcggct caaggcactc 720
aacacctgca tgtcacacat ctgtgcagtg ctggcctttt atgtgcccac aattgctgtc 780
tccatgattc accgcttctg gaaaagtgtc ccacctgttg ttcattgcat gatgtccaat 840
gtctacctgt ttgtaccacc catgctcaac cctatcctct acagtgtgaa aaccaaggag 900
atccgcaaag ggattctcaa gttcttccat aaatccagg cc 942

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<210> 632

<211> 936

<212> DNA

<213> Unknown (H38g481 nucleotide)

<220>

<223> Synthetic construct

<400> 632

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ggaaatacag tgatcctgca ggctgtgcca gtggagccca gcctccatga gcccattgtac 180
tacttctctg ccatgttgtc cttcagtgtg gtggccatat ccatggccac actgcccact 240
gtactccgaa ccttctgcct caatgcccgc aacatcactt ttgatgcctg tctaattcag 300
atgtttctta ttcacttctt ctccatgatg gaatcaggta ttctgctggc catgagtttt 360
gaccgctatg tggccatttg tgaccctctg cgctatgcaa ctgtgctcac cactgaagtc 420
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tttcttatta agaggctgcc tatctgcaga tccaatgttc tttctcactc ctactgcctg 540
caccagaca tgatgaggct tgccctgtgct gatatcagta tcaacagcat ctatggactc 600
tttgttcttg tatccacctt tggcatggac ctgtttttta tcttctctc ctatgtgctc 660
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tgtgtgtcac atatcctggc tgtacttgca ttttatgtgc caatgattgg ggtctccaca 780
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ctatttgtgc ctctgtgtc caaccctctc atttatagcg ccaagacaaa ggaaatccgc 900
cgagccattt tccgcatggt tcaccacatc aaaata 936

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<210> 633

<211> 467

<212> DNA

<213> Unknown (H38g482 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(467)

<223> n = A,T,C or G

<400> 633

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atggaaagca atcagacctg gatcacagaa gtcactctgt tgggattcca ggtggaccca 60
gctctggagt tgttctctct tgggtttttc ttgctattct acagcttaac cctgatggga 120
aatgggatta tcttggggct catctacttg gactctagac tgcacacacc catgtatgtc 180
ttctgtcac acctggccat tgtggacatg tctatgcct cgagtactgt ccctaagatg 240
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tttttgtatt tggcgtttgc tattacagag tgtctgattt tgggtgatgat gtgctatgat 360
cggtatgtgg caatctgtca ccccttgca atacaccnt cattatgaac tggagagtgt 420
gcactgtcct ggctcaact tgctggatat ttagctttct cttggct 467

```

<210> 634

<211> 988

<212> DNA

<213> Unknown (H38g483 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(988)

<223> n = A,T,C or G

<400> 634

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gcactggcga	ttctcatctn	gtgaactctt	ctctgtcttc	tatacactca	ccctgctggg	120
gaatgggggc	atctttggga	ttatctgcct	ggactctaag	cttcacacac	ccatgtactt	180
cttcctctca	cacctggcca	tcattgacat	gtcctatgct	tccaacaatg	ttcccaagat	240
gttggcaaac	ctaataaacc	agaaaagaac	catctccttt	gttccatgca	taatgcagac	300
ttttttgtat	ttggcttttg	ctgttacaga	gtgcctgatt	ttgggtggga	tgctctatga	360
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tctccttcta	aggttgccct	tctgtgggcc	cgggatgtg	aaccacctct	tctgtgaaat	540
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cccagactct	aatcaacgag	aggagcagga	gaaaatgctg	tccctgtttc	acagtgtctt	840
gaacccaatg	ctgaaccccc	tgatctacag	cctgaggaat	gctcagttga	agggcgccct	900
ccacagagca	ctccagagga	agaggtccat	gagaacggtg	tatgggcttt	gcctttaaaa	960
catgtggttt	gctgaagcaa	gaattttg				988

<210> 635

<211> 941

<212> DNA

<213> Unknown (H38g484 nucleotide)

<220>

<223> Synthetic construct

<400> 635

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aatggcatga	tcttgggact	catctgtctg	gaccacattc	tgctacccc	catgtacttc	180
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ttggcaaatc	tgatgaacaa	gaaaagaacc	atctcctttc	ttccatgcat	aatgcagacc	300
tattttgtatt	tctcttttgc	tgctacagag	tgtctgattt	tggtgggtgat	gtcctatgat	360
aggtatgtgg	ccatttgcca	ccctctccag	tacactgtca	tcattgagctg	gagagtgtgc	420
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tcccagactc	taatcaacga	gaggagcagg	agaaaatgct	gtccctgttt	cacagtgtct	840
tgaacccaat	tctgaacccc	ctgatctaca	gtctgaggaa	tgctcaggtg	aagggcgccc	900
tccacagagc	actgcagagg	acgctgtcta	tgtaaggagt	g		941

<210> 636

<211> 1002

<212> DNA

<213> Unknown (H38g485 nucleotide)

<220>

<223> Synthetic construct

<400> 636

atgtgttate	tttctcagct	atgcctcagc	cttgggggaac	acactttaca	tatgggggatg	60
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gtgagacata ccaatgagag caacctagca ggtttcatcc ttttaggggtt ttctgattat 120
cctcagttac agaagggttct atttgtgctc atattgattc tgtattttact aactattttg 180
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gtaaccgcga tgcttaacct tcttatttat accttgagga tcaaggaggt gaaaggggca 960
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<210> 637

<211> 510

<212> DNA

<213> Unknown (H38g486 nucleotide)

<220>

<223> Synthetic construct

<400> 637

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atggaaggca acaagacatg gatcacagac atcaccttgc cgcgattcca ggttgggtcca 60
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<210> 638

<211> 924

<212> DNA

<213> Unknown (H38g487 nucleotide)

<220>

<223> Synthetic construct

<400> 638

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<210> 639
 <211> 669
 <212> DNA
 <213> Unknown (H38g488 nucleotide)

<220>
 <223> Synthetic construct

<400> 639
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 tgacatggcc tatgcttcca acaatgttcc caagatgtcg gtggatcttg caaactagaa 240
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 gacacctggc tcaaccaggt ggtcatcttt gcaagctgca tgttcacctt ggtagggtga 600
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 ccaaaaagg 669

<210> 640
 <211> 927
 <212> DNA
 <213> Unknown (H38g489 nucleotide)

<220>
 <223> Synthetic construct

<400> 640
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 ggaaacttca ccataatcat catctcatat ctggatcccc ctcttcatac cccaatgtac 180
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 tgctcctccc accttacagt ggtgattata ttctatggca ccataatcta cgtgtacctg 780
 caacctagt acagctatgc ccaggaccaa ggggaagtta tctccctctt ctacaccatg 840
 gtgaccccca ctttaaatcc tatcatctat actttaagga acaaggatat gaaagaggct 900
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<210> 641
 <211> 1012
 <212> DNA
 <213> Unknown (H38g490 nucleotide)

<220>
 <223> Synthetic construct

<400> 641
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 tggggaacct gctcatcacc ctggccatca gccctgactc ccacctccac atccccatgt 180

acttcttctct	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcattct	ctatgcaggc	tgcttgactc	300
agatgtctct	ctttgccatt	tttgaggca	tggaagagag	acatgctcct	gagtgtgatg	360
gcctatgacc	ggttttagtc	catctgtcac	cctctatatc	attcagccat	catgaacccg	420
tgtttctgtg	gcttcctagt	tttggtgtct	ttttttttct	gtcctcagtc	tttttagactc	480
ccagctgcac	aacttgattg	ccttacaagt	gacctgcttc	aaggatgtgg	aaattcctaa	540
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tggaggttac	ctcagttcag	atgatgtgtc	atcttcccc	agaaagggtg	cagtggcctc	840
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ggatattaaa	agtgtcctgc	ggcgcccgca	cggcagcaca	gtctaattct	aatatcttct	960
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<210> 642

<211> 879

<212> DNA

<213> Unknown (H38g491 nucleotide)

<220>

<223> Synthetic construct

<400> 642

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ctccaaaccc	caatgtattt	ctttttgaga	aacttgtctt	tcttagattt	ttgttacatc	180
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tgtggattca	tgcattgtat	agcaacattc	tcattaccat	tctgtgggcg	caatagaata	480
cgtcaatttt	tctgtaatat	tccacagctc	ctaagcctct	tagaccccaa	agtaattacc	540
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tcaaaaacat	tttctacctg	cattccacat	cttgtgggtg	taacactctt	tatgatattc	720
ggcagcattg	cctatgtgaa	gccaaattca	aattctcccc	ccgttctgga	tgttttctctg	780
tctgcgttct	acacagtcgt	gcccccgacc	ctgaaccccg	tcattctatag	tctgaggaat	840
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<210> 643

<211> 1020

<212> DNA

<213> Unknown (H38g492 nucleotide)

<220>

<223> Synthetic construct

<400> 643

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cagaaaatac	gctcatgatc	ctcctcattc	gcagtgactc	ccgactccac	actccaatgt	180
attttctgt	cagccatctc	tccttaattg	atatcttgca	tgtttccaac	atcgttccca	240
aaatgggtcac	taagtttctg	tcaggcagca	gaactatttc	atttgcagggt	tgtgggttcc	300
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gtgatcgcta	tgtggctatc	tgccacccgc	tgcgctatcc	gattcttatg	aaggagtatg	420
ccagcgctct	catggctgga	ggctcctggc	tcattgggggt	tttcaactcc	acagtccaca	480
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aagtccctgc	catgttgaag	ttgtcctgtg	cagacacaac	acgctatgaa	cgagggtttt	600
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tcctcacacc	cacactcaac	cctttcatct	acagcttttag	gaataaagat	gttctggcgg	900
tgatgaaaaa	tatgctcaaa	agtaactttc	tgcaaaaaaa	aatgaatagg	aaaattcctg	960
aatgtgtgtt	ctgtctattt	ctatgttaaa	tgccctgaagg	atactcatga	gaggtttcct	1020

<210> 644

<211> 932

<212> DNA

<213> Unknown (H38g493 nucleotide)

<220>

<223> Synthetic construct

<400> 644

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gggaacgccc	tcctcatagg	gctgaacgtg	ctgcaccctc	gcctgcacaa	ccccatgtac	180
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acctgaccct	ggcgtgtgga	tcaacggagt	gcctgtctgt	ggctgtgatg	gcataatgacc	360
gttatgtggc	tatctgccag	ccgcttaggt	acccagagct	catgagtggg	cagacctgca	420
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ttgtctggca	cctccccctc	tgtggccacg	tcatcaacta	cttctatgag	atcttggcag	540
tgctaaaact	ggcctgtggg	gacatctccc	tcaatgcgct	ggcattaatg	gtggccacag	600
ccgtcctgac	actggccccc	ctcttgcctc	tctgcctgtc	ttaccttttc	atcctgtctg	660
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accgcacagt	ggtggtggtt	ttttatggga	caatctcctt	catgtacttc	aaaccaagg	780
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tgaaccccat	catttacagc	ctgaggaatg	cagaggtgaa	agctgccgtc	ctaactctgc	900
tgagaggagg	tttgcctctc	aggaaagcat	cc			932

<210> 645

<211> 957

<212> DNA

<213> Unknown (H38g494 nucleotide)

<220>

<223> Synthetic construct

<400> 645

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ttgggcaatg	gcatacatcat	tctggtctcc	catacagatg	tgacacctca	cacacctatg	180
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ctttgccttg	ggctagcttt	ggcctccttg	ctgggggggtc	tgaccaccag	catggtgggc	480
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gtagtcactc	ctgcgctgaa	cccacttatt	tacaccctga	ggaacacgga	ggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

<210> 646

<211> 792

<212> DNA

<213> Unknown (H38g495 nucleotide)

<220>

<223> Synthetic construct

<400> 646

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atggacgtga	tgctggtttc	caccactgtg	cccaaatgg	cggtgacta	cttgaccgga	180
agtaaggcca	tctcccgccg	tggtgtgtgt	gcgcagatct	tcttccctcc	cacactgggt	240
ggtggagagt	gcttctctct	agcagccatg	gcctatgacc	gctatgcggc	tgtctgccac	300
ccactccgat	atcccactct	catgagctgg	cagctgtgcc	tgaggatgaa	cctgtcgtgt	360
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aaccacgaca	aggttgtgtc	agccttctat	actatgttca	cccctttact	aaacccctc	780
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<210> 647

<211> 662

<212> DNA

<213> Unknown (H38g496 nucleotide)

<220>

<223> Synthetic construct

<400> 647

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atgatgctgg	gtccaccga	gtgcgtcttc	ctggttgtca	tgteccatga	ccgctatgtg	180
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cagctctccc	ggtgtggacg	tcgcaggggtg	gaccacttcc	tgtgtgagat	gcctgtctct	360
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ggtgctgagg	atgaagtcag	cagcagggcg	aaagaaagcc	ttccacacct	gctcttctca	540
cctcacagt	gtctctctct	tctacggaac	catcatctac	ggtgtacctg	aagccggcca	600
acagctactc	ccaagatcag	gggaagttcc	tgactctctt	ctacaccatc	gtcattccca	660
gc						662

<210> 648

<211> 936

<212> DNA

<213> Unknown (H38g497 nucleotide)

<220>

<223> Synthetic construct

<400> 648

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gggaacacag	ccatcatggc	ggtgagcgtg	ctagatatcc	acctgcacac	gcccggttac	180
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atgtgtctga	gcctgtccac	gggtccacg	gagtgccctg	tactggccat	cacggcctat	360
gaccgctacc	tggtccatctg	ccagccactc	aggtaccacg	tgctcatgag	ccaccggctc	420
tgcgtgctgc	tgatgggagc	tgctgggtgc	ctctgcctcc	tcaagtcggg	gactgagatg	480
gtcatctcca	tgaggctgcc	cttctgtggc	caccacgtgg	tcagtcactt	cacctgcaag	540

atcctggcag	tgctgaagct	ggcatgcggc	aacacgtcgg	tcagcgaaga	cttcctgctg	600
gcgggctcca	tcctgctgct	gcctgtaccc	ctggcattca	tctgcctgtc	ctacttgctc	660
atcctggcca	ccatcctgag	ggtgccctrg	gccgccaggt	gctgcaaagc	cttctccacc	720
tgcttggcac	acctggctgt	agtgtgtctt	ttctacggca	ccatcatctt	catgtacttg	780
aagcccaaga	gtaaggaagc	ccacatctct	gatgaggtct	tcacagtcct	ctatgccatg	840
gtcacgacca	tgctgaacct	caccatctac	agcctgagga	acaaggaggt	gaaggaggcc	900
gccaggaagg	tgtggggcag	gagtcgggac	tccagg			936

<210> 649

<211> 940

<212> DNA

<213> Unknown (H38g498 nucleotide)

<220>

<223> Synthetic construct

<400> 649

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agagcccttg	ggggcctcct	ctttgtgatt	ttttatcagc	ctatttggtg	acagtccttg	120
gaaacaccct	tattattatc	ctgattcttg	tggattacag	gctccactca	cccatgtatt	180
tcttcttcag	caatctctct	ttcagtgaag	cattaacat	aacctgtgct	gttcctaaga	240
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cctattttcta	ttttctttcc	ggatgcaactg	agtttattcc	ttttgctgtc	atgtcctatg	360
accgctatgt	ggccatttgc	agtcctcttc	agtaccctgc	aattatgacc	agtcactctt	420
gtgcccacct	cgtcactctc	tcctgggtgg	gtggctttct	cctcatgctc	ccatccacca	480
tcctcaaggc	aggactgcca	cactgtgggtc	ccaacgtgat	tgagcacttt	ttctgtgaca	540
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tcagctgcta	ggctctgata	ctcagctccc	tctcactcac	agtggctctc	tatgtttaca	660
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gtgcctctca	cttcacggtg	gtctccgtgg	gctatgggat	ctccatcttt	gtctatgttc	780
acccctcaca	gaagagcagc	ctgcacctca	acaagatcct	ctttatcttc	tccagcatca	840
tcacaccctt	cctgaatccc	ttcgtcttca	gtctgtggaa	tgaacccatg	aaagatgcac	900
tgaaggacgc	ctcgcccgga	ggacagagct	tgctcaaagg			940

<210> 650

<211> 927

<212> DNA

<213> Unknown (H38g499 nucleotide)

<220>

<223> Synthetic construct

<400> 650

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atgtgcattt	tgcattcgat	tctcttcttg	ttgatttatt	tgtgtgccct	gatgggggat	120
gtcctcatta	tcatgatcac	aactttggac	catcatctcc	acacccccgt	gtatttcttc	180
ttgaagaatc	tatctttctt	ggatctctgc	cttatttcag	tcacggctcc	caaattctatc	240
gccaatcttt	tgatacacia	caactccatt	tcattccttg	gctgtgtttc	ccagggtcttt	300
ttgttgcttt	cttcagcate	tgagagctg	ctcctcctca	cgggtgatgtc	ctttgaccgc	360
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accttctcct	tatcctactg	tgggtccaac	atgggtccatc	agttcttctg	tgacattccc	540
cagttattag	ctatttcttg	ctcagaaaat	ttaataagag	aaattgcaact	catccttatt	600
aatgtagttt	tggatttctg	ctgttttatt	gtcatcatca	ttacctatgt	ccacgtcttc	660
tctacagtca	agaagatccc	ttccacagaa	ggccagtcac	aagcctactc	tatttgccctt	720
ccacacttgc	tggttgtgtt	atttctttcc	actggattca	ttgcttatct	gaagccagct	780
tcagagtctc	cttctatttt	ggatgctgta	atttctgtgt	tctacactat	gctgccccca	840
acctttaatc	ccattatata	cagtttgaga	aacaaggcca	taaagggtggc	tctgggggatg	900
ttgataaagg	gaaagctcac	caaaaag				927

<210> 651

<211> 942

<212> DNA

<213> Unknown (H38g500 nucleotide)

<220>

<223> Synthetic construct

<400> 651

atgggggatg	tgaatcagtc	ggtggcctca	gacttcattc	tggtgggcct	cttcagtcac	60
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ggcaacaccg	ttcttctctt	cttgatccgt	gtggactccc	ggctccacac	acccatgtac	180
ttcctgtctc	gccagctctc	cctgtttgac	attggctgtc	ccatgggtcac	catccccaag	240
atggcatcag	actttctgcg	gggagaaggt	gccacctcct	atggagggtg	tgcagctcaa	300
atattcttcc	tcacactgat	gggtgtggct	gagggcgctc	tgttggctct	catgtcttat	360
gaccgttatg	ttgctgtgtg	ccagcccctg	cagtatcctg	tacttatgag	acgccaggta	420
tgtctgtctg	tgatgggctc	ctcctgggtg	gtagggtgtg	tcaacgcctc	catccagacc	480
tccatcaccc	tgcattttcc	ctactgtgcc	tcccgtattg	tggatcactt	cttctgtgag	540
gtgccagccc	tactgaagct	ctcctgtgca	gataacctgtg	cctacgagat	ggcgtgtgcc	600
acctcagggg	tgctgatcct	aatgctccct	ctttccctca	tcgccacctc	ctacggccac	660
gtgttgccagg	ctgttcttaag	catgcgtcca	gaggaggcca	gacacaaggc	tgccaccacc	720
tgctcctcgc	acatcacggg	agtggggctc	ttttatgggt	ccgccgtgtt	catgtacatg	780
gtgccttgcg	cctaccacag	tccacagcag	gataacgtgg	tttccctctt	ctatagcctt	840
gtcaccacct	cactcaacct	ccttatctac	agtctgagga	atccggaggt	gtggatggct	900
ttgggtcaaa	tgcttagcag	agctggactc	aggcaaatgt	gc		942

<210> 652

<211> 936

<212> DNA

<213> Unknown (H38g501 nucleotide)

<220>

<223> Synthetic construct

<400> 652

atggatctta	aaaatggatc	tctagtgacc	gagtttattt	tactaggatt	ttttggacga	60
tggaacttc	aaattttctt	ctttgtgaca	ttttccctga	tctacgggtg	tactgtgatg	120
ggaaacattc	tcattatggg	cacagtgaca	tgtagggtcaa	cccttcattc	tcccttgtag	180
tttctccttg	gaaatctctc	ttttttggac	atgtgtctct	ccactgccac	aacacccaag	240
atgatcatag	atttgcctac	tgaccacaag	accatctctg	tgtggggctg	cgtgaccacg	300
atgttcttca	tgcacttctt	tggggggtgt	gagatgactc	ttctgataat	catggccttt	360
gacaggtatg	tagccatatg	taaacccctg	cactatagga	caatcatgag	ccacaagctg	420
ctaaaggggt	ttgcgatact	ttcatggata	attggttttt	tacactccat	aagccagata	480
gttttaacaa	tgaacttgcc	tttctgtggc	cacaatgtca	taaacaacat	attttgtgat	540
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atcctgggtca	gtgtacaaa	aaaatcatca	catgggctct	ccaaggcgct	gtccacattg	720
tctgccacac	tcattgtggg	cactctgttc	tttggacctt	gtatttttat	ctatgtttgg	780
ccattcagta	gtttggcaag	caataaaact	cttgccgtat	tttatacagt	tatcacaccc	840
ttactgaatc	cgagtattta	taccctgaga	aataagaaaa	tgcaagaggc	cataagaaaa	900
ttacgggttc	aatatgttag	ttctgcacag	aatttc			936

<210> 653

<211> 972

<212> DNA

<213> Unknown (H38g502 nucleotide)

<220>

<223> Synthetic construct

<400> 653

atgccaacag	acaaacaaat	ggaaaaacaa	aatcagttcca	tggtgcctga	atttattttt	60
------------	------------	------------	-------------	------------	------------	----

ttgggattca	aaaatctcat	gagctacaga	ttttctttat	cttatttttc	cattctctac	120
atatccataa	ttaagtaacc	taatcattat	ctttgtagtg	aaactggatc	ctcaattgca	180
ttctcccatg	tacttcctac	tggccaacct	gtcatctact	gatatgcccc	tggcctcctt	240
tgctactcct	aagaaaatcg	ataatgtaat	tagtgaatat	aggaccatct	cttatgaagg	300
ctgcatgaca	tagagatttt	tccttcactt	tttaagtggg	agtgagatgg	ttttactctt	360
agccatggca	atcgatagat	aatttgccat	atgcaaacc	ctccattaca	agtccattgc	420
atcggacttg	ctcctcgctc	ctggactatg	gatttcatgc	acaccatgag	ccaaattggt	480
ctcacagtga	ctttgccatt	ctgtggtctc	agtgttggtg	atatttttgt	gtgtgtgtga	540
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cagacagtgg	actactttct	ttgctgtgtt	tcatgtttct	gttaatctcc	tatagcaccg	660
tcctgattat	tatttgacat	cattcctcca	gggggtcttc	caaaactctg	tccacgcttt	720
cagcccatat	tatggtgggtg	gtactgttct	ttggagcttg	catctttacc	tgtgaaagac	780
cattcagcac	tgtctccatt	gatgtctgtg	ttttaaacta	tttttgctcc	ccttttaaat	840
ccaatcatct	acacattcag	gaataacgac	atgaagaaag	cattaagaaa	aatgaagatt	900
aactttgtga	gttctagatc	aacttgataa	ctaaaatatt	ataatcacta	aaagcatcat	960
cattattgtt	gt					972

<210> 654

<211> 936

<212> DNA

<213> Unknown (H38g503 nucleotide)

<220>

<223> Synthetic construct

<400> 654

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cggaagatcc	agctcctcct	cttctctttt	ttctcagtg	tctatgtgtc	aagcctgatg	120
ggaaatctcc	tcattgtgct	aactgtgacc	tctgaccctc	gtttacagtc	ccccatgtac	180
ttcctgctgg	ccaacctttc	catcatcaat	ttggtatttt	gttcctccac	agctcccaag	240
atgatttatg	accttttcag	gaagcacaag	accatctctt	ttgggggctg	tgtagttcag	300
atcttcttta	tccatgcagt	tgggggaact	gagatgggtg	tgctcatagc	catggctttt	360
gaccgatatg	tggccatatg	taagcctctc	cactacctga	ccatcatgaa	cccacaaagg	420
tgcattttgt	tttttagtcat	ttcctggatt	atagggtatta	ttcactcagt	gattcagttg	480
gcttttgttg	tagacctgct	gttctgtggc	cctaataaat	tagatagttt	ccttttgtat	540
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gccaatagtg	gatttatttc	tctggcttct	tttttaattc	tcataatctc	ttacatcttt	660
attttggtga	ctgttcagaa	aaaatcttca	ggtgggtatat	tcaaggcttt	ctctatgctg	720
tcagctcatg	tcattgtggg	ggttttggtc	tttggggccat	taatcttttt	ctatattttt	780
ccatttccca	catcacatct	tgataaattc	cttgccatct	ttgatgcagt	tatcactccc	840
gttttgaatc	cagtcactta	tacttttaga	aataaagaga	tgatggtggc	aatgagaaga	900
cgatgctctc	agtttgtgaa	ttacagtaaa	atcttt			936

<210> 655

<211> 967

<212> DNA

<213> Unknown (H38g504 nucleotide)

<220>

<223> Synthetic construct

<400> 655

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tgggagactc	aagatttttc	ttttttgctt	ttcttgtctt	ttctatgtgt	ccgggtgtgat	120
ggcaaacctc	attgtagtgg	tcattgtaac	ctctgacctt	tacttgcaact	cctccttgta	180
tattttgctg	gccaaacctc	ctgtcattga	tctcacattt	tgtccatttg	cagcacgcaa	240
gatgatttgg	gatattttca	ggaaacagaa	agtcatttcc	ttttggggct	gtgtagtcca	300
gatcttcttt	agccatgctg	ttggggggcac	tgagatgggtg	ctgctcatag	ccatggcctt	360
tgacagatat	gttgccgtat	gtaagccctt	tactacctg	accatcatgc	atccaagaat	420
gtgcattttg	attctagtgg	cttctgtggc	cattggtctc	attcactcat	tgggtccaatt	480
gtcttttgta	gtaaacttgc	ccttctgtgg	ccctaagtgt	ttggacagct	tttactgtga	540

catacctcag	ctcatcaaac	ttgcttgac	aaatacctat	aaactgcagt	tcattggttac	600
tgctaatagt	gggttcattt	ccttgagtgc	tttcttcttg	ctcatcctct	cttacatctt	660
cattctggcc	actcttcaga	aacactcctc	aggaggctca	tccaaggctg	tctctactct	720
gtcagctcat	attactgttg	tggttttatt	cttgggtcca	ctgatttttt	tctatgtatg	780
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ttttctgaat	ccagtcctct	acacattcag	gaacaaggaa	atgaagattg	caataaggag	900
agtgttcggt	caatttatgg	gttttagaa	aactacttaa	gtggccttat	taaaacacag	960
aatttcc						967

<210> 656

<211> 873

<212> DNA

<213> Unknown (H38g505 nucleotide)

<220>

<223> Synthetic construct

<400> 656

atggttgggg	caaatcactc	cgtgggtgtca	gagtttgtgt	tcctgggact	caccaattcc	60
tgggagatcc	gacttctcct	ccttggtgttc	tcctccatgt	tttacatggc	cagtatgatg	120
ggaaactctc	tcattttgct	cactgtgact	tctgacctc	acttgcactc	ccccatgtat	180
tttctgttag	ccaacctctc	cttcattgac	ctgggtgttt	cctctgtcac	ttctcccaaa	240
atgatttatg	acctgttcag	aaagcacgaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tggcgggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccatatg	taagccccctc	cagtacctga	ccattatgag	cccaagaatg	420
tgcattgtct	ttcttagtggc	tgccctgggtg	accggcctta	tccactctgt	agttcaattg	480
gtttttgtag	taaacttgcc	cttctgtggt	cctaattgat	cggacagctt	ttactgtgac	540
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gccaacagtg	gattcatctc	tctgggctcc	ttcttcatac	tgatcatttc	ctatgtggtc	660
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ccatctccct	ccacacacct	ggataagttt	ctggccatct	ttgatgcagt	tctcactcct	840
gttttaaate	ctatcatcta	cacattcagg	aat			873

<210> 657

<211> 936

<212> DNA

<213> Unknown (H38g506 nucleotide)

<220>

<223> Synthetic construct

<400> 657

atgaatggaa	tgaatcactc	tgtgggtatca	gaatttgtat	tcattgggact	caccaactca	60
cgggagattc	agcttctact	ttttgttttc	tctttgttgt	tctactttgc	gagcatgatg	120
ggaaaccttg	tcattgtatt	cactgtaacc	atggatgctc	atctgcactc	ccccatgtat	180
ttcctcctgg	ctaacctctc	aatcattgat	atggcatttt	gtcgaattac	agccccctag	240
atgatttgtg	atattttcaa	gaagcacaa	gccatctcct	ttcggggatg	tattactcag	300
atcttcttta	gccatgctct	tgggggact	gagatgggtgc	tgctcatagc	catggccttt	360
gacagataca	tggccatatg	taaacctctc	cactacctga	ccatcatgag	cccaagaatg	420
tgtctatact	ttttagccac	ttcctctatc	attggcctta	tccactcatt	ggtccaatta	480
gtttttgtgg	tagatttacc	tttttgtggt	cctaataatct	ttgacagttt	ttactgtgat	540
ctccctcgge	tcctcagact	tgccctgtacc	aacacccaag	aactggagtt	catgggtcact	600
gtcaatagtg	gactcatttc	tgtgggctcc	tttgtcttgc	tggttaatttc	ctacatcttc	660
attctgttca	ctgtttggaa	acattcttct	ggtggtctag	ccaaggccct	ctctaccttg	720
tcagctcatg	tcactgtggt	catcttgttc	tttgggccac	tgatgttttt	ctacacatgg	780
ccttctccca	catcacacct	ggataaatat	cttgctattt	ttgatgcatt	tattactcct	840
tttctgaatc	cagttatcta	cacattcagg	aacaaagaca	tgaaagtggc	aatgaggaga	900
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<210> 658

<211> 980
 <212> DNA
 <213> Unknown (H38g507 nucleotide)

<220>
 <223> Synthetic construct

<400> 658
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 ggacagaaaa tattatttct tgtgttcttg ctcactctacg ttgtgacaat ggtaggcaac 120
 atattcattg ttgtgactgt ggtgggcagc ccaacttttg atgccccatg tacttcttcc 180
 ttggctactt atcattttatg gatgctgttc attctactac agttacccca aatatgatta 240
 tagacttact ctatgagaag aaaaccattt cgttccaagc ttgattaccc agatttttat 300
 aggacaccta ttggggggtg ctgagatttt actccttgtt gtcattggcct atgatggcta 360
 cgtgaccatc tgcaaaacccc tgcattattt gaccatcatg aaccaacggg tgtgcattct 420
 actgctgctg ttggcctggg ctggagggtt cttgcatgct gtagttcaac ttctttttgt 480
 ttacaacctt cccttctgtg gcccacatgt cattgaccat ttcactctgtg acatgtaccc 540
 ttatttaaaa cttgcctgca ctgacaccta tgttactggc ctcactgtgg ttgccaatga 600
 tggggcaatc tgtgtgggtc tctttatgct cttactcttc tcctatgggg tcattctgca 660
 ctccctgaag aatcttagtc aggaaggag gcacaaagcc ttatccacct gtggctccca 720
 tatcactgtg gtgactctct tctttgtccc ttgtattttc atgtatgtga gacctccttt 780
 gaccttacct attgataaat ccttgactgt gttttacact gttatcacac ctatgttgaa 840
 ccctctaata tatactttaa gaaatgcaga gatgaaaaat gctatgaaga agctctggac 900
 tagaaaaaga aaatgagggt gcagacaaat gtatcatcta ttttcagtga agagttgctc 960
 cctccaggaa agccatttgt 980

<210> 659
 <211> 917
 <212> DNA
 <213> Unknown (H38g508 nucleotide)

<220>
 <223> Synthetic construct

<400> 659
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 tgggaacttc aaattttctt ctttgtgaca ttttccctga tctacggtgc tactgtggtg 120
 ggaaacattc tcattatggt cacagtgaca tgtagtgcga cccttcattc tcccttgtag 180
 tttctccttg gaaatctctc ttttttggac atgtgtctct ccaactgccac aacacccaag 240
 atgatcacia gaccatctct gtgtggggct gcgtgaccca gaagttcttc atgcacttct 300
 ttgggagtgc tgagatgact cttctgataa tcatggcctt tgacaggatg gtagccatat 360
 gtaaacccct gcactatagg acaatcatga gccacaagct gctaaagggg tttgcgatac 420
 tttcatggat aattggtttt ttacactcca taagccagat agttttaaca atgaacttgc 480
 ctttctgttg ccacaatgtc ataaacaaca tattttgtga tcttcccctt gtgatcaagc 540
 ttgcttgcat tgaaacatac accctggaat tatttgtcat tgctgacagc gggctgctct 600
 ctttcacctg tttcactctc ttgcttgttt cttacattgt catcctggtc agtgtaccaa 660
 aaaaatcatc acatgggctc tccaaggcgc tgtccacatt gtctgccac atcattgtgg 720
 tcaactctgt ctttggacct tgtattttta tctatgtttg gccattcagt agtttggcaa 780
 gcaataaaac tcttgcctga ttttatacag ttatcacacc gttactgaat ccgagtattt 840
 ataccctgag aaataagaaa atgcaagagg ccataagaaa attacggtc caatatgtta 900
 gttctgcaca gaatttc 917

<210> 660
 <211> 1008
 <212> DNA
 <213> Unknown (H38g509 nucleotide)

<220>
 <223> Synthetic construct

<400> 660

tctacagacc	cacagaatct	aacagatgtc	tctatatccc	tcctcctaga	acctcagagg	60
atccagaatg	acagccgggc	ctcgcctggc	tggtcctgtc	catgtgcctg	gtcacgggtg	120
tggggaacct	gctcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acatcttctt	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgactgt	ggacatccag	tctcacagca	gagtcactct	ctatgcaggc	tgcctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgttcct	gagtgtgatg	360
gcctatgacc	ggttttagtc	catctgtcac	cctctatatc	attcagctat	catgaaccgg	420
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cagctgcgca	acttgattgc	cttacaaatg	acctgcttca	aggatgtgga	aattcctaata	540
ttcttctgtg	acccttctca	actcccccat	cttgcattgt	gtgacacctt	caccaataaac	600
ataatcctgt	atttccctgc	tgccatatct	ggttttcttc	ccatcttggg	gacctttttc	660
tcttactata	aaatcgtttt	ctccattctg	aggggtttcat	catctgggtg	gaagtataag	720
gccttctcca	cctgtgtgtc	tcacctgtca	gtgggtttgct	gatttttatg	aacaggcggt	780
ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	aggctgcagt	ggcctcagtg	840
atgtacacgg	tggtcacccc	catgttgaac	cccttcatct	acagcctgag	aaacagggat	900
attaaaagtg	tcctgcggcg	gccgcacagc	agcacgggtct	aatcttgata	tcttcttctc	960
tgttccattc	ctttttagtg	gtgggttaaa	aaaggcagca	aggtcaaa		1008

<210> 661

<211> 957

<212> DNA

<213> Unknown (H38g510 nucleotide)

<220>

<223> Synthetic construct

<400> 661

atgatggaaa	tagccaatgt	gagttctcca	gaagtctttg	tcctcctggg	cttctccaca	60
cgaccctcac	tagaaactgt	cctcttcata	gttgtcttga	gtttttacat	ggtatcgatc	120
ttgggcaatg	gcacatcat	tctggtctcc	catacagatg	tgcacctcca	cacacctatg	180
tacttctttc	ttgccaacct	ccccttccctg	gacatgagct	tcaccacgag	cattgtccca	240
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tatgaccgct	acgctgccat	ctgcaggcca	ctccattaca	ctgtcattat	gcacccacag	420
ctttgccttg	ggctagcttt	ggcctcctgg	ctgggggggc	tgaccaccag	catgggtggc	480
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tacctggcca	gctttgtctt	tggtgtcctg	cctctggggc	tcacccctgt	ctcttacggc	660
cacattgccc	gggcccgtgt	gaagatcagg	tcagcagaag	ggcggagaaa	ggcattcaac	720
acctgttctt	cccacgtggc	tgtgggtgtc	ctgttttacg	ggagcatcat	cttctatgat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagtctt	gttctacacc	840
gtagtcactc	ctgcgctgaa	cccacttatt	tacacctga	ggaacacgga	gggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

<210> 662

<211> 912

<212> DNA

<213> Unknown (H38g511 nucleotide)

<220>

<223> Synthetic construct

<400> 662

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caaaatcttc	agattttatt	cttcttgagg	ttctctgtgg	tcttcgtggg	gattgtgtta	120
ggaaacctgc	tcatcttggt	gactgtgacc	tttgattcgc	tccttcacac	accaatgtat	180
tttctgctta	gcaacctctc	ctgcattgat	atgacccctg	cttcttttgc	tacccttaag	240
atgattgtag	atttctcccg	agaacgtaag	accatctcat	gggtggggatg	ttattcccag	300
atgttcttta	tgcacctcct	gggtggggagt	gagatgatgt	tgctttagtc	catggcaata	360
gacaggtagt	ttgccatatt	caaacccttc	cattacatga	ccatcatgag	cccacgggtg	420
ctcactgggc	tactgttatt	ctcctatgca	gttggatttg	tgcaactcat	tagtcaaata	480

gctttcatgt	tgactttgcc	cttctgtggt	cccaatgtta	tagacagctt	tttctgtgac	540
cttccccttg	tgattaaact	tgcttgcaag	gacacctaca	tcctacagct	cctgggcatt	600
gctgacagtg	ggctcctgtc	actggctctgc	ttcctcctct	tgcttgtctc	ctatggagtc	660
ataatattct	cagttaggta	cgtgctgtct	agtcgaccc	ctaaggcttt	ctccactctc	720
tcagctcaca	tcacagttgt	gactctgttc	tttgcctcgt	gtgtctttat	ctacgtctgg	780
cccttcagca	gatactcggt	agataaaatt	cttctgtgtg	tttacacaat	tttcacacct	840
ctcttaaatc	ctattattta	tacattaaga	aatcaagagg	taaaagcagc	cattaaaaaa	900
agactctgca	ta					912

<210> 663

<211> 963

<212> DNA

<213> Unknown (H38g512 nucleotide)

<220>

<223> Synthetic construct

<400> 663

atgggtcaatt	tgacttcaat	gagtggattc	cttcttatgg	ggttttctga	tgagcgtaag	60
cttcagattt	tacatgcatt	ggtattttctg	gtgacatacc	tgctggcctt	gacaggcaac	120
ctcctcatta	tcaccatcat	taccgtggac	cgtcgtctcc	attcccccat	gtattacttt	180
ttaaagcacc	tctctcttct	ggacctctgc	ttcatctctg	tcacagtccc	ccagtcatt	240
gcaaattcac	ttatgggcaa	cggttacatt	tctcttggtc	agtgcattct	tcagggtttc	300
ttcttcatag	ctctggcctc	atcagaagtg	gccattctca	cagtgatgtc	ttatgacagg	360
tacgcagcaa	tctgtcaacc	acttcattat	gagactatta	tggtatccccg	tgctgttagg	420
catgcagtga	tagctgtgtg	gattgctggg	ggcctctctg	ggctcatgca	tgctgccatt	480
aacttctcca	tacctctctg	tggaagaga	gtcattcacc	aattcttctg	tgatgttcct	540
cagatgtcga	aactagcctg	ttcttatgaa	ttcattaatg	agattgcact	ggctgcattc	600
acaacgtctg	cagcattttat	ctgtttgatc	ttcattatgt	tctcctacat	tcgcactctc	660
tctacagtgc	tgagaatccc	atcagctgag	ggccggacca	aggtcttctc	cacctgccta	720
ccacacctat	ttgtagccac	cttctttctt	tcagctgcag	gctttgagtt	tctcagactg	780
ccttctgatt	cctcatcgac	tgtggacctt	gtattctccg	tattctatac	tgtgatacct	840
ccaacactca	atccagtcac	ttatagctta	cggaaatgatt	ccatgaaggc	agcactgagg	900
aagatgctgt	caaaggaaga	gcttcctcag	agaaaaatgt	gcttaaaagc	catgtttaaa	960
ctc						963

<210> 664

<211> 930

<212> DNA

<213> Unknown (H38g513 nucleotide)

<220>

<223> Synthetic construct

<400> 664

atggaccac	agaactattc	cttgggtgtca	gaatttgtgt	tgcatggact	ctgcacttca	60
cgacatcttc	aaaatttttt	ctttatatatt	ttctttgggg	tctatgtggc	cattatgctg	120
ggtaaccttc	tcatttttgg	caactgtaatt	tctgatccct	gcctgcactc	ctccccatg	180
tacttctctg	tggggaacct	agctttcctg	gacatgtggc	tgacctcatt	tgccactccc	240
aagatgatca	gggatttcct	tagtgatcaa	aaactcatct	cctttggagg	atgtatggct	300
caaatcttct	tcttgcaatt	tactgggtggg	gctgagatgg	tgtcctgggt	ttccatggcc	360
tatgacagat	atgtggccat	atgcaaacc	ttgcattaca	tgactttgat	gagttggcag	420
acttgcac	ggctgggtgt	ggcttcatgg	gtcgttggat	ttgtgcactc	catcagtcac	480
gtggctttca	ctgtaaattt	gccttactgt	ggccccaatg	aggtagacag	cttcttctgt	540
gacctccctc	tggtgatcaa	acttgcctgc	atggacacct	atgtcttggg	tataattatg	600
atctcagaca	gtgggttgg	ttccttgagc	tgttttctgc	tcctcctgat	ctcctacacc	660
gtgatccctc	tcgtatcag	acagcgtgct	gccggtagca	catccaaagc	actctccact	720
tgtctgtcac	atatcatgg	agtgcagctg	ttctttggcc	cttgcatttt	tgtttatgtg	780
cggcctttca	gtaggttctc	tgtggacaag	ctcgtgtctg	tgttttatac	catttttact	840
ccactcctga	acccattat	ctacacattg	agaaatgagg	agatgaaagc	agctatgaag	900
aaactgcaaa	accgacgggt	gacttttcaa				930

<210> 665

<211> 957

<212> DNA

<213> Unknown (H38g514 nucleotide)

<220>

<223> Synthetic construct

<400> 665

atggaaaagaa	agaatcaaac	agctataact	gaattcatca	tcttgggatt	ctccaaccta	60
aatgaattgc	agtttttact	attcaccatc	ttctttctga	cttatttctg	tactttggga	120
ggaaatatat	taattatctt	gacgactgtg	actgatccac	acctgcatac	acctatgtat	180
tatttttctag	ggaacttggc	ctttattgac	atctgtctaca	ccaccagcaa	tgteccccag	240
atgatggtgc	acctcctctc	aaagaaaaaa	agcatttctt	atgtgggggtg	tgtgggtcaa	300
cttttttgc	ttgttttctt	tgtaggatca	gagtgtctcc	tactggcagc	aatggcatat	360
gatcgttaca	ttgcaatctg	caatccttta	aggatttcag	ttattctgag	caaggttcta	420
tgcaatcaat	tagcagcctc	atgctgggct	gctgggttcc	ttaactcagt	ggtgcataca	480
gtgttgacat	tctgcctgcc	cttctgtggc	aacaatcaga	ttaattactt	cttctgtgac	540
atccccccctt	tgctgatctt	gtcttgtgga	aacacttctg	tcaatgagtt	ggcactgcta	600
tccactgggg	tcttcattgg	ttggactcct	ttcctttgta	tcgtactttc	ctacatttgc	660
ataatctcca	ccatcttgag	gatccagtcc	tcagagggaa	gacgaaaagc	cttttctaca	720
tgtgcctccc	acctggccat	tgtctttctc	ttttatggca	gcgccatctt	tacatatgta	780
cggccccatct	caacttactc	attaaagaaa	gatagggttg	tttcagtgtt	gtacagtgtt	840
gttaccacca	tgctaaaccc	tataatttac	acattgagga	ataaggacat	caaagaagct	900
gtcaaaaacta	tagggagcaa	gtggcagcca	ccaatttctt	ctttggatag	taaactc	957

<210> 666

<211> 910

<212> DNA

<213> Unknown (H38g515 nucleotide)

<220>

<223> Synthetic construct

<400> 666

atgagagaat	ttttcttgtc	agggttctca	cagacaccat	ctattgaagc	agggtctattt	60
gtactatttc	ttttcttcta	tatgtccatt	tgggttggca	atgtcctcat	catggtcaca	120
gtagcatctg	ataaatacct	gaattcatca	cccatgtatt	tccttcttgg	caacctctca	180
tttctggacc	tatgttatcc	aacagtaacg	acccttaagc	ttctggctga	cttctttaat	240
catgaaaaac	tcatttccta	tgaccaatgc	attgtgcaac	tcttcttctt	gcattttgta	300
ggggcagctg	agatgttctt	gctcacagt	atggcgtagc	atcgctatgt	tgcaatctgt	360
cgcccgctgc	actacaccac	tgtcatgagt	cgggggttat	gctgtgtgtt	ggttgctgcc	420
tcctggatgg	gaggatttgt	gcactccact	gtccagacca	ttctcactgt	ccatctaccc	480
ttttgtgggc	caaatcaggt	ggaaaacttt	ttttgtgat	gttccccctg	tcatcaaact	540
tgcttgtgct	gacacttttg	tcattgaatt	gctcatggta	tctaacagt	ggttgatctc	600
caccatctcc	tttgtgggtc	tgatttcttc	ctacaccact	atcctagtca	agattcgctc	660
caaggaagga	aggcgaaagg	cactctccac	gtgtgcctct	cacctcatgg	tggtaacact	720
gttttttggga	ccctgtattt	tcactctacg	tcgtcctttc	tctacatttt	ctgtggacaa	780
gatggtgtct	gtactctaca	atgttattac	cccaatgcta	aacccccctc	tctacacact	840
tcggaacaaa	gaggtaaagt	cagccatgca	gaagctctgg	gtcagaaatg	ggcttacttg	900
gaaaaagcag						910

<210> 667

<211> 945

<212> DNA

<213> Unknown (H38g516 nucleotide)

<220>

<223> Synthetic construct

<400> 667

atggagaatg	tcactacaat	gaatgagttt	cttctacttg	gcctgactgg	tgttcaggag	60
ctgcagcctt	tcttcttttg	gattttctta	atcattttacc	tgataaactt	gattggaaat	120
ggatctatat	tgggtgatgg	tgttttgga	ccacaactcc	actcccctat	gtattttttt	180
ctgggaaacc	tttcttctct	ggatatttct	tattcttcag	tgacactgcc	caagctgctc	240
gtaaaacctg	tgtgcagtcg	cagggctata	tcttttctag	gctgtatcac	ccagctacac	300
ttcttccact	ttttgggaag	gacagaggcc	attttactgg	ctatcatggc	ctttgaccgt	360
tttgttgcca	tctgcaatcc	tcttcgctac	actgtcatca	tgaacccccca	gggtgtgtatt	420
ctgtttggcag	ctgcggcctg	gctcatcagc	ttctttttacg	ctctgatgca	ttctgtcatg	480
actgcacacc	tgagtttttg	tggctctcag	aaactcaatc	acttcttcta	cgatgtcaag	540
ccgctcttag	aattggcctg	tagtgacaca	ttactcaatc	aatggcttct	ttccattgtc	600
acaggcagca	tatccatggg	agctttcttt	ctgactcttc	tctcctgctt	ctatgtaatt	660
ggcttccctc	tgtttaagaa	caggtcctgc	agaatactcc	acaaggctct	gtccacttgt	720
gcctcccatt	ttatgggtgg	atgtcttttc	tatggacctg	tgggcttcac	atatattcgt	780
cctgtctcag	ccacctccat	gattcaggac	cggataatgg	ccatcatgta	tagcgccgtc	840
accctgtac	tgaatccact	aatctacacc	cttaggaaca	aagaagtgat	gatggctctg	900
aagaaaatct	ttggtaggaa	gttgttttaa	gactggcagc	aacac		945

<210> 668

<211> 966

<212> DNA

<213> Unknown (H38g517 nucleotide)

<220>

<223> Synthetic construct

<400> 668

atgaatgaga	caaatcattc	tcgggtgaca	gaatttgtgt	tgctgggact	gtctagttca	60
agggagctcc	aacctttctt	gtttcttaca	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcactatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttttgc	taccctaaa	240
atgattgcag	actttctggg	tgagcgcaag	actatttctt	ttgatgcctg	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctctc	cactacatga	cagtcatgag	ccgtcgtgta	420
tgtgttggtg	tcgtcctcat	ttcatgggtt	gtgggcttca	tccatactac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagacagttt	tttctgtgac	540
cttctcttag	tgaccaagtt	agcctgcata	gacacttatg	ttgtcagctt	actaatagtt	600
gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttgtctc	ctacactgta	660
atacttgta	cagttaggaa	tcgctcctct	gcaagcatgg	cgaaggcccg	ctccacattg	720
actgctcaca	tcactgtggg	cactttatct	tttggaccat	gcattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	cttgctgtat	tctacaccat	cttcacgctt	840
attttaaacc	ctgtaatcta	cacgctaaga	aacaaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatctgaa	gcctagtcag	gtttctgtag	tcataagaaa	tgttcttttc	960
ctagaa						966

<210> 669

<211> 594

<212> DNA

<213> Unknown (H38g518 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(594)

<223> n = A,T,C or G

<400> 669

gnncggctac	tactacccat	gtactgtttc	ctgnctatac	tgtccgccac	tgacctcggc	60
ctgtccatat	ccactctggg	caccatgctg	agtatattct	ggttcaatgt	gagggaaatc	120
agctttaatg	cctgcttgtc	ccacatgttc	tttattaaat	tcttctactgt	catggaatcc	180

tcagtgtgt	tggccatg	ttttgatcgt	tttgtggc	tctctaate	ccttaggtat	240
gccatgatt	taactgact	cagaatagct	caaattggag	tggcaagtgt	catcagggg	300
ctcctaata	tgacaccaat	ggtagcactt	cttataagac	tttctactg	ccacagccc	360
agtactccac	cactcctact	gctaccaccc	tgatgtgatg	aagttctcat	gcacagacgc	420
cagaatcaac	agtgcagttg	ggctgactgc	catgttctct	actgggtggg	gtagacttac	480
tcttcatect	cctttcttat	gttttgatca	ttaggactgt	ccttancgtt	gcttccccag	540
aagagaggaa	ggaaaccctt	cagtacatgt	gtctcccaca	ttgggggctt	ttgc	594

<210> 670

<211> 939

<212> DNA

<213> Unknown (H38g519 nucleotide)

<220>

<223> Synthetic construct

<400> 670

atgagccctg	agaaccagag	cagcgtgtcc	gagttcctcc	ttctgggect	ccccatccgg	60
ccagagcagc	aggctgtgtt	cttcaccctg	ttcctgggca	tgtacctgac	cacgggtgctg	120
gggaacctgc	tcacatgct	gctcatccag	ctggactctc	accttcacac	ccccatgtac	180
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atgctgatgg	acatgcggac	taagtacaaa	tcgatcctct	atgaggaatg	catttctcag	300
atgtattttt	ttatattttt	tactgacctg	gacagcttcc	ttattacatc	aatggcataat	360
gaccgatatg	ttgccatatg	tcaccctctc	cactacactg	tcacatgag	ggaagagctc	420
tgtgtcttct	tagtggtgtg	atcttggatt	ctgtcttgtg	ccagctccct	ctctcacacc	480
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cttgctgccc	tgctcaagct	gtcctgtctc	gatattcttc	tcaatgagct	ggctcatgttc	600
acagtagggg	tgggtggcat	taccctgcc	ttcatgtgta	tctgggtatc	atatggctac	660
attggggcca	ccatcctgag	ggtcccttca	accaaaggga	tccacaaagc	attgtccaca	720
tgtggctccc	atctctctgt	ggtgtctctc	tattatgggt	caatatttgg	ccagtacctt	780
ttcccagactg	taagcagttc	tattgacaag	gatgtcattg	tggctctcat	gtacacgggtg	840
gtcacaccca	tgttgaaccc	ctttatctac	agccttagga	acagggacat	gaaagaggcc	900
cttgggaaac	tcttcagtag	agcaacattt	ttctcttgg			939

<210> 671

<211> 586

<212> DNA

<213> Unknown (H38g520 nucleotide)

<220>

<223> Synthetic construct

<400> 671

ckactactac	tacctatgta	ttttttctk	kgcaacctgt	cactgttaga	tctctgcctt	60
ccttcaatcc	ctgtgccc	gatgctgcag	aatttattaa	ctcaaaggta	aaccatctct	120
atgtggta	gcattgtcca	gagtttcttt	ctcatattct	ctgggagcac	agaagcctgc	180
ctactccttg	ccatggcctg	tgatcactct	acttccaact	gccaccctcg	gctcaacgat	240
gtggttatga	atcagcctgt	ctgtgtcagg	atgggtgattg	cagcatgggc	agtgggatcc	300
ctaaactcct	tgacaaagaa	tcttttcatt	tacaacttac	acttctgtgg	ccccagtgtc	360
atccctcaact	tctgctgtga	gctgccttca	ctcttccctc	tctcttgtat	tgatccagct	420
gccagtgagg	tccttctctg	tgggtcatgt	acattgctag	gatttgtgac	ttgccgctgg	480
tcctcttttc	ttactctaac	accatctctg	cctcctagcc	atttgktttt	ctgagggtca	540
aggcaaagcc	ttctccacct	gctcctccca	cctcaccgtg	gtgctt		586

<210> 672

<211> 918

<212> DNA

<213> Unknown (H38g521 nucleotide)

<220>

<223> Synthetic construct

<400> 672

atgagccctg	agaaccagag	cagcgtgtcc	gagttccctc	tcctgggcct	ccccatccgg	60
ccagagcagc	aggccgtgtt	cttcgccctg	ttcctgggca	tgtacctgac	cacgggtgctg	120
gggaacctgc	tcatacatgt	gctcaccag	ctagactctc	accttcacac	ccccatgtac	180
ttcttcccta	gccacttggc	cctcactgac	atctcctttt	catctgtcac	tgtccctaag	240
atgctgatga	acatgcagac	tcagcaccta	gccgtctttt	acaagggatg	catttcacag	300
acataatttt	tcataatttt	tgtgacttta	gacagtttcc	ttatcacttc	aatggcatat	360
gacaggatag	tggccatctg	tcatactcta	cattatgcca	ccatcatgac	tcagagccag	420
tgtgtcatgc	tgggtggctgg	gtcctgggtc	atcgcttggt	cgtgtgctct	tttgataacc	480
ctcctcctgg	cccagctttc	cttctgtgct	gaccacatca	tcctcacta	cttctgtgac	540
cttgggtgcc	tgtcaagtt	gtcctgtctc	gacacctccc	tcaatcagtt	agcaatcttt	600
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tgtggatccc	acctctcagt	ggtgactatc	tattatcgga	caattattgg	tctctatttt	780
cttcccccat	ccagcaacac	caatgacaag	aacataattg	cttcagtgat	atacacagca	840
gtcactccca	tgttgaacct	attcattttac	agtctgagaa	ataaagacat	taagggagcc	900
ctaagaaaac	tcttgagt					918

<210> 673

<211> 591

<212> DNA

<213> Unknown (H38g522 nucleotide)

<220>

<223> Synthetic construct

<400> 673

ctactactac	cyatgtat	ttttcttggc	aacctstccc	tcattggacat	ctgcgggcacc	60
tcctcctttg	tgctctcat	cttagacaat	ttcctggaaa	cccagaggac	catttccttc	120
cctggctgtg	ccctgcagat	gtacctgacc	ctggcgctgg	gatcaacgga	gtgcctgctg	180
ctggctgtga	tggcatatga	ccgttatgtg	gctatctgcc	agccgcttag	gtacycagag	240
ctcatgagtg	ggcagacctg	catgcagatg	gcagcgctga	gctggggggac	aggctttgcc	300
aactcactgc	tacagtccat	ccttgtctgg	cacctcccc	tctgtggcca	cgcatcaaac	360
tacttctatg	agatcttggc	agtgtcaaaa	ctggcctgtg	gggacatctc	cctcaatgcg	420
ctggcattaa	tgggtggccac	agccgtcctg	acactggccc	ccctcttggc	catctgctg	480
tcttaccctt	tcactcctgt	tgccatcctt	agggtagcct	ctgctgcagg	ccggtgcaaa	540
gccttctcca	cctgtctcagc	ccaccgcaca	gtgggtgggtg	ttttttatgg	g	591

<210> 674

<211> 985

<212> DNA

<213> Unknown (H38g523 nucleotide)

<220>

<223> Synthetic construct

<400> 674

gttaatggat	ggagtaataa	atcagtgggt	actgaattca	atttggtggg	gctgtctagc	60
tcttgggaac	tccaagtctt	ctttttcttt	atcttctctg	tgttttatgg	agctgcagtg	120
ttgggaaca	tccttatcat	catcacagta	attatagact	ctcatttgca	ttccccaatg	180
tactttcttc	ttagcaatct	ctcttccatc	gatgtgtgtc	aggetacatt	tgccactccc	240
aagatgattg	cagacttcct	caacgaacac	aagaccacca	ctttccaggg	atgcatgtca	300
caaactcttt	tcttgcattg	ttttgggggt	agtgtgagtg	tgcttcttgt	tgccatggcc	360
tatgatagat	acattgctat	atgcaaacct	ctgcactaca	tgaccatcat	gaaccggagg	420
gtgtgaactg	ttctgggtgg	ggtttcctgg	gccattggca	tctcacactc	agccacccac	480
ctggcattca	aagtcaatct	gcctttctgt	ggacccaaca	gggtagacaa	ttttttctgt	540
gacctcctcc	tagtgatcaa	gcttgccctg	ttagacacct	atggttttga	gatactgggtg	600
ctcaactaca	gtggtctgct	ctcaattatg	tgtttctctc	ttttgtcat	ttctgacact	660
atcactcctg	ctactgtgca	tcgccaagcc	tgtgatggga	tgtccaaggc	cctttccact	720
ctgtctgccc	acattactgt	tgtgcttctc	ttctttggcc	cattaatatt	catctatatt	780

tggeccctttg aaagcttccc aattgataaa tttatctctg tggttttttta ctgtcttcac	840
tcctctcctt aaccccatga tttatactct gaggaataaa gatataaagg aagccatgag	900
gaagctaagg agatgacatg tgggttccaa gcagggtttt tagacaacta caaagaagta	960
atacaaattc ctacttttgg gcttt	985

<210> 675

<211> 780

<212> DNA

<213> Unknown (H38g524 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(780)

<223> n = A,T,C or G

<400> 675

atgtatttct tcttgagttt tttgtctctc actgatattt gctttacaac aagcgttgtc	60
cccaagatgc tgatgaactt cctgtcagaa aagaagacca tctcctatgc tgggtgtctg	120
acacagtatg tattttctct atgccttggg caacagtgc agctgccttc tttcgtaant	180
gcctttgacc gctatgttgc cgtctgtgac cctttccact atgtcaccac catgagccac	240
caccactgtg ttctgctggt ggccttctcc tgctcattta cttaccttca ctactcctg	300
cacacacttc tgetgaatcg tctcaccttc tgtgactcca atgttatcca ccactttctc	360
tgtgacctca gccctgtgct gaaattgtcc tgctcttcca tatttgtcaa tgaaattgtg	420
catatgacag aagcacctat tgttttggtg actcgttttc tctgcattgc tttctcttat	480
atacgaatcc tcactacagt tctcaagatt ccctctactt ctgggaaacg caaagccttc	540
tccacctgtg gtttttacct caccgtggtg acgctctttt atggaagcat cttctgtgtc	600
tatttacagc ccccatccac ctacgtgtgc aaggaccacg tggcaacaat tgtttacaca	660
gttttgtcat ccattgctcaa tccttttatc tacagcctga gaaacaaaga cctgaaacag	720
ggcctgagga agcttatgag caagagatcc taggaagcac cctcttgaaa aactcgtaag	780

<210> 676

<211> 576

<212> DNA

<213> Unknown (H38g525 nucleotide)

<220>

<223> Synthetic construct

<400> 676

tactactact accctatgta tttttttctt tgcaacctgt ccttctctgga catgagcttc	60
accacgagca ttgtcccaca gctcctggct aacctctggg gaccacagaa aaccataagc	120
tatggagggt gtgtggtcca gttctatata tcccattggc tgggggcaac cgagtgtgtc	180
ctgctggcca ccatgtccta tgaccgctac gctgccatct gcaggccact ccattacact	240
gtcattatgc atccacagct ttgccttggg ctacgttttg cctcctggct ggggggtctg	300
accaccagca tgggtgggctc cacgctcacc atgctcctac cgctgtgtgtg gaacaattgc	360
atcgaccact tcttttgcca gatgcccctc attatgcaac tggcttgtgt ggataccagc	420
ctcaatgaga tgggagatgt acctggccag ctttgtcttt gttgtcctgc ctctggggct	480
catcctggtc tcttacggcc acattgccgg gccgkgttga agaacaagtc agcagaaggg	540
cggagaaagg cattcaacac ctgttctttc cacgtg	576

<210> 677

<211> 929

<212> DNA

<213> Unknown (H38g526 nucleotide)

<220>

<223> Synthetic construct

<400> 677

atggatataa	gaaacagctc	aataataatc	tgagtttggt	ttgttagaat	tcatcagcac	60
ttgggaactt	gaaattttgt	ttcttaaata	tttttggttg	cctatgcagc	aatcatggca	120
ggaaacctca	ctgcaatcgc	tgtaacctcc	aatcctcccc	tttgctcaac	acctatgtac	180
ttcctccttg	gaaatctctc	ctttctcagt	atgtttatct	ccacagtcac	aatctctaag	240
atggtccaga	cgttctcagg	gagaataaaa	ccacttctct	atggggctgt	atggctcaga	300
tctccacttc	ttaggaggca	gtgagatgac	tcttctcata	tttatggctg	ttgatcagca	360
cattgcaata	tgcagacctc	ttcactgcag	aaccatcacg	actgcaggg	tactcatggc	420
cactcatggg	ctctgtgctg	ctatcacggg	ctgttggttt	tgtgcatact	ataagccaga	480
ttgtttttat	tatcaccttg	cccttctgtg	gccccagtgt	ggtggacaat	ttattttgag	540
accttctctt	agttctgaag	cttgccctgca	ctgagactta	tgatctggag	ttgctggtaa	600
ttgctaaaag	tggacagttg	tctttcatct	gcttcatagt	cttgctcatt	ttctacacta	660
ttattctggt	aactgtgcag	catcgatcct	ctgatgcact	ctccaaggct	ctgtccacac	720
tgtctgctca	tatcactgca	gtcactctat	ttttatgagc	catgtgtcta	catttacact	780
tggccattta	ggagcttttc	agtggataca	tttctttctg	tgttttatct	agttacaccc	840
ttactgaacc	ccattactta	cagtctgaga	tgaaagcatc	tatacatcaa	ctgaggaccc	900
aacacatcat	ctccagacaa	accttctct				929

<210> 678

<211> 595

<212> DNA

<213> Unknown (H38g527 nucleotide)

<220>

<223> Synthetic construct

<400> 678

ctactactac	ccatgtatct	ttttctgtgc	aacctgtccc	tggtggactt	tggttatctc	60
tcagctgtca	ctcccaaggt	gatgggtggg	tttctcacag	gagacaaatt	catattatat	120
aatgcttggt	ccacacaatt	cttcttcttt	gtagccttta	tcactgcaga	aagtttctct	180
ctggcatcaa	tggcctatga	ccgctatgca	gcattgtgta	aacccttgca	ttacaccacc	240
accatgacaa	caaagtgtatg	tgctgcctg	gccataggct	cctacatctg	tggtttctctg	300
aatgcatcca	ttcatactgg	gaacactttc	aggtctctct	tctgtagatc	caatgtagtt	360
gaacactttt	tctgtgatgc	tctctctctc	ttgactctct	catgttcaga	caactacatc	420
agtgagatgg	ttattttttt	ttgtgggtgg	attcaatgac	ctcttttcta	tcctggtaat	480
cttgatctcc	tacttatatta	tatttatcac	catcatgaag	atgcgctcac	ctgaaggacg	540
ccagaaggcc	ttttctactt	gtgcttccca	ccttactgca	gtttccatct	tttat	595

<210> 679

<211> 945

<212> DNA

<213> Unknown (H38g528 nucleotide)

<220>

<223> Synthetic construct

<400> 679

atggaggcca	tgaaactatt	aatcaatct	caagtgtcag	aattcatttt	gctgggactg	60
accagctccc	aggatgtaga	gtttcttctc	tttgccctct	tctcggttat	ctatgtgggc	120
acagttttgg	gtaaccttct	tattatagtc	acagtgttta	acacccttaa	cctgaatact	180
cccatgtatt	ttctccttgg	taatctctct	ttttagata	tgacccttgc	ttcttttgcc	240
acccctaagg	tgattctgaa	cttggttaaaa	aagcagaagg	taatttcttt	tgctgggtgc	300
ttcactcaga	tatttctcct	tcacttactg	ggtggggttg	aaatggtact	gttggtctcc	360
atggcttttg	acagatatgt	ggccatttgg	aagccctac	actacatgac	catcatgaac	420
aagaagggtat	gtgttttgct	tgtagtgacc	tcatggctct	tgggtctcct	tcactcaggg	480
tttcagatac	catttgctgt	gaacttgccc	ttttgtgggc	ccaatgtggt	agacagcatt	540
ttttgtgacc	tcccttgggt	tactaagctt	gcctgtatag	acatatattt	tgtacaggta	600
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tacatttggc	ccttcggcaa	ccactctgta	gataagttcc	ttgctgtggt	ttataaccatc	840
atcactccta	tcttgaatcc	aattatctat	actctgagaa	acaaagaaat	gaagatatcc	900

atgaaaaaac tctggagagc ttttgtgaat tctagagaag atact

945

<210> 680

<211> 951

<212> DNA

<213> Unknown (H38g529 nucleotide).

<220>

<223> Synthetic construct

<400> 680

atggagcccc	aaaatacctc	cactgtgact	aactttcagc	tgtaggatt	ccagaacctt	60
cttgaatggc	aggeccctgt	ctttgtcatt	ttcctgtctc	tctactgcct	gaccattata	120
gggaatgttg	tcatcatcac	cgtggtgagc	cagggcctgc	gactgcactc	ccctatgtac	180
atgttctctc	agcatctctc	ctttctggag	gtctgtgtaca	cgccaccac	tgtgccccct	240
ctcctagcca	acctgctgtc	ctggggccaa	gccatctcct	tctctgcctg	catggcacag	300
ctctacttct	tctgtattct	cggcgccacc	gagtgtcttc	tcttggcctt	catggcctat	360
gaccgttacc	tggccatctg	cagccaccct	cgtaccctt	ttctcatgca	tctgtgggcta	420
tgtgccagg	tggtggtggt	ctcatggtgc	acaggggtca	gcacaggctt	tctgcattcc	480
atgatgattt	ccagggttga	cttctgtggg	cgcaatcaga	ttaaccattt	cttctgcgac	540
ctcccgccac	tcatgcagct	ctcctgttcc	agagtttata	tcaccgaggt	gaccatcttc	600
atcctgtcaa	ttgccgtgct	gtgcatttgt	ttttttctga	cactggggcc	ctatgttttc	660
attgtgtcct	ccatattgag	aatcccttcc	acctctggcc	ggagaaagac	cttttccaca	720
tgtggctccc	acctggtgtg	tgctactctc	tactacggga	ccatgatctc	catgtatgtg	780
tgtcccagtc	cccacctgtt	gcctgaaatc	aacaagatca	tttctgtctt	ctacactgtg	840
gtcacaccac	tgctgaacct	agttatctac	agcttgagga	acaaagactt	caaagaagct	900
gttagaaagg	tcatgagaag	gaaatgtggt	attctatgga	gtacaagtaa	a	951

<210> 681

<211> 1005

<212> DNA

<213> Unknown (H38g530 nucleotide)

<220>

<223> Synthetic construct

<400> 681

tctacagacc	cacagaatct	aacagatgtc	tctatatctc	tctcctaga	agctcagagg	60
atccagaatg	gcagccggtc	ctcactgggc	tgtgcctgtc	catgtgcctg	gtcacgggtgc	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	atccccatgt	180
acttcttctc	ctccaacctg	tccctgcctg	acatcggttt	cacctccacc	acggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcattct	ctacgcaggc	tgccctgactc	300
agatgtctct	ctttgccatt	tttggaggca	tgggaagagag	acatgtctct	gagtgtgata	360
gcctatgagc	ggtttgtagc	catctgtcac	cctctatatc	attcagccat	catgaacca	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttt	ctcagtcttt	tagacgcccc	480
gctgcacaac	ttgattgcct	tacaaaggac	ctgcttcaag	gatgtggaaa	ttcctaattt	540
cttctgtgac	ccttctcaac	tccccatctt	gcataattgtg	gcaccttcac	caataacata	600
atcatgtatt	tccctgccgc	catatttggt	tttcttccca	tctcggggac	gcttttctct	660
tacgataaaa	ttgttttctc	cattctaagg	gtttcatcat	caggtgggaa	gtataaggcc	720
ttctccacct	gtgggtctca	cctgtcagtt	gtttgctgat	tttatggaac	aggcattgga	780
ggctacctca	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcagtggc	ctcagtgatg	840
tacacgggtg	tcatccccat	gccgaacccc	ttcatctaca	gcctgagaaa	cagggatattg	900
aaaagtgtcc	tgcagcggcc	acatggcagc	acgatctcat	ctcaatatct	tcttatttgt	960
tccattcctt	ttgtagtgtg	ggttaaaaaa	ggcagcaagg	tcaaa		1005

<210> 682

<211> 990

<212> DNA

<213> Unknown (H38g531 nucleotide)

<220>

<223> Synthetic construct

<400> 682

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gatccagaac	tgacagccgt	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgaggaacc	tgctcagcac	cctggctgtc	agctctgact	ccccctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	catagtctcc	240
aagatgactg	tgacatgca	gtctcatagc	agagtcattc	ctcatgcggg	ctgcctgaca	300
cagatgtctt	tcttggctct	ttttgcatgt	atagaagaca	tgttcctgac	tgtgatggcc	360
tatgacagat	ttgtagccat	ctgtcgccct	ctttactacc	cagtcattcat	aaatcctcac	420
ctctgtgtct	tcttctgttt	ggtgtccttt	ttccttagcc	tggtggattc	ccagctgcac	480
agttggattg	tgtgacaatt	caccttctcc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcta	ccttgccctgt	tctgacagca	tcattcaatag	catattcata	600
tattttgata	gtactatgtt	tggttttctt	cccatttcaa	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttcacc	720
acctgtggct	ctcacctagc	agttgtttgc	ttatttgatg	gaacaggcat	tggcatgtac	780
ctgacttcag	ctgtggcacc	acccccagg	aatgggtgtg	tggcgctcagt	gatgtacgct	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaaac	900
accctgtgga	ggctgcgcag	cagaagagtg	gaatctcatg	atctgttcca	tccttttttt	960
gtgtgggtga	gaaagggcaa	ccacattaaa				990

<210> 683

<211> 1005

<212> DNA

<213> Unknown (H38g532 nucleotide)

<220>

<223> Synthetic construct

<400> 683

tctacagacc	cacaaaatct	aatagatgtc	tttgatttcc	tcctcctgga	acctcagagg	60
atccagaacg	gcagctgggc	cttgctgggc	tgttcctgtc	catgtgcctg	gtcacgggtg	120
tggggaaacct	gtcatcctc	ctggcggcca	gccctgactc	ccacctccac	acccccatgt	180
acttcttctc	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
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gtctatgacc	ggtttgtagc	catctgtcac	cctctatatc	attcagccgt	catgaacccc	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttc	tcagtctttt	agacgcccag	480
ctgcacaact	tgattgcctt	acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	540
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tacactgtgg	tcacccccat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggatact	900
aaaagtgtcc	tgcgggggcc	gcacggcagc	acggtgtaat	cttgatatct	tcttatctgt	960
tccattcctt	ttgtagtgtg	ggttaaaaaa	ggcagaaagg	tcaaa		1005

<210> 684

<211> 960

<212> DNA

<213> Unknown (H38g533 nucleotide)

<220>

<223> Synthetic construct

<400> 684

cacacagagc	cacggcatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgacagcctg	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacagtg	120
ctaaggaacc	tgctcatcat	cctggctgtg	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtgctgggct	gacatcagtt	tcacctcggc	cacgggttccc	240

aagatgacgg	tggacatgca	gtcgcatagc	agagtcacat	cttatgcggg	ctgcctgaca	300
cggatgtctt	tcttcgtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
taggactgct	ttgtagccat	ctgtcgccct	ctgcactacg	cagtcacgt	gaatccctcac	420
ctctgtgtct	tcttagtttt	ggtgtccctt	ttccttagcc	tggtggattc	ccagctgcac	480
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ctgacttcag	ctgtggcacc	acccccagc	aatggtgtgg	tggcatcagt	gaagtacacc	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacagga	cattcaaagc	900
accctgtgga	ggctgtgcag	cagaacagtt	aaatctcttg	atctgttcca	ttctttttct	960

<210> 685

<211> 982

<212> DNA

<213> Unknown (H38g534 nucleotide)

<220>

<223> Synthetic construct

<400> 685

atttcccttc	ttttctgggt	ccttctcttg	gtcatttcta	gagttttggt	agccatggca	60
tgaggaaaca	gcactgaagt	gactgaattc	tgtcttctgg	gatttggtgc	ctagcaagag	120
ttttgggtga	tcctcttcac	tatattcctt	ctcatctatg	tgacctccat	aatgggtaat	180
agtggataaa	tcttactcat	caacacagat	tccagatttc	aaacacccat	gtactttttt	240
ctacaacatt	tggcttttgt	tgatatctgt	tacacttctg	ctatcactcc	caagatgctc	300
caaagcttca	cggaaagaaa	gaatttgata	tcattttggg	gctgcatgat	acaattattg	360
gtttatgcaa	catttgcaac	cagtgcactg	tatctcctgg	ctatgatagc	agtggaccat	420
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gccaccatcc	tgaatgtgc	ttctagtgc	ggaaggaaaa	aatccttctc	aacatgtgcc	780
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tcccatgttg	aatcctttta	tctatagctt	gagaaataag	gaagtaaaag	aagcttttaa	960
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<210> 686

<211> 927

<212> DNA

<213> Unknown (H38g535 nucleotide)

<220>

<223> Synthetic construct

<400> 686

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catgagtttt	ggtgtatcct	cttcattgta	ttccttctca	tctatgtgac	ctccataatg	120
ggtaaatagtg	gaataatctt	actcatcaac	acagattcca	gatttcaaac	actcacgtac	180
ttttttctac	aacatttggc	ttttgttgat	atctgttaca	cttctgctat	cactcccaag	240
atgctccaaa	gcttcacaga	agaaaagaat	ttgatgttat	ttcagggtctg	tgtgatataa	300
ttcttagttt	atgcaacatt	tgcaaccagt	gactgttate	tcctggctat	gatggcagtg	360
gatccttatg	ttgccatctg	taagccctct	cactatactg	taatcatgtc	ccgaacagtc	420
tgcattccgtt	tggtagctgg	ttcatatact	atgggctcaa	taaagtgcctc	tgtacaaaca	480
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gttcccccta	ttcttgcctt	ttcatgctcc	aatggtgaca	tcaacatcat	gctacttggt	600
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atcatggcca	ccatcctgaa	aatgtcttct	agtgcaggaa	ggaaaaaatc	cttctcaaca	720

tgtgcttccc	acctgaccgc	agtcaccatt	ttctatggga	cactctctta	catgtatttg	780
cagtctcatt	ctaataattc	ccaggaaaat	atgaaagtgg	cctttatatt	ttatggcaca	840
gttattccca	tgttaaatcc	tttaatctat	agcttgagaa	ataaggaagt	aaaagaagct	900
ttaaaagtga	tagggaaaaa	gttatttt				927

<210> 687

<211> 894

<212> DNA

<213> Unknown (H38g536 nucleotide)

<220>

<223> Synthetic construct

<400> 687

atgggtcgag	gaaacagcac	tgaagtgact	gaattccatc	ttctgggatt	tggtgtccaa	60
cacgaatttc	agcatgtcct	tttcattgta	cttcttctta	tctatgtgac	ctccctgata	120
ggaaatattg	gaatgatctt	actcatcaag	accgattcca	gacttcaaac	acccatgtac	180
ttttttccac	aacatttggc	ttttgttgat	atctgttata	cttctgctat	cactcccaag	240
atgctccaaa	gcttcacaga	agaaaataat	ttgataacat	ttcggggctg	tgtgatacaa	300
ttcttagttt	atgcaacatt	tgcaaccagt	gactgttacc	tcctagctat	tatggcaatg	360
tattgttatg	ttgccatctg	taagcccctt	cgctatccca	tgatcatgtc	ccaaacagtc	420
tacatccaac	tcgtagctgg	ctcatatatt	ataggctcaa	taaatgcctc	tgtacataca	480
ggttttacat	tttcactgtc	cttctgcaag	tctaataaaa	tcaatcactt	tttctgtgat	540
ggctctccca	ttcttgccct	ttcatgtctc	aacattgaca	tcaacatcat	tctagatggt	600
gtctttgtgg	gatttgactt	gatgttcact	gagttgggtc	tcactctttc	ctacatctac	660
attatgggtca	ccatcctgaa	gatgtcttct	actgctggga	ggaaaaaatc	cttctccaca	720
tgtgcctccc	acctgacagc	agtaaccatt	ttctatggga	cactctctta	catgtactta	780
cagcctcagt	ctaataattc	tcaggagaat	atgaaagtag	cctctatatt	ttatggcact	840
gttattccca	tgttgaatcc	tttaatctat	agcttgagaa	ataaggaagg	aaaa	894

<210> 688

<211> 444

<212> DNA

<213> Unknown (H38g537 nucleotide)

<220>

<223> Synthetic construct

<400> 688

acgtacgacg	gcgcgagggg	ggctctctgta	ttgtttctta	caatacatgc	aaatctacaa	60
tgatgtcaat	aaaaattcaa	ttaaaaatac	atgtagtaaa	aatagttgct	aatctatgct	120
ggagtttact	tgaatgtcac	tatgtctgatc	gtcaccttca	agtacacaca	tatcttccat	180
catcctgagc	ttgccctctg	ctatgtgtct	ttttccgcag	ttgtcttcca	cctgacagct	240
gtcaccattt	tctttggagc	tctctcttac	atggacttac	aacctgaatc	tactgtgttt	300
caagagcaag	aaaagccagc	atccatattt	tgtggcatta	tgactctcgt	gttaaacttc	360
cttatctact	gcctgtgaaa	ttaggaagta	aaagaagctc	tacagttaac	aaggaaaaag	420
tattaataca	tgtagactga	gggt				444

<210> 689

<211> 888

<212> DNA

<213> Unknown (H38g538 nucleotide)

<220>

<223> Synthetic construct

<400> 689

atgctagtgt	cacaacagga	gcagcctctt	ctgtttggca	tcttccttgg	catgtacctg	60
gtcaccatgg	tggggaacct	gtcattatc	ctggccatca	gctctgacce	acacctccat	120
actcccatgt	acttctttct	ggccaacctg	tcattaactg	atgcctgttt	cacttctgcc	180
tccatcccca	aaatgctggc	caacattcat	accagagctc	agatcatctc	gtattctggg	240

tgtcttgcac	agctatat	ttt	ggtggcc	ttgacaactg	cctgctggct	300
gtgatggcat	atgaccgcta	tgtggccatc	tgccaaccac	tccattacag	cacatctatg	360
agtccccagc	tctgtgcact	aatgctgggt	gtgtgctggg	tgctaaccac	ctgtcctgcn	420
ctgatgcaca	cactgttgct	gacccgcgtg	gctttctgtg	cccagaaagc	catccctcat	480
ttctattgtg	atcctagtgc	tctcctgaag	cttgctgct	cagataccca	tgtaaacgag	540
ctgatgatca	tcaccatggg	cttgctgttc	ctcactgttc	ccctcctgct	gatcgtcttc	600
tcctatgtcc	gcattttctg	ggctgtgttt	gtcatctcat	ctcctggagg	gagatggaag	660
gccttctcta	cctgtgggtc	tcatctcacg	gtggttctgc	tcttctatgg	gtctcttatg	720
gggtgtgtatt	tacttctctc	atcaacttac	tctacagaga	gggaaagtag	ggctgctgtt	780
ctctatatgg	tgattattcc	cacgctaaac	ccattcattt	atagcttgag	gaacagagac	840
atgaaggagg	ctttgggtaa	actttttgtc	agtggaaaaa	cattcttt		888

<210> 690

<211> 939

<212> DNA

<213> Unknown (H38g539 nucleotide)

<220>

<223> Synthetic construct

<400> 690

atgaagaggg	agaatcagag	cagtgtgtct	gagttcctcc	tcctggacct	ccccatctgg	60
ccagagcagc	aggctgtgtt	cttcaccctg	ttcttgggca	tgtacctgat	cacgggtgctg	120
gggaacctgc	tcacatcct	gtcactcgg	ctggactctc	accttcacac	ccccatgttc	180
ttcttctca	gccacttggc	tctcactgac	atctcccttt	catctgtcac	tgteccaaag	240
atgttattaa	gcatgcaaac	tcaggatcaa	tccattcttt	atgcagggtg	tgtaactcag	300
atgtattttt	tcataatttt	cactgatcta	gacaatttcc	ttctcacttc	aatggcatac	360
gatcggtatg	tggccatctg	tcacccctc	cgctacacca	ctatcatgaa	agagggactg	420
tgtaacttac	tagtcaactg	gtcctggatc	ctctcctgta	ccaatgccct	gtctcacact	480
ctcctcctgg	cccagctgtc	cttttgtgct	gacaacacca	tccccattt	cttctgtgat	540
cttgttgccc	tactcaagct	ctcatgtctc	gacatctccc	tcaatgagct	ggtcattttc	600
acagtgggac	aggcagtcac	tactctacca	ctaataagca	tcttgatctc	ttatggccac	660
attggggta	ccatcctcaa	ggctccatct	actaagggca	tcttcaaagc	tttgtccacc	720
tgtggctctc	acctctctgt	gggtgtctctg	tattatggca	caattattgg	actgtatttt	780
ctccctcat	ccagtgcctc	cagtgacaag	gacgtaattg	cctctgtgat	gtacacgggtg	840
atcaccccat	tgctgaatcc	cttcatttat	agcctaagga	acagggacat	aaagggagcc	900
ctggagagac	tcttcaacag	ggcaacagtc	ttatctcaa			939

<210> 691

<211> 933

<212> DNA

<213> Unknown (H38g540 nucleotide)

<220>

<223> Synthetic construct

<400> 691

atggaaaacc	aatccagcat	ttctgaattt	ttctcccgag	gaatatcagc	gcctccagag	60
caacagcagt	ccctcttcgg	aattttcctg	tgtatgtatc	ttgtcacctt	gactgggaac	120
ctgctcatca	tcctggccat	tggtcttgac	ctgcacctcc	acacccccat	gtactttttc	180
ttggccaacc	tgtcttttgt	tgacatgggt	ttaacgtcct	ccacagttac	caagatgctg	240
gtgaatatac	agactcggca	tcacaccatc	tcctatacgg	gttgccctcac	gcaaagtgtat	300
ttctttctga	tgtttggtga	tctagacagc	ttcttctgga	ctgccatggc	gtatgaccgc	360
tatgtggcca	tttgccaccc	cctctgctac	tcacagtcac	tgaggcccca	agtcgtgtgc	420
ctaattgctg	cattgtgctg	ggctcctcacc	aatatcgttg	ccctgactca	cacgttccctc	480
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cctgtcctga	agctgtcatg	ttctgacacc	cacatcaacg	agatgatggg	ttttgtcttg	600
ggaggcaccg	tactcatcgt	ccccttttta	tgcattgtca	cctcctacat	ccacattgtg	660
ccagctatcc	tgagggtccg	aacccgtggg	gggggtgggca	aggccttttc	cacctgcagt	720
tcccacctct	gcgttgtttg	tgtgttctat	gggacctctc	tcagtgccta	cctgtgtcct	780
ccctccattg	cctctgaaga	gaaggacatt	gcagcagctg	caatgtacac	catagtgtact	840

cccatgttga acccctttat ctatagccta aggaacaagg acatgaaggg ggccctaaag 900
aggctcttca gtcacaggag tattgtttcc tct 933

<210> 692

<211> 945

<212> DNA

<213> Unknown (H38g541 nucleotide)

<220>

<223> Synthetic construct

<400> 692

atgggaggca agcagccctg ggtcacagaa ttcactcttg tgggattcca ggttggtcca	60
gcactggcga ttctctcttg tggactcttc tctgtcttct atacactcac cctgctgggg	120
aatgggggtca tctttgggat tatctgcttg gactctaagc ttcacacacc catgtacttc	180
ttcctctcac acctggccat cattgacatg tcctatgctt ccaacaatgt tcccaagatg	240
ttggcaaacc taatgaacca gaaaagcacc atctcctttg ttccatgcat aatgcagact	300
tttttgtatt tggcttttgc tgttacagag tgcttgattt tgggtggtgat gtcctatgat	360
aggatgtgg ccactctgcca ccctttccag tacactgtca tcatgagctg gagagtgtgc	420
acgatcctgg cctcaacatg ctggataatt agctttctca tggctctggt ccatataact	480
catattctga ggccgccttt ttgtggccca caaaagatca accactttat ctgtcaaadc	540
atgtccgtat tcaaattggc ctgtgctggc cctaggctca accaggtggt cctatatgcg	600
ggttctgcgt tcatcgtaga ggggcccgtc tgcttgagc tggctccaa cttgcacatc	660
ctgtcgcgcc atcttgagga tccagtaatg gggaggggcg cagaccgact tactcttct	720
gctccttccc acctttgcat ggtgggactc ctttttggca gcaccatggt catgtacatg	780
gcccccaagt cccgccaccc tgaggagcag cagaaggctc ttccctgtt ttacagcctt	840
ttcaaccoga tgctgaaccc cttgatctac agcctgagga acgcagaggt caaggggtgcc	900
ctgaaaagag tgttgtggaa acagagatca aagtgagggg tgcca	945

<210> 693

<211> 575

<212> DNA

<213> Unknown (H38g542 nucleotide)

<220>

<223> Synthetic construct

<400> 693

ttgaagggttt attaaaaggc aatatgagtg cagaagcaag gtaagttttt tgtaataatt	60
ttttgttaat aatgtgaaat gtaaggaaaa aatatacaac tttaagtttc tgactgtcct	120
gctagaaact agttttgccc tgcagcgacc cctctgtggg aatctcattg atgacaagtg	180
aaattctgga agtgctaaag ttagtttgct caagttcact gctcatggat atgatcatga	240
tgggtgggtca acattcttct cttgccaatt ccaatgtact tatttataac tatgtgctct	300
gtaatcttat ttttaaagag atcttatggt aatcttccaa gggagtttag tttctgcatt	360
tcctggatat atgggttttc gtatattgcc tggctataat ttttagagct ctttacaac	420
tcacaaagat atggggctca acaatgaatg aaattgtacg gtggatgtat tagtattaaa	480
cgtattagta ttaaattgtg tgacataaac tggctcttaa atataatcac aaattagtat	540
ctacaatgct tcaagcattg ttgtcctttt tgaaa	575

<210> 694

<211> 942

<212> DNA

<213> Unknown (H38g543 nucleotide)

<220>

<223> Synthetic construct

<400> 694

atggctgaag aaaatcatat catgaaaaat gagtttatcc tcacaggatt tacagatcac	60
cctgagctga agactctgct gtttgggtg ttctttggca tctatctgat caccgtgggtg	120
gggaatatta gtttgggtggc actgatattt acacaccgtc ggcttcacac accaatgtac	180

atctttctgg	gaaatctggc	tcttggtgat	tcttgctgtg	cctgtgctat	tacccccaaa	240
atgttagaga	acttcttttc	tgagaacaaa	aggatttccc	tctatgaatg	tgagtagacag	300
ttttattttc	tttgcaactgt	ggaaactgca	gactgctttc	ttctggcagc	aatggcctat	360
gaccgctatg	tggccatata	caaccactg	cagtaccaca	tcatgatgtc	caagaaactc	420
tgcatcaga	tgaccacagg	ggccttcata	gctggaaacc	tgcatcccat	gattcatgta	480
gggcttgtat	ttaggttagt	ttctgtgga	tcgaatcaca	tcaaccactt	ttactgtgat	540
attcttccct	tgtatagact	ctcttggtt	gacccctata	tcaatgaact	ggttctattc	600
atcttctcag	gttcagttca	agtctttacc	ataggttagt	tcttaataatc	ttatctctat	660
attcttctta	ctattttcaa	aatgaaatcc	aaagagggaa	gggccaaagc	ttttctacc	720
tgtgcacccc	actttttgtc	agtttcatta	ttctatggat	ctcttttctt	catgtacggt	780
agaccaaatt	tgcttgaaga	aggggataaa	gatataccag	ctgcaatttt	atttacaata	840
gtagttccct	tactaaatcc	tttcatttat	agcctgagaa	ataggggaagt	aataagtgtc	900
ttaagaaaaa	ttctgatgaa	agaaataatc	tcaagaagat	gg		942

<210> 695

<211> 948

<212> DNA

<213> Unknown (H38g544 nucleotide)

<220>

<223> Synthetic construct

<400> 695

atgcaaggag	aaaacttcac	catttgaggc	atctttttct	tggagggatt	ttcccagtag	60
ccagggttag	aagtggttct	cttcgtcttc	agccttgtaa	tgtatctgac	aacgctcttg	120
ggcaacagca	ctcttatttt	gatcactatc	ctagattcac	gccttaaaac	ccccatgtac	180
ttattccttg	gaaatctctc	tttcatggat	atttggtaca	catctgcctc	tgttcctact	240
ttgtgggtga	acttgcgtgc	atcccagaaa	accattatct	ttctgggtg	tgctgtacag	300
atgtatctgt	cccttgccat	gggtccaca	gagtgtgtgc	tcctggcgt	gatggcatat	360
gaccgttatg	tggccatttg	taaccgcgtg	agatactcca	tcatcatgaa	caggtgcgtc	420
tgtgcacgga	tggccacggg	ctcctgggtg	acgggttgcc	tgaccgctct	gctggaaacc	480
agttttgccc	tgcatatacc	cctctgtggg	aatctcatcg	atcacttcac	gtgtgaaatt	540
ctggcgggtg	taaagtttag	ttgcacaagt	tcactgctca	tgaacaccat	catgctgggtg	600
gtcagcattc	tcctcttgcc	aattccaatg	ctcttagttt	gcattcttta	catcttcate	660
ctttccacta	ttctgagaat	cacctcagaa	gagggagaaa	acaaggcttt	ttctacctgt	720
ggtgcccat	tgactgtggt	gattttgtat	tatggggctg	ccctctctat	gtacctaaag	780
ccttcttcat	caaatgcaca	aaaaatagac	aaaatcatct	cgttgcttta	cggagtgcct	840
accctatgt	tgaaccccat	aatttacagt	ttaagaaaca	aggaagtcaa	agatgctatg	900
aagaaattgc	tgggcaaaat	aacattgcat	caaacacacg	aacatctc		948

<210> 696

<211> 936

<212> DNA

<213> Unknown (H38g545 nucleotide)

<220>

<223> Synthetic construct

<400> 696

atgatgggta	gaaggaataa	cacaaatgtg	gctgacttca	tccttatggg	actgacactt	60
tctgaagaga	tccagatggc	tctgtttatg	ctatttctcc	tgatatacct	aattactatg	120
ctgggggaatg	tggggatgat	attgataatc	cgcttgacc	tccagcttca	cactcccatg	180
tattttttcc	ttactcacct	gtcatttatt	gacctcagtt	actcaactgt	cgtcacacct	240
aaaaccttag	cgaacttact	gacttccaac	tatatttcc	ttacgggctg	ctttgcccag	300
atgttctttt	ttgccttctt	gggtactgct	gaatgttacc	ttctctcctc	aatggcccat	360
gatcgctatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgtc	caaaaggctc	420
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gtttccatga	gcagattgca	tttctacgac	tcaaacgtaa	ttcatcactt	tttctgtgac	540
acttccccaa	ttttagctct	gtcctgcact	gatacataca	acaccgaaat	cctgatattc	600
attattgttg	gttccaccct	gatgggtgcc	cttttcacaa	tatctgcate	ctatgtgttc	660
attctcttta	ccatcctgaa	aattaattcc	acttcaggaa	agcagaaagc	tttctctact	720

tgcgtctctc atctcttggg agtcaccatc ttttatagca ctctgatttt tacttattta	780
aaaccaagaa agtcttattc cttgggaaga gatcaagtgg cttctgtttt ttatactatt	840
gtgattcccc tgctgaatcc actcatttat agtcttagaa acaaagaggt gaaaaatgct	900
gtcatcagag tcatgcagag aagacaggac tccagg	936

<210> 697

<211> 634

<212> DNA

<213> Unknown (H38g546 nucleotide)

<220>

<223> Synthetic construct

<400> 697

acaatgttct ataaaaattag tgctttgttc taatgttttg tatcacttta ttttagtaaa	60
aattgagtaa gcaaaaaata tactgggttc tgactatctt tggcttttta gaggcattca	120
ttgccatgaa taaattataa aagttatata gttctctaata atgtttatat ttataaatat	180
gaatatttag ttctctaata tgtttatatt ttataaatat aatatttctg tacattattt	240
cctaaaatgt atttttttct ttgtatctg ttgtcttttag ctattaattt ttgatagttt	300
ttctacccat cctcctcttc ccctacttta agaggcagat atctgtgcaa attcctagcc	360
atgctacact aatactacag ctccctgatg acacttttac attatcctca acttttgcct	420
ctcttattga ccctctgtat catcgatgct ctatggaaga ctgttcctta tgtacttaat	480
gctcagaaaa ttctcttgac acagacagga tggcctctgt cttctacaca gtagtcattc	540
ccatgttaaa ccattgatc tggagcccca ggaacaagga tgtgacattg ccctgaggaa	600
agtcatggct aatagaaaac aggcattatt ttgc	634

<210> 698

<211> 682

<212> DNA

<213> Unknown (H38g547 nucleotide)

<220>

<223> Synthetic construct

<400> 698

tgcatgttct cctttttattt taattttttac cattttttttt cccacatgaa aggtcttgca	60
gtcacttaga aatgctgaga taaattgact ggtataaagt aaggatatctg attaatgaaa	120
tttactctaa aactaattgg cctttttcatg gactataaga ctatgcacaa ccacttcgta	180
ctcaaacatg caattctctt tccaatgttg tatgaccag taccagctc ttcaaagcac	240
attttttttt cttggtagat ctccaggtctt ccttctgttg ctgatggcct agacaactat	300
agggccatct gaaagtcctt gcagtatattg gttgtcatga agcaatggct gtgtgttggtg	360
ctgctgggtg tgccctgggc tggaggattt ttgcacacag taattcaact tggccttatt	420
catgggctcc catcttatga cccaatgct attggctggt ttgtctgtga catggacccc	480
ttaatgaagc ttgtctgtga ctatacactc aacagatttg tctattttgc aggtcattgac	540
ttaaatacta ggttttatat atttcgttta tattcagact ggactgtttc cttttgggtga	600
tttgactttg gtatcctttt gtaatttttt ccctagagga catgattcta taaatcttgt	660
tatacatagt tattatccct gt	682

<210> 699

<211> 897

<212> DNA

<213> Unknown (H38g548 nucleotide)

<220>

<223> Synthetic construct

<400> 699

atggagccaa ggaaaaatgt gactgacttt gtcctcttgg gcttcacaca gaatccaaag	60
gagcagaaag tactttttgt tatgttcttg ctcttctaca ttttgaccat ggtgggcaac	120
ctgctcattg tagtgaccgt aactgtcagt gagaccctgg gctcaccaat gtccttcttt	180
cttgctggct taacatttat agatatcatt tattcttcat ccatttcccc cagattgatt	240

tcagacttgt	tctttgggaa	taattccata	tccttccaat	ctttcatggc	ccagctcttt	300
atcgagcacc	tttttggtgg	gtcagaggtc	tttctcctgt	tggtgatggc	ctatgaccgc	360
tatgtggcca	tctgtaagcc	cttg cattat	ttggttatca	tgagacaatg	gggtgtgtgt	420
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cccttattga	aactggcctg	cactgacacc	catgttattg	gcctcttagt	gggtggccaat	600
ggaggactyt	cttg cactat	tgcgtttctg	ctcttactca	tctcttatgg	tgatcatcctg	660
cactctctaa	agaaacttag	tcagaaaagg	aggcaaaaag	cccactcaac	ctgcagtcc	720
cacatcactg	tggttgtctt	cttctttgtt	ccttgtattt	ttatgtgtgc	tagacctgct	780
aggaccttct	ccattgacaa	atcagtgagt	gtgttttata	cagtcataac	cccaatgctg	840
aacccttaa	tctacactct	gagaaattct	gagatgacaa	gtgctatgaa	gaagctt	897

<210> 700

<211> 945

<212> DNA

<213> Unknown (H38g549 nucleotide)

<220>

<223> Synthetic construct

<400> 700

atgagtcctg	atgggaacca	cagtagtgat	ccaacagagt	tcgtcctggc	agggtccca	60
aatctcaaca	gcgcaagagt	ggaattattt	tctgtgtttc	ttcttgtcta	tctcctgaat	120
ctgacaggca	atgtgttgat	tgtgggggtg	gtaagggtg	atactcgact	acagaccctt	180
atgtacttct	ttctgggtaa	cctgtcctgc	ctagagatac	tgctcacttc	tgatcatcatt	240
ccaaagatgc	tgagcaattt	cctctcaagg	caacacacta	tttcttttgc	tgcatgtatc	300
acccaattct	atttctactt	ctttctcggg	gcctccgagt	tcttactgtt	ggctgtcatg	360
tctgcggatc	gctacctggc	catctgtcat	cctctgcgct	accccttgct	catgagtggg	420
gctgtgtgct	ttcgtgtggc	cttggcctgc	tggttggggg	gactcgtccc	tggtgttggg	480
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tacggcctca	ttgtgtctgg	agtcctgagc	atcccctctg	cttcaggccg	tcagaaggcc	720
ttctctacct	gtacctccca	cttgatagtg	gtgacctctt	tctatggaa	tgccattttt	780
ctctatgtgc	ggccatcgca	gagtggttct	gtggacacta	actgggcagt	gacagtaata	840
acgacatttg	tgacaccact	gttgaatcca	ttcatctatg	ccttacgtaa	tgagcaagtc	900
aaggaagctt	tgaaggacat	gtttaggaag	gtagtggcag	gcgtt		945

<210> 701

<211> 772

<212> DNA

<213> Unknown (H38g550 nucleotide)

<220>

<223> Synthetic construct

<400> 701

gtactctgtg	tcataattttg	taaatgaaat	catcatataa	gtttattgag	tttttttgag	60
tacctaataga	cttaataaaaa	aaaatatggg	agcatatgta	gtaccatgct	tgtatcaata	120
cggataaagt	atctggaagt	ctttgctgag	aatctttttg	tgctgctgag	attattccac	180
tgatgtggat	gggtccatggc	tggttatgtga	ccgtctgtac	tacatgacca	tcgtgaatca	240
atataggtgt	agccatctca	ctggaatggc	atgtactgaa	agctttatcc	aggcacagtt	300
tagatcctct	ccccagtctg	acttcctttc	tatgacccca	atgtcatagc	tcattcatgt	360
gtgacttaaa	cacttttttg	aaactcctct	gcatgggtac	tactaataca	attggtttct	420
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aagtggccat	ccatgtgtact	ttgaaaactc	acagcttggg	ggaaagatgc	taaagttctc	540
tacctgcac	tctcacacca	ccatgggtcat	cttatctttg	agttctgtat	atctgtgtat	600
ctgtgcccag	tgacccttcc	ccaatcaata	aagcaatggc	tgtgtttcat	accgtgataa	660
atcctatgtt	aaaaccttta	gtctaaccct	cagaaatgca	gagggtgaaa	gtgctttgag	720
aaaggtctgg	gtcaaaaagat	gacctgaaga	gagaaataat	ctaaacataa	ga	772

<210> 702
<211> 954
<212> DNA
<213> Unknown (H38g551 nucleotide)

<220>
<223> Synthetic construct

<400> 702
atggaatggg aaaaccacac cattctggtg gaattttttc tgaagggact ttctgggtcac 60
ccaagacttg agttactctt ttttgtgctc atcttcataa tgtatgtggt catccttctg 120
gggaatggta ctctcatttt aatcagcatc ttggaccctc accttcacac ccctatgtac 180
ttctttcttg ggaacctctc cttcttggac atctgctaca ccaccacctc tattccctcc 240
acgctagtga gcttcctttc agaaagaaag accatttccc tttctggctg tgcagtgcag 300
atgttctca gcttggccat ggggacaaca gagtgtgtgc ttctgggcgt gatggccttt 360
gaccgctatg tggctatctg caacctctg agatatccca tcatcatgag taaggatgcc 420
tatgtaccca tggcagctgg gtccctggatc ataggagctg tcaattctgc agtacaaaca 480
gtgtttgtgg tacaattgcc tttctgcagg aataacatca tcaatcattt cacctgtgaa 540
attctagctg tcatgaaact ggcctgtgct gacatctcag gcaatgagtt catcctgctt 600
gtgaccacaa cattgttctt attgacacct ttgttattaa ttattgtctc ttacacgtta 660
atcattttga gcatcttcaa aattagctct tcggagggga gaagcaaacc ttccctacc 720
tgctcagctc gtctgactgt ggtgataaca ttctgtggga ccatcttctt catgtacatg 780
aagcccaagt ctcaagagac acttaattca gatgacttgg atgccactga caaacttata 840
ttcatattct acagggtgat gactcccatg atgaatcctt taatctacag tcttagaaac 900
aaggatgtga aggaggcagt aaaacaccta ctgagaagaa aaaattttaa caag 954

<210> 703
<211> 999
<212> DNA
<213> Unknown (H38g552 nucleotide)

<220>
<223> Synthetic construct

<400> 703
atggaaagga ccaattggac agagatagag ttcattctgc aaggactttc agggtagcca 60
agagctgaaa aattccctttt cgtgatgtgc ttagtgatgt acctgggtgat tctcctaggt 120
aatggcacct tgatcattct gacactcctg gatgctcgtc tccacacacc catgtacttc 180
ttccttggga atctttcctt cctagacatt tggtagacat cctcctccat cccctcaatg 240
ctgatacact tcctatcaga gaagaaaacc atctccttca ctagatgtgt gattcaaagt 300
tctgtctctt acactatggg atccaccgag tgtgtgcttc tagcagtgat ggcataatgac 360
cgttatgtag ccactctgaa cctcttgaga tatcccatca tcatgggcaa ggcactttgt 420
attcagatgg tggctgtctc ttggggacta ggctttctca actcattgac agaaactgtt 480
cttgcaatac ggttaccctt ctgtggaaaa aaatgtcatt aatcattttg tttgtgaaat 540
attggccttt gtcaagctgg ctgtcacaga tacttccctg aatgagatta ttataatgtt 600
gggcaatgta atatttttgt tttctccatt actgctgatt tgtatctcct acatctttat 660
cctttctact gtactaagaa tcaattcagc tgaaggaagg aaaaaggcct tttccacctg 720
ctcagccac atgacagtgg tgattgtgtt ttatgggaca atcctcttca tgtacatgaa 780
ggcaaagtcc aaagactctg cttttgacaa actgattgcc ctgttctatg gcatagtcac 840
cccatgtc aatcctatca tctatagcct gaggaatata gaggtgcatg gagctatgag 900
gaaattaatg agtagaccct ggttctggag gaaatgatga cacactgaca cctttgagtt 960
tatgcacaaa atacgctcac aagtttgaga caacacttt 999

<210> 704
<211> 966
<212> DNA
<213> Unknown (H38g553 nucleotide)

<220>
<223> Synthetic construct

<400> 704

cacacagagc	catggaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggg	cctcgccttg	ctctccctgt	ccctgtccat	gtgtctgggc	120
atgggtgctga	ggaacctgtc	cagcatcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccgtgtact	tcttcctctc	taaactgtgc	tyggctgaca	tcggtttcac	cttggccacg	240
gttcccaaga	tgatttggtg	catgcagtcg	catagcagag	tcattctctca	tgcgggctgt	300
ctgacgcaga	tgtctttctt	catccttttt	gcatgtatag	aaggcatgct	cctgacagtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccacgt	catcgtgaat	420
cctcacctct	gtgtctcctt	cctttttggtg	tcctttttcc	ttagcatggt	ggattcccag	480
ctgcacagtt	gaatttggtt	acaattcaca	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctgttctg	acagcgtcat	caatagcata	600
ttcatatatt	tcaatagtag	tatgtttggt	tttcttccca	tttcagggat	cctatggctc	660
tactgtaaaa	tcgtcccttc	cattctaagg	atttcatcat	cagatgggaa	gtataaagcc	720
ttctccacat	gtggctctca	cctagcagtt	gtttgtgat	tttatagaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaatg	gtgtgggtggc	gtcagcgatg	840
ttctctgtgg	tcaccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcgagggt	gctcagcaga	acagtcgaat	cttatgatct	gttccatcct	960
ttttct						966

<210> 705

<211> 937

<212> DNA

<213> Unknown (H38g554 nucleotide)

<220>

<223> Synthetic construct

<400> 705

atggctgggg	aaaaccatac	tacactgcct	gaattcctcc	ttctgggatt	ctctgacctc	60
aaggccctgc	agggccccc	gttctgggtg	gtgcttcttg	tctacctggg	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaactctc	agtgggtggg	ctcttctaca	ccactgacat	cgtgcccagg	240
acctgggcca	atctgggctc	cccgcacccc	caggccatct	ctttccaggg	ctgtgcagcc	300
caatgtatag	tcttcattgt	cctgggcate	tcggagtgtc	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgtatt	ccacctctt	gagcccacgg	420
gcctgcatgg	ccatgggtgg	tacctcctgg	ctcacaggca	tcatacaggc	caccacccat	480
gcctccctca	tcttctctct	accttttcgc	agccaccgca	tcataccgca	ctttctctgt	540
gacatcctgc	cagtactgag	gctggcaagt	gctgggaagc	acaggagcga	gatctccgtg	600
atgacagcca	ccatagtctt	cattatgata	cccttctctc	tgattgtcac	ctcttacatc	660
cgcatacctg	gtgccatcct	agcaatggcc	tccaccagga	gccgccgcaa	ggtcttctcc	720
acctgtctct	cccatactgt	cgttggtctc	tctcttctt	ggaacagcca	gcatcaccta	780
catccggccg	caggcaggct	cctctgttac	cacagaccgc	gtcctcagtc	tcttctacac	840
agtcatacaca	cccatactca	accccatcat	ctacaccctt	cggacaagga	acgtgaggag	900
ggccctgcga	cacttggtga	agaggcagcg	cccctca			937

<210> 706

<211> 930

<212> DNA

<213> Unknown (H38g555 nucleotide)

<220>

<223> Synthetic construct

<400> 706

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cctgaattac	aagtcagtct	tttcttgatg	tttctcttca	tttatctatt	cactgttttg	120
ggaaacctgg	gactgatcac	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
tttttctctg	gcaatttagc	atattattgac	atattttact	cctctactgt	aacacctaaag	240
gcattgggtg	atttccaatc	caatcggaga	tccatctcct	ttgttggtctg	ctttgttcaa	300
atgtactttt	ttgttggtg	ggtgtgtgtg	gagtgtttcc	ttctgggatc	aatggcctac	360
aatcgctaca	tagcaatctg	caatccctta	ctgtattcag	tagtcatgtc	ccaaaaagtg	420

tccaactggc	tgggagtaat	gccatatgtg	ataggcttca	caagctcgct	gatatctgtc	480
tgggtgataa	gcagtttggc	gttctgtgat	tccagcatca	atcatttttt	ttgtgacacc	540
acagctcttt	tagcactctc	ctgtgtagat	acattcggca	cagaaatggt	gagctttgtc	600
ttagctggat	tcactcttct	tagctctctc	cttatcatca	cagtcactta	tatcatcctc	660
atctcagcca	tcctgaggat	ccagtcagca	gcaggcaggc	agaaggcctt	ctccacctgc	720
gcacccacc	tcctggctgt	aactatcttt	tatgggtctc	tgattttcac	ctatttgcaa	780
cctgataaca	catcatcgct	gacccaggcg	cagggtggcat	ctgtattcta	tacgattgtc	840
attcccatgc	tgaatccact	catctacagt	ctgaggaaca	aagatgtgaa	aaatgctctt	900
ctgagagtca	tacatagaaa	actttttcca				930

<210> 707

<211> 471

<212> DNA

<213> Unknown (H38g556 nucleotide)

<220>

<223> Synthetic construct

<400> 707

atctgtagcc	ccttgctgta	cagtgtcatc	atatccaata	aggcttgctt	ttctctgatt	60
ttaggggtgt	atataatagg	cctggtttgt	gcacagttc	atacaggctg	tatgtttagg	120
gttcaattct	gcaaatttga	tttgattaac	cattatttct	gtgatcttct	tcccctccta	180
aagctctctt	gctctagtat	ctatgtcaac	aaactactta	ttctatgtgt	tggtgcattt	240
aacatccttg	tcccagctt	gaccatcctt	tgctcttaca	tctttattat	tgccagcatc	300
ctccacattc	gctccactga	gggcagggtc	aaagccttca	gcactttagt	ctccacatg	360
ttggcggttg	taatcttttt	tggatctgca	gcattcatgt	acttgcagcc	atcttcaatc	420
agctccatgg	accaggggaa	agtatcctct	gtgttttata	ctattattgt	g	471

<210> 708

<211> 529

<212> DNA

<213> Unknown (H38g557 nucleotide)

<220>

<223> Synthetic construct

<400> 708

ctggccccgt	cctccagtct	ggccttgggg	acatggcggt	ggcaatggca	cagcatgact	60
gagcttggtt	tgttggtgct	ctcaggtttt	ggttccgtcc	ggggccttct	gttttgggca	120
gtgctctgca	aacatctggt	gaccctgctg	gacaaactccc	tgatcgctgt	cctcgccctg	180
gcagcctctg	cctgcgctgg	cccacgcact	tcctcctgca	ccacttctcc	ttagggggagg	240
tcccacgcca	cagcggcgga	gtctcggatg	caggccgatt	cccttcccc	gccgcactag	300
ccaccggta	ggcggttcc	cgctgctggg	tttcttcgcc	ctccctggca	tcgccgaatg	360
cgcttgcgca	gggccatggc	ctccgcccgt	gtgacgccat	ctgccggccg	ctgcattcta	420
ctacctgagg	agccctagtc	ttccgagccc	gcttcgcctt	caccttgccc	ttctgcggcg	480
cagcaccacc	cgctacttcc	ggctggattc	tcggcctgtg	ctgagacct		529

<210> 709

<211> 942

<212> DNA

<213> Unknown (H38g558 nucleotide)

<220>

<223> Synthetic construct

<400> 709

atgaccagaa	aaaattatac	ctcactgact	gagttcgctc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttttgttt	tttcttgtga	tttatacact	tacagtactg	120
ggaaatctcg	ggatgatcct	cttaatcagg	atcgattccc	agcttcacac	acccatgtat	180
ttcttctctg	ctaacctgtc	ctttgtggac	gtttgttaact	caactaccat	caccccaaag	240
atgctggcag	atttattatc	agagaagaaa	accatctctt	ttgctggctg	cttctctacag	300

atgtacttct	ttatctccct	ggcgacaacc	gaatgcatcc	tctttggggt	aatggcctat	360
gacaggtatg	cggccatag	tcgcccgtg	ctttactcct	tgatcatgtc	caggaccgtc	420
tacctaaaaa	tggcagccgg	ggcttttgct	gcagggttgc	tgaacttcct	ggtcaacaca	480
agccatgtca	gcagcttgct	attctgtgac	tccaatgtca	tccatcactt	cttctgtgac	540
agtccccac	ttttcaagct	ctcttgttct	gacacaatcc	tgaagaaaag	cataagttct	600
attttggtg	gtgtgaatat	tgtggggact	ctgcttgta	tcctctctct	ctactcctac	660
gttctcttct	ccattttttc	tatgcattcg	ggggagggga	ggcacagagc	tttctccacg	720
tgtgcctctc	acctgacagc	cataattctg	ttctatgcca	cctgcatcta	tacttacctg	780
agacctagtt	ccagctactc	cctgaatcag	gacaaagtgg	cttctgtgtt	ctacacagtg	840
gtgattccca	tgttgaatcc	tctgatctac	agcctcagga	gtaaggaagt	aaagaaggct	900
ttagcgaatg	taattagcag	gaaaaggacc	tcttccttct	tg		942

<210> 710

<211> 941

<212> DNA

<213> Unknown (H38g559 nucleotide)

<220>

<223> Synthetic construct

<400> 710

atgaccagaa	aaaattatac	ctcactgact	gagttcatcc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttctgtta	tttcttgtga	tttacacact	taccgtactg	120
ggaaatatcg	ggatgatcct	cttaatcagg	atcgattccc	ggcttcacac	acccatgtat	180
ttcttccctg	ttaacctgtc	ctttgtggac	atttggtact	caaccacat	caccccaaag	240
atgctggcag	atttattatc	agagaagaaa	accatctctt	ttgctggctg	cttctacag	300
atgtacttct	ttatcgccct	ggcgacaacc	gaatgcatcc	tctttggggt	aatggcctat	360
gaccggtatg	tgaccatag	tcgcccgtg	ctttactcct	tgatcatgtc	caggacagtc	420
tgcctaaaaa	tggcagccgg	ggcttttgct	gcagggttgc	tgaactccat	ggtcaacact	480
agctatgtca	gcagcttgct	attctgtggc	tccaatgtca	tccatcactt	cttctgcaac	540
agtccccac	tttttaagct	ttcttgttct	gacacacact	tgaaggaaaag	catattttcc	600
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tgtgcctctc	acctgacagc	cataatcctc	ttctacacca	cctccatcta	tacctacctg	780
agacctagtt	ccagctactc	cctgatcagg	acaaagtggg	ttctgtgttc	tacacagtg	840
tgatcccat	attgaatcct	ctgatctaca	gcctcaggaa	taaggaagta	aagaaggctt	900
tagcgaatgt	aattagcagg	aaaaggatcc	cttcatttct	g		941

<210> 711

<211> 939

<212> DNA

<213> Unknown (H38g560 nucleotide)

<220>

<223> Synthetic construct

<400> 711

atgagtgggg	agaatgtcac	caaggtcagc	accttcatcc	tggtgggcct	ccccagggcc	60
ccagggctgc	agtacctgct	cttctcctc	ttcctgctca	cctacctctt	tgctctgggtg	120
gagaacctgg	ccatcatcct	catcgtctgg	agcagcacct	ccctccacag	gcccattgtac	180
tactttctga	gtcccatgtc	tttctgggag	atctgggtacg	tgtctgacat	cacccccaag	240
atgctggagg	gcttctcct	ccagcagaaa	cgcattctct	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	ggtgtgcacc	gagtgtgtgc	ttctgcctcc	atggcctacg	360
accgctacgt	ggccatctgc	cacccgctgc	gctaccacgt	ccttgtgacc	gccgggctgt	420
gctccagctg	gtgggcttct	cctttgtgag	tgcttctcca	tctccatgat	caaggtctgt	480
tttatctcca	gcgtcacgtt	ctgtggctcc	aacgtcttga	accacttct	tctgtgacat	540
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accctggctg	tcctgcgcac	cccctcggcc	accggctgct	ggagagcctt	ctctacctgc	720
gcctctcacc	tcaccgtgg	caccgtcttc	tatacagcct	tgcttttcat	gtatgtccgg	780
ccccaaagcca	ttgattccca	gagctccaac	aagctcatct	ctgccgtgta	cactgttgtc	840

acgcccaataa ttaacccttt gatttactgc ctgaggaaca aggaatttaa ggacgccttg 900
 aaaaaggcct tgggcttggg tcaaacttca cactaagac 939

<210> 712

<211> 642

<212> DNA

<213> Unknown (H38g561 nucleotide)

<220>

<223> Synthetic construct

<400> 712

ctggctgacc	tctgtttctc	taccaacata	gttcctcagg	cactagtcca	cctgctttcc	60
agaaagaagg	tcattgtatt	cacactgtgc	gcagctcgac	ttctctttct	cctcattggg	120
gggtgtaccc	agtgcgcctc	tcttggagtg	atgtctctatg	atcgctatgt	tgcaatctgc	180
aatcctctgc	gttaccctaa	catcatgacc	tggaaagtgt	gtgtccagct	ggcaacagca	240
ccatggacca	gtggtattct	ggtgtctgtg	gtagacacca	ccttcacact	gaggctaccc	300
taccgaggca	gtaacagcat	tgctcatttc	tgggtgtgagg	cccctgcact	attgatctta	360
gcattccacag	acacccatgc	atcagagatg	gccatttttc	ttacgggggt	tgtgattctc	420
ctcatacctg	ttttctgat	tctgggtatcc	tatggccgta	tcatagtaac	tgtgggtcaag	480
atgaagtcaa	ctgtggggag	tctcaaggca	ttttctacct	gtgggtccca	cctcatgggtg	540
gtcatacttt	tttatggatc	agcaattatc	acttacatga	cacccaagtc	ttccaaacag	600
caggaaaaat	cggtgtctgt	tttctatcca	atagtgactc	cc		642

<210> 713

<211> 948

<212> DNA

<213> Unknown (H38g562 nucleotide)

<220>

<223> Synthetic construct

<400> 713

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ctacctctca	gagtcacact	gttcttggta	ttccttcttg	tatatacatt	aactatggtc	120
ggaaatatac	tcttaataat	tctagttaat	attaattcaa	gccttcaa	tcccatgtat	180
tattttctta	gcaacttate	tttcttagac	atcagctgtt	ctacagcaat	cactcctaaa	240
atgctggcaa	acttcttggc	atccaggaaa	agcatctctc	cttatgggtg	tgactacaa	300
atgtttttct	tcgcttcttt	tgctgatgct	gagtgcctta	tcctggcagc	aatggcttat	360
gaccgctatg	cagccatctg	caacccactg	ctctatacta	cactgatgtc	taggagagtc	420
tgtgtctgct	tcatttgtgt	ggcatatttc	agtggaaagta	caacatcact	ggtccatgtg	480
tgccctcacat	tcaggctgtc	atthttgtggc	tccaatatcg	tcaatcattt	tttctgtgat	540
atcccacctc	ttctggcttt	atcatgtaca	gacactcaga	tcaaccagct	tctgtctctt	600
gctttgtgca	gcttcatcca	gaccagcact	tttgtggtaa	tatttatttc	ttacttctgc	660
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tgtgcttccc	acctcatagc	agtcacctta	ttctatggag	cgctcctgtt	tatgtactta	780
cagcccacca	ctagctattc	cctagacact	gataagggtg	tggcagtgtt	ttatactgtt	840
gtatttccca	tgtttaatcc	aataatttat	agtttcagaa	acaaggatgt	gaaaaatgct	900
ctcaaaaagc	tattagaaag	aattggatat	tcaaatgaat	ggtattta		948

<210> 714

<211> 939

<212> DNA

<213> Unknown (H38g563 nucleotide)

<220>

<223> Synthetic construct

<400> 714

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ggacttgagg	gtggcctgga	gaaccaggcc	ctgctctttg	ctgtgttccc	aggtctatac	120

atggtgacca	tcccgggaaa	cctcaccatg	accatgggtca	tcatacctgga	cacgcacctg	180
cacttcccag	tgaacttctt	cctcaggagc	ctcccccttc	ctggaccttg	gccatgcctc	240
catcacccca	atgccctggg	taacttctct	tcctcgtcca	aggtcgtcac	ctttgcaggc	300
tgtgctgccc	ggttcttttt	ctccttgctg	tctaccactg	agactttcct	gctggccgtg	360
atggcctatg	actgcttcgt	ggccatctgt	agtctgggtg	ggtgccaggt	gaccacgtgc	420
ctctcgatct	gcatcatcct	gggaccaggc	acctactgca	gggtctgcct	cagctccatc	480
gtgcagaccg	gcctcatgtt	ccagctccct	tctgcaggga	ccaaccacat	tgaccactct	540
gtgacatgcc	ccagctgctc	cggctggcct	gtgcatgcct	ggccctcaat	gagctgacca	600
agttcagcct	ttgtgggctc	atgatgggaa	cgccactctt	gtggtcctcg	tctcctttgg	660
ctgtgtcaca	gtgaccatcc	tgaggacacc	ctccgcagcc	agtgcataaa	ggtcttcacc	720
tgtagctccc	acgtgatgac	cgtgtccctg	tttgatggga	ctgtgtttgt	cacatatgcc	780
cagccaggga	ctatggagtc	catggagcag	ggcaagggtg	tgtctgtctt	ctacagcctg	840
gtcatcccg	tgcttgggcc	cttcatctac	agcctacgaa	acaaggacat	gaaggaggcc	900
ctgcggaggc	tgggccagag	acaagcactc	atgggaagg			939

<210> 715

<211> 756

<212> DNA

<213> Unknown (H38g564 nucleotide)

<220>

<223> Synthetic construct

<400> 715

atgtacttct	tccttgga	cctctccttt	tgtgatatct	gctactctac	tgtctttgct	60
cctaagatgc	tagtcaattt	cctatcaaaa	cataagtcca	gtacattttc	tggctgtgtt	120
ctacagagtt	tcccttttgc	agtatatgta	accacaaagg	acatttctct	gtccatgatg	180
gcttatgacc	attacgtggc	catagcta	cccttggtgt	atacagtc	tatggcccaa	240
aaagtttgta	ttcagatggg	ccttgcttct	tacttaggtg	ggctcattaa	ttccctgaca	300
cacacaatag	gtttgtc	attagacttc	tgtggctcta	atattgtgaa	tcattatttc	360
tgtgatgttc	ctcctcttct	gaggctttct	tgctctgatg	ctcatatcaa	tgaaatgctg	420
cccttgggtct	tctctgggct	cattgcaatg	ttcactttca	ttgtcattat	ggtgtcttat	480
atctgcatca	tcattgccat	ccagagaatc	catgcagctg	aggggaaggta	caaagccttc	540
tccactttgt	tctccacact	aaccacgggt	accttattct	atgggtctgt	ttcttttagt	600
tatatccagc	caagttctca	gtattccttg	gaacaggaga	aggtcttggc	tgtgttttat	660
acactgggtga	tcccatgct	aaaccactt	atttatagcc	tgagaaataa	ggatgtaaaa	720
gatgcagcca	aaaggttgat	atgggtgggg	gaaaaa			756

<210> 716

<211> 954

<212> DNA

<213> Unknown (H38g565 nucleotide)

<220>

<223> Synthetic construct

<400> 716

atgagtggg	agaatgtcac	cagggtcgcc	accttcaccc	tgggtgggctt	ccccacggcc	60
ccagggtctg	agtacctgct	cttcctcctc	ttcctgctca	cctacctctt	tgtcctgggtg	120
gagaacctgg	ccatcatcct	caccgtctgg	agcagcacct	ccctccacag	gcccattgtac	180
tactttctga	gtccatgtc	tttcttagag	atctgggtacg	tgtctgacat	cacccccaaag	240
atgctggagg	gcttcctcct	ccagcagaaa	cgcactctct	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	ggtgtgcacc	gagtgtgtgc	ttctggcctc	catggcctac	360
gaccgctacg	tggccatctg	ccaccgcgtg	cgctaccacg	tccttgtgac	cccgggctgt	420
gctccagct	ggtgggcttc	tcctttgtga	gtggcttcac	catctccatg	atcaaggctct	480
gtttttatctc	cagcgtcacg	ttctgtggct	ccaacgtctt	gaaccacttc	ttctgtgaca	540
tttcccccat	cctcaagctg	gcctgcacgg	acttctccac	tgacagagctg	gtggatttca	600
ttctggcctt	catcatcctg	gtgtttccac	tcctggccac	catgctgtca	tatgcgcaca	660
tcacctgggc	tgtcctgcgc	atccccctgc	caccggctgc	tggagagcct	tcttcacctg	720
cgctctcac	ctcaccgtgg	tcaccgtctt	ctatacagcc	ttgcttttca	tgtatgtccg	780
ccccaggcca	ttgattcccc	gagctccaac	aagctcatct	ctgttttgta	cacagttatc	840

acccccatct tgaacccctt gatatactgc ctgaggaata aggaatttaa gaatgccttg 900
 aaaaacagtc ggcttgacga ctgcgccgta gagggggaggc tttctagtct tctg 954

<210> 717

<211> 960

<212> DNA

<213> Unknown (H38g566 nucleotide)

<220>

<223> Synthetic construct

<400> 717

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gctgaactga agatgggtcct cttegtgttg ttctgtctga tctacacat ttccctgggtg	120
ggaaatatag gaatgctctt tctaactctat gtaactccca aactccacac acccatgtat	180
tatttcctca gctgtctgtc atttggtgat gcctgtctatt catcagtttt tgcacccaga	240
atgctgctga acttctttgt tgagcgggag acaatcttat tctctgcatg tattgtgcag	300
tattttttat tcgtgtctct ccttaccact gagggcttct tgctggccac aatggcttac	360
gaccgttaca tggccattgt gaacccttta ctttatacag tagctatgac taaaatagtt	420
tgtattgtgc tcgcatttgg gtcattgtat ggaggtttta tcaactcatt gacacatata	480
attggcttgg tgaaactgtc tttctgtggg ccaaagtca tcagtcactt cttctgtgat	540
cttccccac tggtgaagct gtcattgtct gagacatcta tgaatgaatt gttgcttttg	600
atcttctctg gcattattgc cacgtcact ttttgactg tggatgatct ctacatcttc	660
attgttgcctg ctatcctgag gatccgctaa gcagcaggta gacgtaaagc cttctccacc	720
tgcacctctc acctgattac cgtgacctta ttctatggat cgataagctt tagttacatt	780
cagccaaact cccagtatct cctagaacaa gaaaagggtg tgtctgtatt ttataccctg	840
gtgggttccca tgttaaacc attgatttac agcctaagga acaaggaagt gaaggaagct	900
gtgaaaaggg ctatagaaat gaaacatttt ccttgttaat ttcatttttc catatccaaa	960

<210> 718

<211> 938

<212> DNA

<213> Unknown (H38g567 nucleotide)

<220>

<223> Synthetic construct

<400> 718

atgttgggga attactctag cgccactgaa ttttttctct taggcttccc tggctcccaa	60
gaagtacgcc gtatcctttt tgtgaacttc ttcttcttgt acgcagtgc agtgatggga	120
aacacggtca tcacgtcac tgtctgtgtt gataaacatc tgcagtcccc catgtatttt	180
ttcctgggcc acctctgtgt cctggagatc ctgatcacat ccaccgtgc cccttttatg	240
ctgggggggt gctgcttcca agcaccaga tcattgtctt gacagcctgt gctgcacagc	300
tatatacctt tctttgggta cctcggagtt ggcattaatg ggagtgatgg ctgtggacca	360
ttatgtggct gtgtgtaacc ctttgaggta caacatcatt atgaacagca gcacatgtgt	420
ctggatggtc attgtatcat ggggtgtttg gttccttttt caaatctggc cagtttatgc	480
cacttttcag cttactttct gcaaatcaaa tgtgttagat catttttact gtgactgagg	540
acaattgctc aagggtatcct gtgaggacac tcttttcaca gagtttatte tttttctaat	600
ggctgttttc attatcattg gttccttttg tccctacgat tgtctcctac acctacatca	660
tctccaccat cctcaagatc ccgttagcct ctggctggag gaaatccttt tccactgtg	720
cctcccactt cactgtgtt gtgacggct acagcagctg cttgtttctc tacacgaaac	780
ccaagcaaac acaggcagcc aagtataacc gtagcgcgc actgctgggt ttagtggtga	840
ccccttttct gaacccttct atcttcaccc tgaggaaatga caaattcata caggcctttg	900
gagatggcat gaaacactgc tatcaactcc tcagaatt	938

<210> 719

<211> 942

<212> DNA

<213> Unknown (H38g568 nucleotide)

<220>

<223> Synthetic construct

<400> 719

atataaatgg	ctgacagaaa	tgtcactgtg	ataactgaat	tcatectect	ggggttgact	60
gataaccctg	aaatgaatgt	tgtectttct	gtgctctttc	tattaatcta	tctcattact	120
gtcttgggca	acttttggat	tatcataata	attctggcta	gtgcccaact	ccattcaccc	180
atgtactttt	tccttagcca	gttggctttc	ttagatttct	gctattcttc	agtcttgatt	240
cctaaaatgt	tgggtgaatta	catagcagga	cagaaagtca	tctcttatca	cggttgcctc	300
cttcagtatt	cctttgtcag	cttggttctg	actactgaat	gcttctctct	ggctgccaatg	360
gcatgtgatc	ggtatctcgc	tgtttgccac	ccacttcaact	acaaagggtct	catgactcct	420
actttctgaa	tctatttggg	gactgtttct	tacctgctgg	gctctgtaaa	ctccctcacc	480
cacctgagta	gcttactcag	tttgtctttc	tgtgggtcca	atgttatcaa	ccgttatctc	540
tgtgacattc	cattgctctt	ccaactctcc	tgttccaaca	cccaacacag	taagatttta	600
tttactgtcc	tttctggagc	aacatcagtg	actacctttt	tgatagtggg	tagttcctat	660
ctggtaatcc	tactcattgt	cctgaagata	cattccacca	ggggcagaaa	taaagccata	720
tccacatgtg	cctcccacct	aatggtagtg	actctcttct	acagaacagt	gatatttact	780
tatctgggag	ccaaccctgg	atactcacag	gatagaccca	aaattctgcc	tgtggagtgc	840
acacttttgt	tgtcaatact	aaatcttcta	atatatagcg	tgagaaacag	agaagtcaaa	900
gaagccataa	aaataattat	taagagaaaa	atacttcttc	ag		942

<210> 720

<211> 942

<212> DNA

<213> Unknown (H38g569 nucleotide)

<220>

<223> Synthetic construct

<400> 720

atgttgatga	attactctag	tgccactgaa	ttttatctcc	ttggcttccc	tggctctgaa	60
gaactacatc	atatcctttt	tgctatatte	ttctttttct	acttggtgac	attaatggga	120
aacacagtca	tcatcatgat	tgtctgtgtg	gataaacgtc	tgagtcctcc	catgtatttc	180
ttcctcggcc	acctctctgc	cctggagatc	ctgggtcacaa	ccataatcgt	ccccgtgatg	240
cttttggggat	tgtctgctccc	tgggatgcag	acaatatatt	tgtctgcctg	tgttgtccag	300
ctcttcttgt	accttgtctg	ggggacaaca	gagttcgcat	tacttggagc	aatggctgtg	360
gaccgttatg	tggctgtctg	taaccctctg	aggtacaaca	tcattatgaa	cagacacacc	420
tgcaactttg	tgggttcttg	gtcatgggtg	tttgggtttc	tttttcaaat	ctggccgggc	480
tatgtcatgt	ttcagcttac	ttactgcaaa	tcaaatgtgg	tgaacaattt	tttttgtgac	540
cgagggcaat	tgtcacaact	atcctgcaat	aatactcttt	tcacggagtt	tatctctctc	600
ttaatggctg	tttttgttct	ctttgggtct	ttgatcccta	caattgtctc	caacgcctac	660
atcatctcca	ccattctcaa	gatcccgtca	tcctctggcc	ggaggaaatc	cttctccact	720
tgtgcctccc	acttcacctg	tgttgtgatt	ggctacggca	gctgcttgtt	tctctacgtg	780
aaacccaagc	aaacgcaggc	agctgattac	aattgggtag	tttccctgat	ggtttcagta	840
gtaactcctt	tcctcaatcc	tttcatcttc	accctccgga	atgataaagt	catagaggcc	900
cttcgggatg	gggtgaaacg	ctgctgtcaa	ctattcagga	at		942

<210> 721

<211> 936

<212> DNA

<213> Unknown (H38g570 nucleotide)

<220>

<223> Synthetic construct

<400> 721

atgatgggta	gaagggaatga	cacaaatgtg	gctgacttca	tccttacggg	actgtcagac	60
tctgaagagg	tccagatggc	tctgtttatg	ctattttctcc	tcataatact	aattactatg	120
ctgggggaatg	tggggatgct	attgataatc	cgccctggacc	tccagcttca	cactcccatg	180
tattttttcc	ttactcacct	gtcattttatt	gacctcagtt	actcaactgt	cgtcacacct	240
aaaaccttag	cgaacttact	gacttccaac	tatatttctc	tcacgggctg	ctttgcccag	300
atgttctgtt	ttgtcttctt	gggtactgct	gaatgttatc	ttctctcttc	aatggcctat	360

gategctatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgcc	caaaaggctc	420
tgccctgctc	tcatactg	gccttatgtg	attggcttta	tggaactcct	tgtcaatgtg	480
gtttccatga	gcagattgca	tttctgtgac	tcaaacataa	ttcatcactt	tttctgtgac	540
acttcccca	ttttagctct	gtcctgcact	gacacagaca	acactgaaat	gctgatattc	600
attatcgctg	gttccaccct	gatgggtgcc	cttatcaca	tatctgcate	ctatgtgtcc	660
attctctcta	ccatccctgaa	aattaattc	acttcaggaa	agcagaaagc	tttctctact	720
tgcgtctctc	atctcttggg	agtcaccatc	ttctatggaa	ctatgatttt	tacttactta	780
aagccaagaa	agtcttattc	cttgggaaga	gatcaagtgg	ctcctgtgtt	ttatactatt	840
gtgattccca	tgctgaatcc	actcatttat	agtcttagaa	acagagaagt	gaaaaatgct	900
ctcattagag	tcatagcagag	aagacaggac	tccagg			936

<210> 722

<211> 730

<212> DNA

<213> Unknown (H38g571 nucleotide)

<220>

<223> Synthetic construct

<400> 722

atgtcatgat	gaattttctg	cctgccccaa	ataatcatta	ctttatttga	gtaggagtgg	60
gatgctttta	atttagagac	acgggttttt	ctggaagagg	acttcccatg	tggaattcagc	120
ttgtggattg	tacgtcaatt	gtcttttttc	ttggaaataa	attaatttgc	tcattttaaaa	180
aaatgatgca	ggaagcatac	gagtactttt	tctctgagca	acttggtttt	tttaagtttct	240
gttatgcttc	agtcattaca	tccaaaatgt	ttggaagttt	cttgtaaaaa	caaaaaaaat	300
taaccttcaa	tgcacatagg	ctgctctctc	accttcatga	ccaccgagtg	cttgctctag	360
ctttcatggc	ctgtgatcaa	tacctgggtc	tttgtaatcc	tcctttgtat	atgggtcacca	420
tgcccccccc	gcaaggagtc	tgcatccagc	ttatgcctgc	ctcctatagc	tatagcttcc	480
tgatgacact	ttcacattat	cctcagcctt	tgtctccctt	attgccccct	tgtatcattg	540
atgttcaatt	gaagcctgtt	ctttatgtac	ttaatgtctc	gaaaattctc	ttgacacaga	600
caggatggcc	tctgtcttct	acacagtagt	cattcccatg	ttgagccctt	tgatctggag	660
cctcaggaac	aaggatgtga	aagatgcctt	gaggaaagtc	attgtcaaca	gaaaccaggc	720
attattttgt						730

<210> 723

<211> 936

<212> DNA

<213> Unknown (H38g572 nucleotide)

<220>

<223> Synthetic construct

<400> 723

atggctcctg	aaaatttcac	cagggtcact	gagttttattc	tcacaggtgt	ctctagctgt	60
ccagagctcc	agattccctt	cttcctgggc	ttcctagtgc	tctatgtgct	gaccatggca	120
gggaacctgg	gcatcatcac	cctcaccagt	gttgactctc	gacttcaaac	ccccatgtac	180
tttttcttga	gacatctagc	tatcatcaat	cttggaact	ctactgtcat	tgccccataa	240
atgctgatga	actttttagt	aaagaagaaa	actacctcat	tctatgaatg	tgccacccaa	300
ctgggagggt	tcttgttctt	tattgtatcg	gaggtaaatga	tgctggctgt	gatggcctat	360
gaccgctatg	tgccattttg	taacctctctg	ctctacatgg	tggtgggtgc	tcggcggtc	420
tgccctctgc	tggtgtccct	cacgtacctc	tatggctttt	ctacagctat	tgtggtttca	480
ccttgatat	tctctgtgtc	ttattgtctt	tctaataataa	tcaatcattt	ttactgtgat	540
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atatctgcag	caacaaattt	gtttttttcc	atgattacag	ttctagtatc	ttatttcaat	660
attgttttgt	ccatttctaag	gatacgttca	ccagaaggaa	ggaaaaaagc	cttttccacc	720
tgcgcttcgc	atatgatagc	agtcacggtt	ttctatggga	caatgctatt	tatgtatttg	780
cagccccaaa	ccaaccactc	actggatact	gataagatgg	cttctgtgtt	ttacacattg	840
gtgattccca	tgctgaatcc	cttgatctac	agcctgagga	ataatgatgt	aaatgttgcc	900
ttaaagaaat	tcataggaaa	tccatgttac	tccttt			936

<210> 724

<211> 481
 <212> DNA
 <213> Unknown (H38g573 nucleotide)

<220>
 <223> Synthetic construct

<400> 724
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 taagtatgcc atttgttacc ttcttccttt gtcagtgtatt gtaataagaa attatgtaat 120
 catcatagta tgtgttgaga aatgcctgct gttcctccta tatttattct atggtgacct 180
 ctctgtcatg gaaatcctta tcacatatac tgcgttccc ttgatgctca ggggttgta 240
 ctttccatga ttcaaacaaat acctttaatg acatgtgctg tccaactcta tatgaacttt 300
 tttgggggta cacaaaattt gcattactgg gagtcatgac tgtgaaccat tatgtggctc 360
 tctgtaactc tttgaagtaa aacatcatta tgagcagaca cactgcatct ggctggtaat 420
 tgtattattg attgggttcc tttctgaaat ctggtcagtc tatgccacat ttcagctccc 480
 t 481

<210> 725
 <211> 971
 <212> DNA
 <213> Unknown (H38g574 nucleotide)

<220>
 <223> Synthetic construct

<400> 725
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 gatccagaac tgcagccggg cctcgctttg ctgtccctgt ccctgtccat gtatctggtc 120
 acggtgctga ggaacctcct cagtatcctg gctgtcagct ctgactcccc cctccacacc 180
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcggtttcac ctcgcccatg 240
 gttcccaaga tgattgtgga catgcagtcg catagcagag tcatctctca tgagggtctg 300
 ctgacacaga tgtttttctt ggtccttttt gcatgtatag aaggcatgat cctgactgtg 360
 atggcctatg actgctttgt agccatctgt cgccctctga attaccagat catcgtgaat 420
 cctcacctct gtgtcttctt cattttgatg tcccttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggattgtgtt acaattcaca atcatcaaga atgtggaaat ctctaatttt 540
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 tactataaaa tcgtcacctc cattctcagg atttcatctt cagatgggaa gtataaagcc 720
 ttctccacct gtgactctca cctagcagtt gtttgcgtat tttatggaac agacattggg 780
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 tacgctgtgg tcacccccat gctgaacctt ttcactctaca gcctgagaaa cagggacata 900
 caaagtgcct tgcggaggct gcgcagcaga acagtccaat ctcatgatct gttccatcct 960
 ttttcttgtg t 971

<210> 726
 <211> 960
 <212> DNA
 <213> Unknown (H38g575 nucleotide)

<220>
 <223> Synthetic construct

<400> 726
 cacacaaagc cacggaatct cacaggtgtc tgagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcagcccat cctggctggg ctgtccctgt ccatgtatct ggtcacgggtg 120
 ctgaggaacc tgctcatcat cctggctgtc agctctgact ccacacctca cactcccatg 180
 tgcttcttcc tctccaaact gtgctgggct gacatcggtt tcacctcggc cacggttcct 240
 aagatgattg tggacatgca gtcgcatagc agagtcactt cttatgaggg ctgcctgaca 300
 aggatgtctt tcttggctct ttttgcagtg acagaagaca tgcttctgac tgtgatggcc 360
 tatgactgct ttgtagccat ctgtcgccct ctgcactacc cagtcactct gaatcctcac 420

ctctgtgtct	ttttcatttt	ggtgtccttt	ttccttagcc	tgttggattc	ccagctgcac	480
agttagggtg	tattacaatt	caccttcttc	aataatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttgtaaa	ccttgccagt	tctgacagcg	tcgtcaatag	catattcata	600
tatttcgata	gtactatgtt	tggttttctt	cccattttag	gggtcctttt	gtctcactat	660
aaaattgtcc	cctccattct	aaggatttca	tcgtcagatg	ggaagtataa	agtcttcgct	720
acctgtggct	ctcacctggc	agttgtttgc	tgatttgatg	gaacaggcat	tgacatgtac	780
ctgacttcag	ctgtgtcacc	accccacagg	aatgggtgtg	tygcatcagt	gatgtatgct	840
gttttcaccc	ccatgctgaa	ccctttcatt	tacagcctga	gaaacaggga	catacaaagt	900
gccctgcgga	ggctgctcag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

<210> 727

<211> 806

<212> DNA

<213> Unknown (H38g576 nucleotide)

<220>

<223> Synthetic construct

<400> 727

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aaactagact	cccacctata	cacacctggt	gtatatTTTT	taatcaaaca	catatttttc	120
attgattttt	acaattgtat	tgttatttac	accaataaaa	tgttaaattt	tggtgtggat	180
cagaataaca	tttccattta	tgcattgtgc	acacatatga	ctttcttatg	ttcattatca	240
ctgaactttt	aatcttggtg	agcatggcct	atgattgcta	tgtggtgaac	tccaacctt	300
tgttttacat	tgttatcatg	tgtctgtgac	tgtaacatgt	gctgatgagc	attccatacc	360
tctgtaatac	atttcaatct	ctaattatca	caatgacctt	tttttgacct	tctgtagctt	420
tatcatcagt	cattttctatt	gttatgatgt	tctcttcttc	catatgctat	gctcaaattgc	480
acaggaaaaga	gaattgttga	tcacactgct	tacagcattt	aatttgatcc	ctacctcctg	540
gtattgctag	tgttaaacat	tctgattttg	ttagccatat	gttgaatgca	ttctgcactg	600
ggcaggaaaa	aagctttctc	ctgtgtgtgg	tctcatctta	caatgggtgt	tatgttctat	660
ggatctctac	tttttgatat	ggataaatgg	cctccttggt	ctacacttta	atgatcctca	720
ggtttaacct	cttgatctac	agcttttagca	acttaggggt	taaaaatgtc	ttttatagag	780
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<210> 728

<211> 384

<212> DNA

<213> Unknown (H38g577 nucleotide)

<220>

<223> Synthetic construct

<400> 728

atggggaggca	agcagccctg	ggtcacagaa	ttcatcctgg	tgggattcca	gctctgtgca	60
gagatggaga	tctttctctc	ttgcatcttc	tcgcgatttt	atgccttcag	tctactgagg	120
aatggcatga	acatgggact	cacctatctg	gatgacagag	acgacagact	acacaccttc	180
atatacattt	tcctctcaca	cctggccatc	aatgacatgt	actatgcttc	caacaatgtt	240
ccaaagaggc	aggtgaacca	aatgaaccag	aaaaaaaaaa	actttgttct	atggataaag	300
cagatatttt	tgtatttggc	ttttgtctac	acagagtgcc	taatttaggc	aatgatgtcc	360
tgtaatagat	atgtggcaat	ctgc				384

<210> 729

<211> 921

<212> DNA

<213> Unknown (H38g578 nucleotide)

<220>

<223> Synthetic construct

<400> 729

atggggccaac	acaatctaac	agtgctaact	gaattcattc	tgatggaact	cacaaggcgg	60
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cctgagctgc	agattccccct	ttttggagtc	ttcctcgtca	tctacctaat	cacagtgggtg	120
ggcaacctaa	ctatgatcat	tttgaccaa	ctggactccc	acttacatac	acctatgtac	180
ttttctatca	gacatttggc	ttctgttgat	cttggaatt	ctactgtcat	ttgtcccaag	240
gtgctggcaa	atthttgtgt	ggatcgaaat	actatttctt	attatgcatg	tgctgcacag	300
ctggcattct	tccttatgtt	cattatcagt	gaatttttca	tcctgtcagc	catggcctat	360
gaccgctatg	tggccatttg	taacctcttg	ctctattatg	ttattatgtc	tcagcgactg	420
tgatcatgtac	tgggtggcat	tcaatactc	tacagcacat	ttcaggctct	gatgttcaact	480
attaagattt	ttacattgac	cttctgtggc	tctaattgtca	tcagtcattt	ttactgtgat	540
gatgttccct	tgctacctat	gctttgtctca	aatgcacagg	aaatagaatt	gttgagcata	600
ctattttctg	tatttaattt	gatctcctcc	ttctgtatag	tcctagtgtc	ctacatgttg	660
atthttgttag	ctatgtgtca	aatgcattct	gcagagggga	ggaaaaaggc	ttctccaca	720
tggtgttccc	atthtgacagt	gggtgtgtgt	ttctatgggt	ctctactctt	catgtacatg	780
cagcccaatt	ccactcactt	ctttgatact	gataaaatgg	cttctgtgtt	ttacacttta	840
gtaatcccca	tgcttaacct	tttgatttac	agcttaagaa	acgaagaggt	gaaaaatgcc	900
ttctataagc	tctttgagaa	t				921

<210> 730

<211> 654

<212> DNA

<213> Unknown (H38g579 nucleotide)

<220>

<223> Synthetic construct

<400> 730

ttgcctgaca	tcagtttcac	ctccaccaca	gtccccaaga	tgatttgtga	catccaatct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctattttt	120
ggaggcatgg	aagagaggca	tgctcctgag	tgtgatggcc	tatgactggg	ttgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaaccctgtg	ttctgtggct	tcctagtttt	240
gttgctcttt	ttttctcag	tccttttagat	gcccagctgc	acaacttgat	tgctttacaa	300
gtgacctgct	tcaaggatgt	ggaaattcct	aattttctct	gtgaccttct	tcaactcccc	360
catcttgcat	gttgtagacac	cttcaccatt	aacataatca	tgtatttccc	tgccgcata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttctccatt	480
ctgaggggtt	catcgctcag	tgggaggtat	aaagccctct	ccacctgtgg	gtctcacgtg	540
tcagttgttt	gctgagttta	tgggaacaggc	gttgagggtg	acctcagttc	ggatgtgtca	600
ttttccccc	gaaagggtgc	agtggcctca	gtgatgtacg	cggttgtcac	cccc	654

<210> 731

<211> 683

<212> DNA

<213> Unknown (H38g580 nucleotide)

<220>

<223> Synthetic construct

<400> 731

atgtacttct	tcttctccaa	cctgtccttg	cctgacgacg	gtttcacctc	caccacggtc	60
cccaaagatg	attgtggaca	tccagtctca	cagcagagtc	acctcctatg	caggctgcct	120
gactcagatg	tctctctttg	ccatttttgg	aggcatggaa	gagagacatg	ctcctgagtg	180
tgatggccta	tgaccgggtt	gtagccatct	gtcaccctct	atgtcattca	gccatcacga	240
accctgtgtt	ctgtggcttt	ctagtthttg	tgtctttttt	ttttctcagt	cttttagacg	300
cccagctgca	caacttgatt	gccttacaaa	ggacctgctt	caaggatgtg	gaaattccta	360
atttcttctg	tgacccttct	caattccccc	gtcttgcatt	ttgtggcacc	ttaccaata	420
acataatcat	gtatttccct	gcagccatat	ttggttttct	tcccatctcg	gggacccttt	480
tctcttacga	taaaattgtt	ttctccattc	tgagggtttc	atcatcaggt	gggaagcata	540
aggccttctc	caccaggggg	tctcaccctg	cagttgtttg	ctgattttat	ggaacaggca	600
ttggaggcta	cctcagttca	gatgtgtcat	cttccccgag	aaaggctgca	gtggcctcag	660
tgatgtacac	ggtggccatc	ccc				683

<210> 732

<211> 582

<212> DNA

<213> Unknown (H38g581 nucleotide)

<220>

<223> Synthetic construct

<400> 732

tactttttcc	tctccaacct	ctccttcttg	gacctctgtt	tcaccataag	ttgtgtcccc	60
gggatgctgg	tcaacctctg	ggagccaaag	aagaccatca	tcttactggg	ctgctctgtc	120
cagttcttca	tcttctctgtc	cctggggacc	actgagtga	tcctcctgac	ggtgatggcc	180
tttgaccgct	acatggctat	ctgccagccc	ctccactatg	ccaccatcgt	ccaccctctg	240
ctgtgctggc	agctggcacc	tgtggcctgg	gtcatgagtc	tggttagagtc	agtgggtccag	300
acaccatcca	ccctccactt	gcctttctgc	cccgatcggc	aggtggatga	ttttgtctgt	360
gaggtccag	ctctaattcg	actctcctgt	gaagacacct	cctacaatga	aatccagttg	420
gctgttgcca	gtgtcttcat	cttggctgtg	cctctcagcc	tcctccttgt	ctcttatgga	480
gccattgcct	gggcagtgtc	aaggactaac	tctgcaaaag	ggcagaggaa	agcttttggg	540
acctgtctct	cccatctcac	tgtggtcacc	ctcttctaca	gc		582

<210> 733

<211> 959

<212> DNA

<213> Unknown (H38g582 nucleotide)

<220>

<223> Synthetic construct

<400> 733

atggtcagtt	ccaatcagac	ctccccctgtg	ctgggggttcc	ttctcctggg	gctctctgcc	60
catccaaagc	tggagaagac	attcttctgtg	ctcatcctgc	tgatgtacct	ggtgaccta	120
ctgggcaatg	gggtcctcat	cctgggtgacc	atccttgact	cccgcctgga	cacacccatg	180
tacttcttcc	tggggaacct	ctccttctctg	gacatctgct	atacaacctc	ctcatccttg	240
acagcttctc	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagta	cagatgttcc	300
tctcccttgc	catgggagcc	acagagtgtg	ttctcctgag	catgatggcg	tttgatcgct	360
acgtggccat	ctgcaacccc	ctttgggtacc	ctgaagtcac	gaacaaagct	acttatgtgc	420
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ctgtcctgaa	gttggcctgt	gctgatatct	ctgtcaatgt	gatcagtatg	ggagtggcca	600
atgtgatctt	cctgggggtc	cctgttctgt	tcctctcttt	ctcctatgtc	ttcatcattg	660
ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	acctgctctg	720
cccacctcac	tgtcgtgac	gtcttctacg	ggaccatcct	cttcacgtac	gggaagccca	780
agtctaagga	cccactggga	gcagacaaac	aggaccttgc	agacaaactc	atttcccttt	840
tctatggggt	ggtgaccccc	atgctcaacc	ccatcatcta	cagcctgagg	aacaagggaag	900
tgaaggctgc	tgtgagggaac	ctgggtatttc	agaaacgctt	cctgcagtga	tggtggagg	959

<210> 734

<211> 954

<212> DNA

<213> Unknown (H38g583 nucleotide)

<220>

<223> Synthetic construct

<400> 734

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cacccaaagc	tggagaaaac	gttctttgtg	ctcatcctgc	tgatgtacct	ggtgaccta	120
ctgggcaatg	gggtcctcat	cctgatgact	gtgtccaaact	cccacctgca	catgccccatg	180
tacttcttcc	tggggaacct	ctccttctctg	gacatctgct	atacaacata	ctcagtcctcc	240
ctcatccttg	acagcttctt	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagtg	300
cagatgttcc	tctcctttgc	catgggagcc	acagagtgtg	ttctcctgag	catgatggcg	360
tttgatcgct	acgtggccat	ctgcaacccc	cttaggtacc	ctgtgggtcat	gagcaaggct	420
gcctacatgc	ccatggctgt	cggctcctgg	gtagctggaa	gcactgcttc	catggtgcag	480

acatcccttg	caatgaggct	gcccttctgt	ggagacaaca	tcataaatca	cttcacctgt	540
gagattctgg	ctgtccagaa	gttggcctgt	gctgatatct	ctgtcaatgt	gatcagtatg	600
ggagtgaaca	atgtgatctt	cctgggggtc	ccggttctgt	tcatactctt	ctcctatgtc	660
ttcatcattg	ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	720
acctgctctg	cccacctcac	agtcgtgggc	atcttctatg	ggaccatcct	cttcattgtat	780
gggaagccca	agtctaagga	cccgtggggg	gcagacaagc	aagactttgc	agacaaactc	840
atttcctttt	tctatggggg	ggtgaccccc	atgctcaacc	ccatcatcta	cagcctgagg	900
aacaaggatg	taaaggctgc	tgtgaggggc	ttgatatttc	agaaatgctt	tgcc	954

<210> 735

<211> 962

<212> DNA

<213> Unknown (H38g584 nucleotide)

<220>

<223> Synthetic construct

<400> 735

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cacccatagc	tggagaagac	attcttttgt	ttcatcctgc	tggtgtacct	ggtgatcctg	120
ctgggcaacg	gggtcctcat	cctggtgacc	atccttgact	ccgcctgca	cacacccatg	180
tactttcttc	tggggaacct	ctccttcctg	gacatctgct	atacaacctc	ctcatccttg	240
acagcttctt	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagta	cagatgttcc	300
tctcctttgc	catgggagcc	acagagtgtg	ttctcctgag	catgatggct	tttgatcact	360
acctggacat	gtgcaacccc	cttaggtacc	ctgtgggtcat	gagcaaggct	gcctacatgc	420
ccatggctgt	tggtcctggt	gcagctggta	tcaccaactc	tgtagtacag	atatccctag	480
caatgtgact	gcccttctgt	ggggacaatg	tcataaatca	cttcacctgt	gagatcctgg	540
cagttctaaa	gttggcctgt	gctgacatct	gcataacagt	gatcagcatg	gttgtgacca	600
acatgatctt	ccttgcactc	ccagtcctgt	ttatttttgt	ctcatatgtc	ttcatcattg	660
ccaccatcct	gagaatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	acctgctctg	720
cccacctcac	tgctgtgac	gtcttctatg	ggatgatect	cttcattgtat	gggaagccca	780
agtctaagga	cccaatggga	gcagacaaac	aggaccttgc	agacaaactc	atctccattt	840
tctatggagt	ggtgaccccc	attctcaacc	ccatcatcta	cagcccagg	aacaaagatt	900
tgaagctgc	tatgaggaac	ctggtggctc	aaaaacacct	aacagagtga	ctatcacaga	960
tc						962

<210> 736

<211> 375

<212> DNA

<213> Unknown (H38g585 nucleotide)

<220>

<223> Synthetic construct

<400> 736

agactaaatg	tcatacagtca	cctgcccttc	tatgggggaca	tcataaacca	cttgacctgt	60
gaggtcctgg	ctgtcctgaa	gttggcctgt	gctgacatct	ctatcaacat	gatcaggcaa	120
aaggccttct	ccacctgctc	tgcccacctc	acagttgtgg	tcattcttcta	caggaccatc	180
ctcttcacgc	atgggaagcc	caagtcgaag	gacccactgg	gggcagacaa	gcaggatttt	240
gcagacaaac	tcatactcct	ctcctatgga	gtgggtcaccc	ccatgctgaa	caccatcatc	300
tacagcctga	ggaaaaagg	tgtgaaggct	gctgtgaaga	acctggtatt	tcagaaaccc	360
ctaactgaat	gacag					375

<210> 737

<211> 648

<212> DNA

<213> Unknown (H38g586 nucleotide)

<220>

<223> Synthetic construct

<400> 737

tttgttgaca	tgggtttaac	gtcctccaca	gttaccaaga	tgtgtgtgaa	tatacagact	60
cggcatcaca	ccatcaccta	tacgggttgc	ctcacgcaa	tgtatttctt	tctgatgttt	120
ggtgatctag	acagcttctt	cctggctgcc	atggcgtag	accgctatgt	ggccatctgc	180
cacccccctct	gctactccac	ggatcatgagg	ccccaaagtct	gtgccctaata	gcttgcatgtg	240
tgtgtgggtcc	tcaccaatat	cgttgccctg	actcacacgt	tcctcatggc	tcggttgtcc	300
ttctgtgtga	ctggggaaat	tgctcacttt	ttctgtgaca	tcactcctgt	cctgaagctg	360
tcattgttctg	acacccacat	caacgagatg	atgggttttg	tcttgggagg	caccgtactc	420
atcgtccctct	ttttatgcat	tgtaacctcc	tacatccaca	ttgtgccagc	tatcctgagg	480
gtccgaaccc	gtgtgtgggt	gggcaaggcc	ttttccacct	gcagttccca	cctctgcgtt	540
gtttgtgtgt	tctatgggac	cctcttcagt	gcctacctgt	gtcctccctc	cattgcctct	600
gaagagaagg	acattgcagc	agctgcaatg	tacaccatag	tgactccc		648

<210> 738

<211> 957

<212> DNA

<213> Unknown (H38g587 nucleotide)

<220>

<223> Synthetic construct

<400> 738

atggaaaaag	ccaatgagac	ctccccctgtg	atgggggttcg	ttctcctgag	gctctctgcc	60
caccagagag	tggaaaagac	attcttcctg	ctcatcctgc	tgatgtacct	cgtgatcctg	120
ctgggcaatg	gggtcctcat	cctgggtgacc	atccttgact	ccgcctgca	cagccccatg	180
tacttcttcc	tagggaacct	ctccttctctg	gacatctgct	tcactacctc	ctcagtcacca	240
ctggctcctg	acagcttttt	gactccccag	gaaacctatct	ccttctcagc	ctgtgctgtg	300
cagatggcac	tctccttttg	catggcagga	acagagtgtc	tgctcctgag	catgatggca	360
tttgatcgct	atgtggccat	ctgcaacccc	cttaggtact	ccgtgatcat	gagcaaggct	420
gcctacatgc	ccatggctgc	cagctccttg	gctattgggtg	gtgctgcttc	cgtgggtacac	480
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gaggtgacga	atgtgatctt	cctaggagtc	ccggttctgt	tcattctctt	ctcctatgtc	660
ttcatcatca	ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggtcttctcc	720
acctgctctg	cccacctcac	cgtgggtgatc	gtcttctacg	ggaccttatt	cttcatgtat	780
gggaagccta	agtctaagga	ctccatggga	gcagacaaa	aggatcttct	agacaaactc	840
atcccccttt	tctatggggt	ggtgaccccg	atgctcaacc	ccatcatcta	tagcctgagg	900
aacaaggatg	tgaaggctgc	tgtgaggaga	ctgctgagac	caaaaggctt	cactcag	957

<210> 739

<211> 653

<212> DNA

<213> Unknown (H38g588 nucleotide)

<220>

<223> Synthetic construct

<400> 739

ctgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgtcctctgag	tgtgatagcc	tatgagcggg	ttgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaacctatgt	ttctgtggct	ttctagtttt	240
gttgtctttt	tttttctcag	tcttttagac	gccagctgc	acaacttgat	tgcccttata	300
aggacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gtgaccttct	tcaactcccc	360
atcttgcata	ttgtggcacc	ttcaccata	acataatcat	gtatttccct	gccgccatat	420
ttggttttct	tcccatctcg	gggacctttt	tctcttata	taaaattgtt	ttctccattc	480
taagggtttc	atcatcaggt	gggaagtata	aggccttctc	cacctgtggg	tctcacctgt	540
cagttgtttg	ctgattttat	ggaacaggca	ttggaggcta	cctcggttca	gatgtgtcat	600
cttccccgag	aaaggctgca	gtggcctcag	tgatgtacac	ggtggtcatc	ccc	653

<210> 740

<211> 648
 <212> DNA
 <213> Unknown (H38g589 nucleotide)

<220>
 <223> Synthetic construct

<400> 740

tttgtggatg	tctgcttctc	ctctaccact	gtccctaaag	ttctggccaa	ccatatactt	60
gggagtcagg	ccatttcctt	ctctgggtgt	ctcaccagc	tgtattttct	cgctgtgtgt	120
ggtaacatgg	acaatttctt	gctgggtgtg	atgtcctatg	accgatttgt	ggccatatgc	180
caccctttac	actacacaac	aaagatgacc	cgacagctct	gtgtcctgct	tgttgtgggg	240
tcatgggttg	tagccaacat	gaattgtctg	ttgcacatac	tgctcatggc	tcgactctcc	300
ttctgtgcag	acaacatgat	cccccacttc	ttctgtgatg	gaactcccct	cctgaaactc	360
tcctgtctcag	acacacatct	caatgagctg	atgattctta	cagagggagc	tgtggctcatg	420
gtcaccatcc	ttgtctgcat	cctcatctcc	tacatccaca	tcacctgtgc	tgtcctcaga	480
gtctcatccc	ccaggggagg	atggaaatcc	ttctccacct	gtggctccca	cctggctgtg	540
gtctgcctct	tctatggcac	cgtcatcgct	gtgtatttca	acccatcatc	ctctcaetta	600
gctggggagg	acatggcagc	tgcatgtgat	tatccagtgg	tgacccca		648

<210> 741
 <211> 988
 <212> DNA
 <213> Unknown (H38g590 nucleotide)

<220>
 <223> Synthetic construct

<400> 741

atggcagaag	aaaataagat	tctggtgact	cactttgtcc	tcacaggact	cacagatcat	60
ccagggctgc	aggcgcccct	gttcctggtg	ttcttgggtca	tctacctcat	caccctggtg	120
ggcaaccttg	gcctgatggc	tctcatcttg	aaggaccccc	accttcacac	ccccatatac	180
ttattttctg	gcagtttagc	ctttgcagat	gcattgcactt	catcctctgt	aacttctaag	240
atgcttatca	atttttttat	caaagaatca	tatgctatcc	atggctaagt	gtgccacca	300
gttttacttt	tttggttcca	atgcaaccac	agaatgcttc	ctgctggtag	tgatggccta	360
tgaccgctat	gtagccatat	gcaatcccct	gctttatcca	gtgggtgatgt	ccaatagcct	420
ctgtactcag	tttataggta	tttcatatct	tattggtttt	ctgcattcag	cgattcatgt	480
gggtttgtta	tttagattaa	ctttctgcag	gtccaatatt	atacattatt	tctactgtga	540
aattttacag	ctgttcaaaa	tttcttgcac	caatcctaca	gttaatatatac	ttctgatttt	600
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tattctctct	gccatcctga	aaaagaagtc	tgagaagggt	agaagcaaag	ccttctctac	720
ttgcagtgcc	catctgctct	ctgtctcttt	gttctacggc	accctcttct	tcatgtatgt	780
gagttctagg	tctggatcag	ctgcagatca	ggccaaaatg	tattctttat	tttacacaat	840
aataattcct	ttactaaatc	cttttattta	cagcctaagg	aacaaagagg	ttatagatgc	900
cctgagaaga	atcatgaaga	aataaatagt	tgtcagacaa	cattcaaac	atttcttctt	960
tatattctgc	tgaagaaaac	cccaagtc				988

<210> 742
 <211> 636
 <212> DNA
 <213> Unknown (H38g591 nucleotide)

<220>
 <223> Synthetic construct

<400> 742

tgctactccc	agggtcacgg	ctagcagggc	taggttactt	agagggtagg	aggctaagtt	60
cctcgtacaa	tgcttgtgct	gtcagatgt	tcttttttgt	agccttggcc	acagtggaaa	120
atatcgctgt	tgacatcaat	ggcctatgac	cactatatag	cagtgtgcaa	acccctacac	180
tacactacca	ccacgatagc	cagtgtatgt	gtcatctgg	tcataggctc	ctatgtctgt	240
ggctttctaa	atgcctccct	ccgcattgtg	gacatattca	gtctctcttt	ctgtaagtc	300

aatcttgtcc	atcacctttt	ctgtgatgtt	ccaccagtca	tggctgtgtc	ttgctctggg	360
aaacacatta	gcaagaagat	tctggttttt	atgtcaagct	tcaatgtctt	tttggctctt	420
ctagtatatc	tgacctccta	cctgttcata	ttcatcacca	tcttgaagat	gcactcagct	480
cagggaact	taaaagcttt	gtccacctgt	gcctctcacc	tcattgcagt	ctccatcttc	540
tatggaacta	ctatctttat	gtacttacag	cctagctcca	gccattccat	ggacacagat	600
gaaatggcat	cttgtttcta	tgtctgtgtc	atctcc			636

<210> 743

<211> 942

<212> DNA

<213> Unknown (H38g592 nucleotide)

<220>

<223> Synthetic construct

<400> 743

atgggggaca	accaatcacg	ggtcacagaa	ttcatcctgg	ttggattcca	gctcagtgtg	60
gagatggaag	tgctcctctt	ctggatcttc	tccctgttat	atctcttcag	cctgctgggg	120
aatggggcca	tctttgggct	catctgcctg	gactctaagc	ttcacacccc	catgtacttc	180
ttcctctcac	acctggccgt	cattgacatg	tcctatgctt	ccaacaatgt	tcccaagatg	240
ctggcaaac	tagtgaacca	gaaaagaact	atctcgttca	tctcttgcat	aatgcagact	300
tttttgtatt	tggtttttgc	tgttacagtg	tgcttgattt	tggtgggtgat	gtcctatgac	360
agatttgtgg	ccatctgcca	tcccctgcat	tacactgtca	tcattgagctg	gagagtgtgc	420
actgtcctgg	ctgtggcttc	ctgggtgttc	agcttctccc	tggtctctgg	ccatttagtt	480
ctcattctga	ggctgccctt	ctgtggggcc	caggaggtga	accacttctt	cgggtgaaac	540
ctgtctgtcc	tcaagttggc	ctgtgctgac	acctggctca	accaggtggg	catctttgca	600
gcctgcatgt	tcactcctgg	aggggtgactc	tgcttggtgc	tggtctccta	cttgacatc	660
ctggcggcca	tcttgaggat	ccagtctggg	gagggccgca	gaaaggcctt	ctctacctgc	720
tcctcccacc	tctgcgtggg	ggggcttttc	tttggcagcg	ccattgtcat	gtacatggcc	780
cccaagtcaa	gccattctca	agaacggagg	aagatccttt	ccctgtttta	cagccttttc	840
aaccgcgacc	tgaaccccct	catctacagc	cttaggaatg	cagaggtgaa	aggggctcta	900
aagagagtcc	tttggaacaa	gagatcaatt	gaagaatcat	tt		942

<210> 744

<211> 648

<212> DNA

<213> Unknown (H38g593 nucleotide)

<220>

<223> Synthetic construct

<400> 744

ttctctgacc	tctgtttctc	ttccgtgacc	attcccgaat	tgttacagaa	catgcagaac	60
caggacccat	ccatccccta	tgccgactgc	ctgacccaaa	tgtacttctt	cctgttatatt	120
ggagacctgg	agagcttcc	ccttgtggcc	atggcctatg	accgctatgt	ggccatctgc	180
ttccccctgc	actacaccgc	catcatgagc	cccattgctc	gtctcgccct	ggtggcgctg	240
tcctgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttgtgt	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
gccttctctg	acactcgagt	taatgaatgg	gtgatattta	tcattggagg	gctcattctt	420
gtcatcccat	tcctactcat	ccttgggtcc	tatgcaagaa	ttgtctcctc	catcctcaag	480
gtcccttctt	ctaagggtat	ctgcaaggcc	ttctctactt	gtggctccca	cctgtctgtg	540
gtgtcactgt	tctatggaac	cgttattggg	ctctacttat	gtcatcagc	taatagtctt	600
actctaaagg	acactgtcat	ggctatgatg	tacactgtgg	tgaccccc		648

<210> 745

<211> 936

<212> DNA

<213> Unknown (H38g594 nucleotide)

<220>

<223> Synthetic construct

<400> 745

atggatggag	agaatcactc	agtgggtatct	gagttttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcatttgtgt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcgt	tgggtgggtg	gagatgggtg	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcccttcat	ttctggctgt	tgccctggacc	cttgggtgtc	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttagc	cttctgtggc	cctaattgtg	tggacagctt	ctactgtgac	540
cttctctggc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggctcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgtttggaa	acattcctca	ggtggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagagg	atctca			936

<210> 746

<211> 384

<212> DNA

<213> Unknown (H38g595 nucleotide)

<220>

<223> Synthetic construct

<400> 746

atgaactcag	agaacctcac	ccggggccg	ggtgcccctg	ctgaattcgt	cctcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttctctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcatggatgc	ccggctccac	180
acacctatgt	acttcttctc	ggccaacctc	tcctgtctgg	atgcctgcta	ttcctccgcc	240
atcgccccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgccctcc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttc	aatgcaatta	360
atgccaaaag	tgaacaaaaa	tgta				384

<210> 747

<211> 810

<212> DNA

<213> Unknown (H38g596 nucleotide)

<220>

<223> Synthetic construct

<400> 747

atgaccattg	tcttgctttc	agctctggat	tcccggctgc	acacaccaat	gtatttcttt	60
ttggcaaacc	tctcattcct	ggacatgtgt	ttcaccacag	gttccatccc	tcagatgtct	120
tacaaccttt	gggttccaga	taagaccatc	agctatgtgg	gttgtgccat	ccagctgtac	180
tttgtctctg	ccctgggagg	ggtggagtgt	gtcctcctgg	ctgtcatggc	atatgaccgc	240
tatgctgcag	tctgcaaacc	cctgcactac	accatcatca	tgcacccacg	tctctgtgga	300
cagctggctt	cagtggcatg	gctgagtggc	tttggcaatt	ctctcataat	ggcaccctcg	360
acattgatgc	taccccgctg	tgggcacaga	cgagttgacc	actttctctg	tgagatgcca	420
gcactaattg	gtatggcctg	tgtagacacc	atgatgcttg	aggcactggc	ttttgccctg	480
gcaatcttta	tcatectggc	accactcatc	ctcattctca	tttcttatgg	ttacgttgga	540
ggaacagtgc	ttaggatcaa	gtcagctgct	gggcgaaaga	aagccttcaa	cacttgcagc	600
tcgcatctaa	ttgttgtctc	tctcttctat	ggtacaatca	tatacatgta	cctccagcca	660
gcaaatactt	attcccagga	ccaggggcaag	tttcttacc	tttctacac	aattgtcact	720
cccagtgtta	acccctgat	ctatacacta	agaaacaaag	atgttaaaga	ggccatgaag	780
aagggtgctag	ggaagggggag	tgagaaaata				810

<210> 748

<211> 342
 <212> DNA
 <213> Unknown (H38g597 nucleotide)

<220>
 <223> Synthetic construct

<400> 748
 atttgccttc ctctccacta tcccatccgt ataagcaaaa gagtgtgtgt gatgatgata 60
 acaggatctt ggatgataag ctctatcaac tcttgtgctc acacagtata tgcactctgt 120
 atcccatatt gcaagtccag agccatcaat cattttttct gtgatgttcc agctatgttg 180
 acgctagcct gcacagacac ttgggtctat gagagcacag tgtttttgag cagcaccatc 240
 tttcttgtgc ttcttttcac tggatttgca tgctcctatg gccgggttct ccttgtctgc 300
 taccgcatgc actctgcaga agggaggaag aaggcctatt ca 342

<210> 749
 <211> 635
 <212> DNA
 <213> Unknown (H38g598 nucleotide)

<220>
 <223> Synthetic construct

<400> 749
 tttgtggaca ttgcctgttc ctcagccaca gcacccaaga tgattgtaga ctctgtttct 60
 gagaaaaaga ctatttccta ctggggctgt ataactcaga tgtttacctt ccactttttt 120
 ggttgtgctg acatttttgt tttgactgtc atggcttttg atcgctatgc tgctatctgc 180
 caaccctcc gttacactgt catcatgagt gctaagtctt atactgtgct ggcatcactg 240
 tcctgggttg gggccctggg tcatttcctt gtccagaccc tctgacctt ccagctgccc 300
 ttctgtaatg ctcaggttat agaccattac ttttgtgatg tccaccaggt cctaaaaactt 360
 gcctgtgctg atacaactct ggtaagtatg ttgggtggtg ccaacagtgg tctcatctcc 420
 ctgggggtgt tctcattct tttggcctcc tacacagtca ttctgtttag tcttcaaaaa 480
 cagtctgcag agagctgaca caaagttctc tctacctgtg gatctcatct gactatagta 540
 actttcttct ttgttccgtg tacctttatt tatctccatc cactactttc ccattggata 600
 aagctgtgtc tgtgttctat accaccatca cccca 635

<210> 750
 <211> 633
 <212> DNA
 <213> Unknown (H38g599 nucleotide)

<220>
 <223> Synthetic construct

<400> 750
 tttgttgatt tctgttattc caccacaatt acacccaaac tgctggagaa cttgggtgcg 60
 gaagatagaa ctatctcctt cacaggatgc accatgcagt tattctttgt ctgcatattt 120
 gtagtaacag aaacatgcat gctggcagt atggcctatg accgatatgt ggcggtgtgt 180
 accctcttct ctacacagt gcaatgtacc agaggctttg ctcttggtta gtggctacat 240
 catactgctg ggggatagtc tgttccctga cacttaccta gtttctactg gagttatcct 300
 tcagaggaaa taatatcatt aataactttg tctgtgagca cgctgccatt gttgctgtgt 360
 cttgctctga cccctgtgtg agccagtaga tcactttagt ttctgccaca ttcaatgaaa 420
 taagcagcct gcttccatg ctttcatttt tatcactgtc atgaagacgg cttccactgg 480
 ggggagcaag aaagcgttct ccacgtctgc ctccactga cggccattac cattttccat 540
 gggactatct ttttctcta ctgtgttct aacgccaaaa gttcgtggct catggtcaag 600
 gtggcctctg gcttttacac agtggtcacg ccc 633

<210> 751
 <211> 646
 <212> DNA
 <213> Unknown (H38g600 nucleotide)

<220>

<223> Synthetic construct

<400> 751

tttgttagaca	tctgtgttac	ctccaccaca	gtcccaaaga	cactgtcaaa	catccggaca	60
cagagtaaag	tcatcaccta	tgcaggttg	atcacccaga	tgtacttttt	tgtactcttt	120
atagtgttg	acagcttact	cttgaccgtg	atggcctatg	accagtttgt	ggccatctgt	180
cacccctgc	actacacgg	catcgtgaac	cctcggctct	gtggactgct	ggttctggcg	240
tcctggatca	tgagtgcct	gaattccttg	atagaaagct	taatgggtgt	gccactgctc	300
ttttgtacag	acttgaaaat	ccccacttt	ttctgtgaac	ttaatcagat	aatccgcagt	360
gcctgttctg	acacctttct	taatgacatg	gtgatgtatt	tgtcagctgt	gcttctaggt	420
aggggatgtt	tactgggat	cctgtactct	tactttaaga	cagtttctc	catacgtgca	480
atctcatcag	ctcaggggaa	gtacaaggca	ttttccacct	gtgcatcgca	cctctcagtt	540
gtctccttat	tttattgtat	gggccttggg	gtgtacctta	gtgctgctgc	aaccacaac	600
tcactctcaa	gtgcaacagc	ctctgatgta	cactgtggtc	accccc		646

<210> 752

<211> 342

<212> DNA

<213> Unknown (H38g601 nucleotide)

<220>

<223> Synthetic construct

<400> 752

atttgctttc	ctctccacta	tcccatccgt	atgagaaaaa	gagtgtgtgc	actgatgata	60
acaggatctt	ggatgatagg	ctccatcaac	tcttgtgtct	acacgggtata	tgcactccgt	120
atcccatatt	gcaagtccag	agccatcaat	cattttttct	gtgatgttcc	agctatgttg	180
accctagcct	gcacggatac	ctgggtctat	gagtgcacgg	tgtttttgag	caccaccatt	240
tttcttgtgt	ttcccttcat	ttgtattgca	tgttcctatg	gccggattct	ccttgcgtgc	300
taccacatgc	actctgcaga	agggaggaag	aaggcctatt	cg		342

<210> 753

<211> 648

<212> DNA

<213> Unknown (H38g602 nucleotide)

<220>

<223> Synthetic construct

<400> 753

cttgctgatg	tctcctatgc	cacaagtgtg	gtccctcagc	tgctggcaca	ttttcttgca	60
gaacataaag	ccatcccat	ccagagctgt	gcagcccagt	tatttttctc	cctggccttg	120
ggtgggattg	agtttgttct	cctggcggtg	atgggctatg	accgctatgt	ggctgtgtgt	180
gatgccctgc	gatactcggc	catcatgcat	ggagggtctg	gtgctagggt	ggccatcaca	240
tcctgggtca	gtggcttcat	cagctctcct	gtgcagactg	ctatcacctt	tcagctgccc	300
atgtgcagaa	acaagtttat	tgatcacata	tcctgtgaac	tcctagctgt	ggtcaggctg	360
gctcgtgtgg	acacctctc	caatgaggtc	accatcatgg	tgtctagcat	tgttcttctg	420
atgacaccct	tctgcctgg	tcttttgtcc	tacatccaga	tcctctccac	catcctaaag	480
atccagtcga	gagaaggaag	aaagaaagct	ttccacacgt	gtgcctctca	cctcacagtg	540
gttgccctgt	gctatgggtg	ggccattttc	acttacatcc	agccccactc	cagtcctctc	600
gtccttcagg	agaagttgtt	ctctgtcttt	tatgccattt	taacacca		648

<210> 754

<211> 635

<212> DNA

<213> Unknown (H38g603 nucleotide)

<220>

<223> Synthetic construct

<400> 754

tttgtggaca	ttgcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgctg	agatttttgt	cttgactgtc	atggcttttg	atcgctatgc	tgctatctgc	180
caaccctcc	gttacactgt	catcatgagt	gctaattgctt	atactgtgct	ggcatcactg	240
tcctggttgg	gggccctggg	tcattccctt	gttcagaccg	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaccattac	ttttgtgatg	tccaccctagt	cctaaaaactt	360
gcctgtgctg	atacaactct	ggtaaataatg	ttgggtggtg	ccaacagtgg	tctcatctcc	420
ctgggggtgtt	tcctcattct	tttggcctcc	tacacagtca	ttctgttttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tggtttctat	accaccatca	cccca			635

<210> 755

<211> 342

<212> DNA

<213> Unknown (H38g604 nucleotide)

<220>

<223> Synthetic construct

<400> 755

atatgcaaac	ctttacttta	tccagccatt	atgaccaatg	gactgtgcat	ccggctatta	60
atcttgtcat	atgtaggtgg	tcttcttcat	gctttaatcc	atgaaggatt	tttattcaga	120
ctaaccttct	gtaactccaa	catagtacat	cacatttact	gtgacattat	cccattgtct	180
aagatttctt	gtactgattc	ttctattaat	tttctaattg	tttttatttt	ctcagggttca	240
attcaggat	tcagcattgt	gactattctt	gtatcttata	catttggttct	cttcgcaatc	300
ttaaaaagga	aatctgataa	aggtgtaagg	aaagcctttt	cc		342

<210> 756

<211> 333

<212> DNA

<213> Unknown (H38g605 nucleotide)

<220>

<223> Synthetic construct

<400> 756

atttgtaacc	ctctgagata	ccccatcatc	atgagcaggc	acgtctgtgt	gcagatggcc	60
gccatctcct	gggtgacagg	ctgtctgact	gctctgctgg	taactagttg	tgccctgcag	120
atccccctct	gtgggaatgt	catcgaccat	ttcacatgtg	aaatccttgc	agtgctaaaa	180
ctagcttgtg	tgagttccct	gctcgtggac	atgggttatg	tggtgggcag	tattctcctg	240
ctgcccatac	caatgctttt	gatttgcac	tcgtatggct	tcatcctttc	tacaattctg	300
aggatcggct	caacagaggg	aagaaacaaa	gct			333

<210> 757

<211> 665

<212> DNA

<213> Unknown (H38g606 nucleotide)

<220>

<223> Synthetic construct

<400> 757

ttgcctgaca	tcggttttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagsagag	tcattctcta	tgaggctgc	ctgactcaga	tgtctctctt	tgccatttkt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtagggcc	tatggccggg	ttgtagccat	180
ctgtcacctc	ctatatcggt	cagccatctt	gaacccatgt	ttctgtggct	tcctagattt	240
gttgtcttcg	ttttgttttg	ttttgttttt	ctcagtcctt	tagactccca	gctgcacaac	300
ttgattgcct	tacaaatgac	cggcttcaag	gatgtggaat	tcctaatttc	ttctgggaac	360

cttctcaact	ccccatcttg	catgtttgtga	caccttcacc	aggaacatca	acctgtat	420
cctgtctgcc	gtatttggtt	ttcttcccat	cttggggacc	ttttctctta	ctgtaaaatt	480
gtttctccca	ttctgagggt	ttcatcctca	ggtgggaagt	ataaaccttc	tccacctgtg	540
ggtctcacct	gccagttggt	tgtgtat	gtggaacagg	tgttgagggt	taccttggtt	600
cagatgtgtc	atcttcccca	agaaagagtg	cagtgccttc	agtgatgtac	ccggtgggtca	660
cctcc						665

<210> 758

<211> 646

<212> DNA

<213> Unknown (H38g607 nucleotide)

<220>

<223> Synthetic construct

<400> 758

ttttagaca	tctgtgttac	ctccaccaca	gtcccaaaga	cactgtcaaa	catccggaca	60
cagagtaaag	tcatcaccta	tgcagattgc	atcaccaga	tgtacttttt	tgtactcttt	120
atagtgttgg	acagcttact	cttgaccgtg	atggcctatg	accagtttgt	ggccatctgt	180
cacccctgc	actacacggt	catcgtgaac	cctcggtctt	gtggactgct	ggttctggcg	240
tcctggatca	tgagtgcctt	gaattccttg	atagaaagct	taatggtgtt	gccactgctc	300
ttttgtacag	acttgaaaat	ccccactttt	ttctgtgaac	ttaatcagat	aatccgcagt	360
gcctgttctg	acacctttct	taatgacatg	gtgatgtatt	tgtcagctgt	gcttctaggt	420
aggggatgtt	tactgggat	cctgtactct	tactttaaga	cagtttcttc	catactgca	480
atctcatcag	ctcaggggaa	gtacaaggca	ttttccacct	gtgcacgcga	cctctcagtt	540
gtctccttat	tttattgtat	gagccttggg	gtgtacctta	gtgctgctgc	aaccacaac	600
tcactctcaa	gtgcaacagc	ctctgatgta	cactgtgggtc	acccc		646

<210> 759

<211> 834

<212> DNA

<213> Unknown (H38g608 nucleotide)

<220>

<223> Synthetic construct

<400> 759

atggcaatta	ggaaccattc	caccctccac	aaacccatgt	actttttttt	agctaatatg	60
tcctttcttg	agatttggtg	tgtcactgtc	actattccca	agatgcttgc	tggctttggt	120
ggatccaaac	aggatcatgg	acagctaata	tcctttgagg	gatgcatgac	acagctttac	180
tttttccctg	gcttgggctg	cactgagtg	gtccttctcg	ctgttatggc	caatgatcgc	240
tatatggcca	tctgctatct	tctccacaac	ccagtcattg	tcagtggccg	gctgtgtgtg	300
cagatggctg	ctggctcttg	ggctggaggt	tttggcatct	ccatgggtcaa	agtttttctt	360
atttcgggcc	tctctaacgg	tggccccaac	atcatcaacc	actttttctg	tgatgtctct	420
ccattgctca	acctctcatg	cactgatatg	tccacagcag	agcttacaga	tttcatcctg	480
gccattttta	ttcttctagg	gccactctct	gtcactgggg	cctcctatgt	ggccattact	540
ggtgctgtga	tgcacattcc	ttcggtgtgt	ggacggtata	aggccttttc	cacctgtgccc	600
tctcatttca	atgttgtgat	aattttttat	gcagccagta	tcttcattta	tgctcggcca	660
aaggcacttt	cagcttttga	caccaacaag	ttgggtctctg	tactgtatgc	tgctcattgta	720
ccattgctca	atcccatcat	ttactgcctg	cgcaatcaag	aggtcaagag	agccctatgc	780
tgatatttgc	acctgtacca	gcaccaggat	cctgacccca	agaaaggtag	caga	834

<210> 760

<211> 942

<212> DNA

<213> Unknown (H38g609 nucleotide)

<220>

<223> Synthetic construct

<400> 760

atggaattta	cagatagaaa	ctacacgttg	gtcactgagt	ttattctatt	aggttttcca	60
actcgccctg	aactgcagat	tgtcctgttc	ctcatgtttc	tgacattgta	tgctataatt	120
ctgataggga	acattggatt	gatgctgttg	atcaggattg	atcctcacct	tcaaaccccc	180
atgtattttt	tccttagcaa	cctatcattt	gtagaccttt	gctattttctc	agacattggt	240
cccaaaatgc	tggtaaat	cctctcggag	aacaaatcta	tttcctatta	tgggtgtgcc	300
ctgcagtttt	attttttctg	tacttttgca	gatacagaat	ccttcaccc	ggccgccatg	360
gcctatgac	gctatgtcgc	catctgtaac	cctttattgt	acacagttgt	gatgtcttgy	420
ggcatctgta	tgcggttgat	tgtcttgta	tacctggag	gcaacatgag	ttccctgggt	480
cacacatcct	ttgcctttat	tctgaaatat	tgtgacaaaa	atgttattaa	tcattttttc	540
tgtgacctcc	ctccctgtct	taaactatcc	tgcactgaca	caacaattaa	tgagtggctc	600
ctctccacat	acggcagctc	agtggaaatc	atttgtttta	tcatcatcat	catctcctac	660
tttttcatte	ttctctcagt	cttaaagatc	cgctctttca	gtgggaggaa	gaagaccttt	720
tctacatgcg	cctctcacct	gacttcagt	acgatctacc	aagggaactct	cctctttatt	780
tactcacggc	ccagctacct	gtattctcca	aacactgata	aaattatctc	agtgttctac	840
accattttca	ttccagtgct	gaatccgttg	atttatagtt	tgagaaataa	agatgtaaag	900
gatgcagctg	agaaagttct	aagatcaaa	gtagattctt	ca		942

<210> 761

<211> 948

<212> DNA

<213> Unknown (H38g610 nucleotide)

<220>

<223> Synthetic construct

<400> 761

atggataacc	aaagctccac	accgggcttc	ctccttcttg	gcttctctga	acaccaggg	60
ctgggaagga	ctctcttctg	ggatgtcatc	acttcttacc	tcctaaccct	agtgggcaac	120
acactcatca	tctctgtctc	tgcgctggac	accaagctcc	actctccaat	gtactttttc	180
ctctccaacc	tctccttctt	ggacctctgt	ttcaccacga	gttggtgtcc	ccaaatgctg	240
gccaacctct	ggggcccaaa	gaagaccatc	agcttctctg	actgctctgt	ccagatcttc	300
atcttctctg	ccctggggac	aactgagtgc	atcctcatga	aagtgatggc	ttttgatcgc	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggtcattggg	ctagtggggg	cagtgggtcca	gacaccatcc	480
accctgcacc	tgccttctct	ccccgatcgg	cagggtggatg	attttgtctg	tgaggtccca	540
gctctaattc	gactctctct	tgaagacacc	tcctacaatg	agatccagg	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcctcttg	tctcttacgg	agccattacc	660
tgggcagtgc	tgaggattaa	ctccgccaca	gcatggagaa	aggccttttg	gacctgtctc	720
tcccatctca	ctgtgggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcaact	840
ccttcactta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaag	agactccagg	gaaagctgga	gagctgct		948

<210> 762

<211> 927

<212> DNA

<213> Unknown (H38g611 nucleotide)

<220>

<223> Synthetic construct

<400> 762

atgaaaagag	agaactttac	tctcatcact	gactttgttt	tccaaggttt	ctctagcttc	60
catgagcagc	agatcaccc	ttttggcgtg	ttccttgac	tatacatctt	aaccttagca	120
ggcaatatca	tcattgtgac	catcatccga	attgatcttc	atcttcacac	acccatgtac	180
ttcttctctg	gcatgctgtc	cacttcagag	actgtatata	cattgggtcat	tctcccaaga	240
atgctctcca	gcctcgtagg	tatgagccag	cccatgtcat	tggcaggggtg	tgccacacag	300
atgttctttt	ttgtaacctt	tggcatcact	aactgcttcc	tgctcacagc	aatgggatat	360
gaccgctctg	tggccactctg	caacccctg	agatacatgg	ttattatgaa	caagaggctg	420
cgtatccaac	ttgtcctggg	ggcctgcagc	attgggtgta	ttgtagcaat	aacgcaagtg	480
acatctgtat	tcaggttacc	cttctgtgct	agaaaagggtc	cccacttctt	ctgtgacatc	540

cgccctgtga	tgaagctctc	ctgcattgac	accactgtca	atgaaatcct	gacttttgatt	600
atcagtgtgc	tgggtgcttg	tgtacctatg	ggtctgggtt	tcattttctta	tggtctcatt	660
atctctacaa	tcctcaagat	tgcttcagtt	gagggccgga	agaggcttt	tgccacctgt	720
gcatcccacc	tcactgtggt	cattgtccac	tacagctgtg	cctccattgc	ctacctcaag	780
cccaagtcag	agaacaccag	agaacatgac	cagctgatct	cggtgacct	caactgtcatc	840
actcccctac	tgaaccctgt	ggtatacacc	ctgagaaata	aagaggctca	agatgctctg	900
tgcagggtcg	ttggtgggaa	gttttcc				927

<210> 763

<211> 650

<212> DNA

<213> Unknown (H38g612 nucleotide)

<220>

<223> Synthetic construct

<400> 763

tgggctgaca	tcggtttcac	ctcggccacg	gctcccaaga	tgattgtgga	catgcagtcg	60
cataggagag	ccatctctca	tgcgggctgt	ctgacgcaga	tgtctttctt	gttcctttgt	120
gcatgtgtag	aaggcatgct	cctgactgtg	atggcctatg	actgctttgt	agacatctgt	180
cgccctctgc	actaccagtc	catcggaat	cctcacttct	gtgtcttctt	cgtgggggtg	240
tcctttctcc	ttagcctgtg	ggattcccag	ctgcacagtt	ggattgtgtt	acaatatcac	300
catcttcaag	aatgtggaaa	tctctaattt	tgtctgtgac	ccctctcaac	ttctcaaact	360
tgctgtttct	gacggcgctc	tcaatagcat	attcatatat	ttgatagta	ctatgttttg	420
tttcttctcc	atttcaggga	tcctatggtc	ttactataaa	atcgtcccct	ccattctaag	480
gatttcacgc	tcagatggga	agtataaagc	cttctccacc	tgtggctcct	caccaggcag	540
ttgtttgctg	attttataga	acaggcattg	gcatgtacct	gacttcagct	gtgtcaccac	600
ccccaggaa	tgggtgtggtg	gcatcattga	tatacgtctt	tgctactccc		650

<210> 764

<211> 641

<212> DNA

<213> Unknown (H38g613 nucleotide)

<220>

<223> Synthetic construct

<400> 764

ttcactgacc	tcttctttgt	caccaacaca	atccccaaga	tgctgggtgaa	cctccagtc	60
cagaacaaaag	ccatctccta	cacagggtgt	ctgacacagc	tctacttcct	ggtctccttg	120
gtggccctgg	acaacctcaa	cctggccgtg	atggcgtatg	atcgctatgt	ggccatctgc	180
cgccccctcc	actatgtcac	agccatgac	cctgggctct	gtatcttctg	cctctccttg	240
tggtgggtgt	tctctgccct	ctatggcctc	atccatatcc	tcctcatgac	caggtgacct	300
tctgtgggtc	tcaaaagatc	cactacctct	tctgtgagat	gtacttcctg	ctaaggctgg	360
catgttccaa	catccacgtc	aaccacacag	tactggttgc	cacgggctgc	ttcatcttcc	420
tcacccctt	aggcttcag	atcacatcca	acgccgcac	tgtcagagcc	atcctccaaa	480
taccctcagc	cactgggaag	tacaaagcct	tctccacctg	tgcttcccat	ttggctgtgg	540
tctccctctt	ctatgggact	ctgggtatgg	tgtacctgca	gcccctccaa	acctactcca	600
tgaaggactc	agtagccaca	gtgatgcatg	cggtgggtgac	g		641

<210> 765

<211> 635

<212> DNA

<213> Unknown (H38g614 nucleotide)

<220>

<223> Synthetic construct

<400> 765

tttgttgatt	tctgttattc	caccacaatt	acacccaaac	tgctggagaa	cttgggtgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	accatgcagt	tattctttgt	ctgcatattt	120

gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgccat	tgttgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcagttaa	420
ataagcagcc	tgcttcctat	gctttcattt	ttatcactgt	catgaagacg	ccttccactg	480
gggggcgcaa	gaaagcgctt	tccacgtctg	cctcccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcttc	tactgtgttc	ctaactccaa	aagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgggtca	ttccc			635

<210> 766

<211> 635

<212> DNA

<213> Unknown (H38g615 nucleotide)

<220>

<223> Synthetic construct

<400> 766

ttagttgatt	tctgttattc	caccacaatt	acacccaagc	tgctgaggaa	cttggttgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	accatgcagt	tattccttgt	ctgcatattt	120
gtagtaacag	aaacattcgt	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgccat	tgttgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcagcc	tgcttcctat	gctttcattt	ttatcactgt	catgaggacg	ccttccactg	480
gggggcgcaa	gaaagcgctt	tccacgtctg	cctcccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcttc	tactgtgttc	ctaactccaa	gagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgggtca	ttccc			635

<210> 767

<211> 936

<212> DNA

<213> Unknown (H38g616 nucleotide)

<220>

<223> Synthetic construct

<400> 767

atgtccattt	ccaacatcac	agtctacatg	ccctctgtgt	tgacactagt	agggatccca	60
ggcctagaat	ctgtgcagtg	ctggattggg	attccattct	gtgccattta	tctcattgct	120
atgattggaa	attccttgct	tctgagcatc	atcaaactcg	agcgcagtct	ccatgagccc	180
ttgtacattt	tcttaggcatt	gctaggagcc	acagacattg	cacttgctag	cagcattatg	240
ccaaagatgc	ttggaatatt	ctggtttaat	gtgcctgaaa	tctattttga	ttcctgcttg	300
cttcaaattg	ggttcatcca	cacattgcag	ggtatagagt	caggcatcct	tgtggccatg	360
gccctggacc	gttatgtggc	catctgttat	ccactaagac	atgccaacat	cttcacccac	420
cagcttggtca	ttcagatagg	aactatgggt	gtactcaggg	ctgctattct	tgtagcccca	480
tgccatgtac	tgataaagt	ccggtttcaa	ttttatcaca	caacagtcac	ctcccactcc	540
tactgtgagc	atatggccat	tgtgaaacta	gcagcagcaa	atgttcaagt	caacaaaatc	600
tatggtttgt	ttgtggcctt	cactgtagca	ggatttgacc	tcacattcat	cacattgtcc	660
tacatccaga	tatttatcac	agtttttctg	ttgcccaga	aggaggctag	gtttaaagca	720
ttcaatacct	gcattgctca	catctgtgtc	ttcctccagt	tctacctcct	tgctttcttc	780
tcctttctca	cacataggtt	tgggtctcac	atccccctt	atatccatat	tctcttttct	840
agcatttact	tgctgggtccc	tccatttctc	aatccacttg	tctatggtgc	aaagaccaca	900
cagattcgca	ttcatgtggt	aaaaatgttc	tgttca			936

<210> 768

<211> 954

<212> DNA

<213> Unknown (H38g617 nucleotide)

<220>

<223> Synthetic construct

<400> 768

atgtggcaga	agaatcagac	ctctctggca	gacttcatcc	ttgaggggct	cttcgatgac	60
tcccttacct	accttttctt	tttctccttg	accatgggtg	tcttccttat	tgcggtgagt	120
ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttcctgctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaat	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaacccag	300
cacttcctct	atttgtgtct	agggtggtgt	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcattccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcacttccc	tttctgtggg	cctcggaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagtt	gggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
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cttcaaagtg	tcattcagat	gcgtcctatc	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacgggtgg	ttctcttttg	tttgggtgct	gcattctctc	ctacatgaga	780
cccaggtccc	agtgcactct	attgcagaac	aaagtgtggt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tgttatcacc	cagtgcattc	aacgactgca	attg	954

<210> 769

<211> 881

<212> DNA

<213> Unknown (H38g618 nucleotide)

<220>

<223> Synthetic construct

<400> 769

gccacgtaca	attccagcaa	tactgtgggtg	acagagtttg	tgttttctgag	cttcccagag	60
ctgcaccatc	ttcaagggct	gctatttgg	cactcctcat	catctatgtg	gtgaccatcc	120
tagaggacct	ggctgtcgtg	gggaccatca	gagccagcca	ccacctgcac	atatccacac	180
acctcttctt	ggcccaactc	tcgggtgctg	agactctgta	cacctcggtc	accgtcccaa	240
agctgttggc	cggactccca	gcacgagcga	cgaccatcta	tctccttctc	ggggcacctc	300
acctggctgc	tcctcttctt	ctcactcagc	tcctctgagt	gcgtcctccc	ggccaacatg	360
gactgtgact	ggcaccag	catctgccac	ctgctgcact	accagccca	tcattggactc	420
catgcagctg	gctctgctg	cacctggcca	tcagcgccca	gctcagcagc	ttcccagcct	480
cctttgtgtc	cacggctctc	aactccagcc	tgaggctccg	cagccccgat	gtcctcaacc	540
acttctgtga	tatcccaccc	ccgctagggc	tctcttgctc	cagcaccact	accatagaaa	600
tgcggtactca	ggcagcccag	gtgatccttg	cggtctcctt	gcaggcaacc	acggtctcct	660
acaccacat	cctggccaga	tcgctgagga	ttccagaaa	gcccagcagc	ttaaaggcctt	720
ccccacctat	gcctcccacc	tgggtgtggc	gctcctctaa	cctcatcaag	ctggtgttca	780
gggtgtact	tggttgggat	ccctctgtc	aaacccatca	tctactgcct	gggaactgca	840
acatcaggga	ggccctggcc	aaactcctcc	aggcccttcc	c		881

<210> 770

<211> 880

<212> DNA

<213> Unknown (H38g619 nucleotide)

<220>

<223> Synthetic construct

<400> 770

gccacataca	attccagcaa	tactgtgggtg	acagagtttg	tctttctgag	cttcccagag	60
ctgcgccatc	ttcaagggct	gctatttgg	cactcctcat	catctatgtg	gtgaccatcc	120
tagaggacct	ggctgtcgtg	gggaccatca	gagccagcca	ccacctgcac	atatccacac	180
acctcttctt	ggccaaactc	tcgggtgctg	agaccctgta	cacctcggtc	accgtcccaa	240
agctgttggc	cggactccca	gcacgagcga	cgaccatcta	tctccttctc	ggggcacctc	300

acctggctgc	tectcttctc	ctcactcagc	tcctctgagt	gcacccctcc	ggccaacatg	360
gactgtgact	ggcaccgggt	catctgccac	ctgctgact	acccagccca	tcattggactc	420
catgcagctg	gctctgcctg	cacctggcca	tcagcgccca	gctcagcagc	ttcccagcct	480
cctttgtgtc	cacggctctc	aactccagcc	tgaggctccg	cagccccgat	gtcctcaacc	540
acttctgtga	tatcccaccc	ccgctagggc	tctcttgctc	cagcaccact	accatagaaa	600
tgccgactca	ggcagcccag	gtgatccctg	cggcttcctt	gcaggcaacc	acggctctcct	660
acaccacat	cctggccaga	tcgctgagga	ttccagaaaag	gccagcagc	ttaaaggcctt	720
ccccacctat	gcctcccacc	tgggggtggc	gctcctctaa	cctcatcaag	ctgggtgtcag	780
gggtctactt	ggttgggac	cctctgctca	aacccatcat	ctactgcctg	ggaactgcaa	840
catcagggag	gccctggcca	aactcctcca	ggcccttccc			880

<210> 771

<211> 524

<212> DNA

<213> Unknown (H38g620 nucleotide)

<220>

<223> Synthetic construct

<400> 771

ctcctaattg	cagcagacaa	ccacacagcg	tagaggcggt	tgctctgcag	ggttttctctg	60
aagaccttcc	actccagggc	tgctgctttg	cttttttcc	cctttacctg	atggcacttg	120
taggaaacat	cctcatggtc	atggccatca	gtctgaatcc	aggcctccac	acgccagtgt	180
acttctttct	caccaacctg	gcccttttag	acatcgctctg	cacatccatg	gacaaagca	240
gagtggtggc	tgctgtgtac	acagtggtca	gccccaccct	gaacccctca	cctactccct	300
gcggaacaag	gacttatcag	tagcactgag	gagagtgttt	tcttgcatca	ggtaaaagga	360
agggaagttt	ctagtgtgaa	atgttccagg	tgtaacaaa	ctaatttcaa	catatgactt	420
tgagaatctc	atgcaagcag	caaggaacaa	gaaagtaatt	aatgccacat	atttataaat	480
aatgtgctcc	cgcacggggc	tgccatcatt	caatgtggaa	ctcc		524

<210> 772

<211> 951

<212> DNA

<213> Unknown (H38g621 nucleotide)

<220>

<223> Synthetic construct

<400> 772

atggaaagga	ccaacgatcc	cacgtcgaca	gaatttttcc	tggtagggtc	ttctgcccac	60
ccaaagctcc	agacagtttt	cttcgttcta	attttgtgga	tgtacctgat	gacccgtgctt	120
ggaaatggag	tccttatctc	agttatcacc	tttgattctc	acctgcacac	ccccatgtat	180
ttcttctctc	gtaatctttc	cttctctgac	gtttgttaca	caagttcttc	tgteccacta	240
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atgtttatatt	cttttgccat	ggggggccac	gagtgcatga	tcttaggcac	gatggcactg	360
gaccgctatg	tggccatctg	ctacccactg	agataccctg	tcattcatgag	caaggggtgcc	420
tatgtggcca	tggcagctgg	gtcctgggtc	actgggcttg	tggactcagt	agtgcagaca	480
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attctggcta	tcttgaaact	ggcctgtgct	gatatttcaa	tcaatgtgat	tagtatgaca	600
gggtcgaaac	tgattgttct	ggttattcca	ttgttagtaa	tttccatctc	ttacatattt	660
attgttgcca	ctattctgag	gattccttcc	actgaaggaa	aacataaggc	cttctccacc	720
tgctcagccc	acctgacagt	ggtgattata	ttctatggaa	ccatcttctt	catgtacgca	780
aagcctgagt	ctaaagcctc	tggtgattca	ggtaatgaag	acatcattga	ggccctcatc	840
tcccttttct	atggagtgat	gactcccatg	cttaatcttc	tcattctatag	tctgcgaaac	900
aaggatgtaa	aggctgctgt	caaaaacata	ctgtgttaga	aaaacttttc	t	951

<210> 773

<211> 954

<212> DNA

<213> Unknown (H38g622 nucleotide)

<220>

<223> Synthetic construct

<400> 773

atggaatggg	aaaaccaa	cattctggtg	gaattttttc	tgaagggaca	ttctgttcac	60
ccaaggcttg	agttactctt	ttttgtgcta	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcatc	ttggaccctc	accttcacac	ccctatgtac	180
ttctttcttg	ggaacctctc	cttcttggac	atctgctaca	ccaccacctc	tattccctcc	240
acactagtga	gcttcctttc	agaaagaaag	accatttcct	tttctggctg	tgcagtgcag	300
atgttccttg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caaccctctg	agatatecca	tcacatgag	caagaatgcc	420
tatgtacca	tggctgttgg	gtcctggttt	gcagggattg	tcaactctgc	agtacaaact	480
acatttgtag	tacaattggc	tttctgcagg	aagaatgtca	tcaatcattt	ctcatgtgaa	540
attctagctg	tcataaggtt	ggcctgtgct	gacatctcag	gcaatgagtt	cctcatgctt	600
gtggccacaa	tattgttcac	attgatgcc	ctgctcttga	tagttatctc	ttactcatta	660
atcatttcca	gcacccctca	gattcactcc	tctgagggga	gaagcaaagc	tttctctacc	720
tgctcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtatatg	780
aagcccaagt	ctaaagagac	acttaattca	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aagaggcagt	aaaacaccta	cgaacagaa	ggttctttag	caag	954

<210> 774

<211> 369

<212> DNA

<213> Unknown (H38g623 nucleotide)

<220>

<223> Synthetic construct

<400> 774

ttcctccttt	aggccaacta	cagcgcagag	gagcgccttc	tcctgctggg	tttctccgac	60
tggccttccc	tgcagccggt	cctcttccgc	cttgctctcc	tgtgctacct	cctgaccttg	120
acgggcaact	cggcgctggt	gctgctggcg	ggtcgaccgc	cgctgcaca	cgcccatgta	180
ctacttcttc	tccacctggc	cttggtagac	gcgggcttca	ctactagcgt	ggtgccgcgc	240
ctgctggcca	acctggcgga	ccagcgcctc	cgtgcgcgca	gccactgcac	ggcccagctg	300
tgcgcacgc	tggctctggg	ttccgcccga	tgcgtccatc	tggcggtgat	ggctctgggc	360
cgcgcggtc						369

<210> 775

<211> 945

<212> DNA

<213> Unknown (H38g624 nucleotide)

<220>

<223> Synthetic construct

<400> 775

atgagacaga	ataacaatat	tacagaattt	gtcctcctgg	gcttttctca	ggatcctggg	60
gtgcaaaaaag	cattatttgt	catgttttta	ctcacatact	tgggtgacagt	ggtggggaac	120
ctgctcattg	tgggtgat	tattgccagc	ccttccttgg	gttccccaat	gtatttcttc	180
cttgccctgcc	tgtcatttat	agatgctgca	tattccacta	ccatttctcc	caagttaatt	240
gtaggcttat	tctgtgataa	aaagactatt	tccttccaag	gttgcatggg	ccagctattt	300
atagaccatt	tctttgggtg	ggctgaggtc	ttccttctgg	tgggtgatggc	ctgtgatcgc	360
tatgtggcca	tctgtaagcc	actgcaactat	ttgaccatca	tgaatcgaca	ggtttgcttc	420
cttctgttgg	tgggtggccat	gattggaggt	tttgtacatt	ctgcgtttca	aattgttgtg	480
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ttacttgaac	tggcatgcac	tgacacctac	tttataggcc	tcactgttgt	tgtcaatagt	600
ggagcaatct	gtatgggtcat	tttcaacctt	ctgttaatat	cctatggagt	catcctaagc	660
tcccttaaaa	cttacagtca	ggaaaagagg	ggtaaagcct	tgtctacctg	cagctccggc	720
agtaccgttg	ttgtcctctt	ttttgtaccc	tgtattttca	tatatgttag	acctgtttca	780
aactttccta	ctgataagtt	catgactgtg	ttttatacca	ttatcacaca	catgctgagt	840

cctttaatat atacgttgag aaattcagag atgagaaatg ctatagaaaa actcttgggt 900
 aaaaagttaa ctatatttat tataggagga gtgtccgtcc tcatg 945

<210> 776

<211> 352

<212> DNA

<213> Unknown (H38g625 nucleotide)

<220>

<223> Synthetic construct

<400> 776

cgctgtgccc	cccgcctgct	ggaccacttc	atctgtgagc	tgccggcggt	gctcaagctg	60
gcctgaggag	gcgacggaga	cactaccgag	aaccagatgt	tcgccgcccg	cgtgggtcatc	120
ctgctgctgc	cgtttgccgt	cactctggcc	tcctacgggtg	ccgtggcccg	agactgtctg	180
ttgcatgcgg	ttcagcggag	gccggcagag	aggcggtggg	cacgtgtggg	tcccacctga	240
cagccgtctg	cctgttctac	ggctcggcca	tctacacctg	cctgcagccc	gcgcagcata	300
caaccaggca	cggggcaagt	tcgtatcgct	cttctacacc	gtgggtcacac	ct	352

<210> 777

<211> 937

<212> DNA

<213> Unknown (H38g626 nucleotide)

<220>

<223> Synthetic construct

<400> 777

ggactgagta	ataatgttac	agaatttgct	ctcttgggca	acactcagtg	tcctgatgtg	60
caaaatgcat	tatttgtcat	ggttttactc	acatacgttg	tgagtatggc	gggaaacttg	120
cttgcctgtg	tggtatttat	ttccagccct	tcctttggct	ccccaatgta	cttcttcttc	180
acagcctggt	atztatatat	gctgcatatt	ccaataccat	ttctcccaaa	ttgattatag	240
gcttactcca	tgataaaaag	actattttct	tcacagcatg	catggggcag	ctatttatag	300
accacttatt	tggtgggtgct	gaggtcttcc	tacttgtggg	gatgtcctac	gatttctatg	360
tgcccatctc	taagccactg	cactatttga	ccatcatgaa	tcaacagggt	tgtatccttc	420
tgttgggtgg	ggctgtgact	ggaggttttg	tgagttgtgt	gtttcaaatt	gttgttgtgt	480
acactctctc	gttctgtggc	caaattgtcac	tgaccacttt	gtctgtgaca	tgtaccatt	540
attggaactg	gtttgcactg	atacctactt	tataggtctc	actgttggtg	ccaatgggtc	600
agcaatctgt	atggctcgtc	tcacccttct	actaatctcc	tatggagtca	tcctaaacaa	660
ctttaaaact	tatagtcagg	aagggaggct	taaagccctg	tctgcctgca	tctcctacat	720
aacagtcact	gtcctgtttc	ttgttccctg	tattttccct	ttcgtttagac	ctgtttcgaa	780
ctttcctatt	gataaattca	tgactgtgtt	ttatacagtt	atcatacaca	tgttgaatcc	840
attaatatac	acactgagaa	atttagagat	gagaattgct	gtaaaatcca	atgtaaaaaa	900
actctggcat	taaaaactta	actatagtta	gaatgag			937

<210> 778

<211> 970

<212> DNA

<213> Unknown (H38g627 nucleotide)

<220>

<223> Synthetic construct

<400> 778

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ctgcccattg	tggtgactat	tattgccacc	cccaccttag	gctccccagt	gtacttcttc	180
attgtctgct	tgtcatttat	agatgtttgt	tattccacca	ccattcctcc	caaattgatt	240
gtaagctatc	ttcatgataa	aaagactatt	tccttccgag	cttgcagggg	tcagcccttt	300
tatagaccac	ttagtgtgtg	gtgctgaggt	cttcattctg	ttggtgatgg	cctataatcg	360
ctatgtagcc	atctgtgaagc	cactgcacta	tttcaccatc	atgaattgac	aggtttgcac	420

ccttctgttg	gtgggtggctg	tcactgcggg	ttttgtgcat	tctgtgtttc	aaatttttagt	480
tgcgtacagt	ctccttttct	gtgggtcccaa	tatcattgac	cactttttct	gtgacatgta	540
cccattattg	gaactggcac	acactgacac	ctactttata	ggcctcactg	ttgttgccaa	600
tggtggagga	atctgtatgg	tcttgttcat	ccttctacta	atctcctgtg	gggtcactct	660
aatctccctt	aaaacttata	gtcaggaagg	gaggcataaa	gccctgtcta	cctgcagctc	720
ccacattacc	gtggttggtc	tgttttttgt	tccctgtatt	ttcctgtatg	ttagacctgt	780
ttcaaacttc	cctattaata	aattcattac	tgtgttttat	acagttatca	cacccatgtt	840
gaatccatta	atatacacat	tgagaaactg	agagatgaaa	aatgctatag	gaaacctctg	900
gtgtaaata	taactctaga	tagaataaga	gggtacattt	tcatgtaggt	acagggtaat	960
gcaggtaaag						970

<210> 779

<211> 704

<212> DNA

<213> Unknown (H38g628 nucleotide)

<220>

<223> Synthetic construct

<400> 779

cccattgtact	tgttccctcg	caatttgtcc	ttcattgata	tctgttattc	atttgtcttt	60
acccccaaaa	tgctgatgag	ctttatttca	gagaggaaca	tcattctcct	tccaggatgc	120
ataactcagc	tcttttttct	ctgctttttt	gtccactctg	agtgtctatg	gctgacagcc	180
atggcctatg	atcgctatgt	ggccatctgc	aaaccccttc	tgtacatggt	caccacgtcc	240
ctcagatctg	ttctctactg	atgcttgggt	catatgtgat	ggggtttgct	ggggccatgg	300
tccacacaga	gtgtatgatg	aagctcatct	tttgtgactc	caacgtcatc	aaccataaca	360
tgtgtgacat	cttcccactg	ctccagctct	cctgcagcag	cacctaggcc	aatgagctgg	420
tgatgtctgt	tattgtaggc	acagttgtta	tagtatcaag	cctcattatc	ttaatctctt	480
atgctttgat	tcttttcaat	atccttcaca	tgtcctcagc	cgaggggttg	ttcaaagcca	540
tcggtagctg	tggctcccac	ataataactg	ttggcctatt	ctatgaattt	gggctgatca	600
ctcatgttaa	gttatcatct	gattgggtata	tgggtcaggg	gaagtttctc	tcagtgtttt	660
atacaaatgt	ggttcccatg	ctgaaccctt	tcattctactg	tctg		704

<210> 780

<211> 924

<212> DNA

<213> Unknown (H38g629 nucleotide)

<220>

<223> Synthetic construct

<400> 780

atgaggcaga	ataacaatat	tacagaattt	gtcctcctgg	gcttctctca	gtatcctgat	60
gtgcaaaaatg	cattattttgt	catgttttta	ctcatatata	ttgtgactat	ggtggggaac	120
ctgctcattg	tggtgtctat	tattgccagt	cccttttttg	gtccccagct	gtacttcttc	180
cttgccctg	tgctatttat	agatgctgtg	tattccacca	ccatttctcc	tgtattgatt	240
gtagacttac	tctgtgataa	aaagactatt	tccttcccag	cttgcatggg	tcagctattt	300
atagagcact	tgtttggtga	tactgacgtc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tacgtggcca	cctgtaagcc	actgcgctat	ttgaccatca	tgaattgaca	ggtttgcatc	420
cttctgttgg	tggtggctgt	gactggaggt	tttctgcatt	ctgtgtttca	aatttttagt	480
gtgtacagtc	tcccttttctg	tggccccaat	gtcattttatc	acttttttctg	taacatatac	540
ccttttattgg	acctggaatg	cactgacacc	tacttctgtg	gcctcgctgt	ggttttcaat	600
gggtggagcaa	tctgtatggt	catcttcacc	cttctactaa	tctcctatgg	ggtcatccta	660
aaactccctta	aaacttatag	tccggaaggg	aggcataaag	ctccgtttat	ctgcagctcc	720
cactttatca	tggttatctt	gttttttgtt	ccctgtattt	tcttatatgt	tagaccctgt	780
tcaaacttttc	ctattgataa	attcctgact	gtgtttttatt	cagttatcac	acccaagttg	840
aatcctttta	tatacatgtt	gagaaattca	gagatgagaa	atgctataga	aaatctcttg	900
ggataccaaa	gtgggaagac	agga				924

<210> 781

<211> 690

<212> DNA

<213> Unknown (H38g630 nucleotide)

<220>

<223> Synthetic construct

<400> 781

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gtccccaaga tgattgtgga catctaactc cacagcagac tcatctccta ggcaggctgc      120
ctgactccca tgtctctctt tgccattttt ggaggcatgg aagagagaca tgctcctgag      180
tgtgatccct atgaccggtt tgtagccatc tgtcaccctc tatatcattc agccatcatg      240
aaccctgtgt tctgtggctt tctagttttg ttgtcttttt tttctcagtc tcttttagac      300
gcccgagtg cacaacttgat tgccttacaa atgacctgct tcaaggatgt ggaaattcct      360
aatttcttct gggaaacctc tcaactcccc catcttgcat gttgcgacac cttcaccaat      420
aacataatca tgtattcccc tgcgtgccata ttgggttttc tcccatctc ggggacctt      480
ttctcttact ataagattgt ttctccatt cggagggttt catcatcagg tgggaagtat      540
aaggcctgct ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaaacaggc      600
ttttgggggt acctcagttc agatgtgtca tcttccccgg gaaaggctgc agtggcctca      660
gtgatgtaca cgggtggtcac ccccatgctg      690

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<210> 782

<211> 681

<212> DNA

<213> Unknown (H38g632 nucleotide)

<220>

<223> Synthetic construct

<400> 782

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tctttcctgg agattggctt caacctagtc attgtgccca aaatgctggg gacctgctt      60
gcccaggaca caaccatctc cttccttgge tgtgccactc agatgtattt cttcttcttc      120
tttggggtag ctgaatgctt cctcctggct accatggcat atgaccgcta tgtggccatc      180
tgcagtcctt tgcactaccc agtcatcatg aaccaaagga cacgggcaa actggctgct      240
gcttctggtt tcccaggctt tctgtagct actgtgcaga ccacatggct cttcagtttt      300
ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccgcc tgtgctgaag      360
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gtcatgatec cctgcttgct gatcttgtgt tctatactc gcattgctgc tgctatcctc      480
aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgctctc acacctcctt      540
gttgtctctc ttttctatat atcatthaag ctcacgtact tccggcctaa atcaaataat      600
tcacctgagg gcaagaagct gctatcattg tcgtacactg ttatgactcc catgctgaac      660
ccctttcatc tactgtcctg g      681

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<210> 783

<211> 576

<212> DNA

<213> Unknown (H38g633 nucleotide)

<220>

<223> Synthetic construct

<400> 783

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atggtcacag agttcctcct actgggattt ctctggggcc caaggattca gatgctcctc      60
tttgggctct tctccctggt ctatgtcttc accctgctgg ggaatgggac catcctgggg      120
ctcatctcac tggactccag actccacacc cccatgtact tcttctctc acacctggcg      180
gtcgtcgaca tcgcctacgc ctgcaacacg gtgccccgga tgctggtgaa cctcctgcat      240
ccagccaagc ccatctcctt tgcggggccgc atgatgcaga cctttctggt tccactttt      300
gctgtcacag aatgtctcct cctgggtggtg atgtcctatg atctgtacgt ggccatctgc      360
caccctcc gatatttcat catcatgacc tggaaagtct gcatcactct ggccatcact      420
tccggacat gtgggtccct cctggctatg gtccatgtga gcctcactct aagactgccc      480
ttttgtgggc ctggtgaaat caaccactty ytctgtgaaa tccctkctgt cctcaggctg      540
ggctgtgctg atacctggct caaccagggtg gtcac      576

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<210> 784

<211> 924

<212> DNA

<213> Unknown (H38g634 nucleotide)

<220>

<223> Synthetic construct

<400> 784

tatgcagacc	cacagaatct	aacagatgtc	tcwatattcc	tcttcctaga	actctcagag	60
gatccagaac	tgcagccagt	ccttgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	cacgggtcccc	240
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cagatgtctc	tctttgccat	ttttggaggc	atggaagaga	gacatgtctc	tgagtgtgat	360
ggcctatgac	tggttttag	ccatctgtca	cccgtatat	cattcaccat	catgaaccgc	420
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tgcacaactt	gattgcctta	caagtacct	gcttcaagga	tgtggaaatt	cctaatttct	540
tctgtgaccc	ttctcaactc	ccccatcttg	catgttgtga	caccttcacc	aataacataa	600
tcatgtattt	ccctgctgcc	atatttggtt	ttcttcccat	ctcggggacc	cttttctctt	660
actataaaat	tgtttccctc	attctgaggg	tttcatcatc	aggtgggaag	tataaagcct	720
tctccacctg	tgggtctcac	ctgtcagttg	tttgcctgatt	ttatggaaga	gggtgttgag	780
ggtacctcag	ttcagatgtg	tcatcttccc	ccagaaaggg	tgcatgggcc	tgcatgtgatg	840
tacacggtgg	tcacctccat	gctcaacccc	tttatctaca	gcctgagaaa	cagggatatt	900
aaaagtgtct	tgcggcgccc	gcaa				924

<210> 785

<211> 714

<212> DNA

<213> Unknown (H38g635 nucleotide)

<220>

<223> Synthetic construct

<400> 785

atgtacttgt	tctgaggaa	tctgtccttg	cctgacatcg	gtttcacctc	caccattgtc	60
ccaagatga	ttgtggacat	ccagtctcac	agcagagtga	tctcctatgc	aggccgcctg	120
actcagatgt	ctctcttttg	cattttttgga	ggcatggaag	acaacatgct	cctgagtggtg	180
atggcctatg	accggtttgt	agccatctgt	caccctctat	atcattcagc	catcatgaat	240
ccgtgtttct	gtggcttct	acttttgttg	tctttttttt	tttttctcag	tcttttagac	300
accacgtgc	acaacttgat	tgttttataa	atgacctgct	tcaaggatgt	ggaaattcct	360
aatttcttct	gtgaccttc	tcaactcccc	catcttgcac	gttgtgacac	cttcaccaat	420
aacatcatcg	tgtatttccc	tgtgtcata	tttgttttcc	ttcccatctc	ggggaccctt	480
ttctctttta	aactgtttgt	ttctccatt	ctgaggggtt	catcatcagg	cgggaagtat	540
aaaaccttct	ccacctgtgg	gtctcacctg	tcagttattt	gcttatttta	tggaacaggt	600
gttgagggtg	acctcagttc	agatgtgtca	tcttccctga	gaaaggctgc	agtgccctca	660
gtgatgtaca	agatggtcac	ccccatgctg	aaccttcca	tttacaccct	gcgg	714

<210> 786

<211> 962

<212> DNA

<213> Unknown (H38g636 nucleotide)

<220>

<223> Synthetic construct

<400> 786

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gaggcagaac	attatgtgga	tatccatccc	cttctgcctg	atatacacca	tcattcttcc	120
gggaaatggc	atcattcttc	acatcatccg	aattgactct	tccttgacc	aacctatgta	180

ctattttctg	gccatgccgg	cctttgttga	acttgggtgc	tctgcttcca	ccatgcccac	240
tgtgttaagc	atattcctct	ttggcattaa	cgatgtcagt	tttgggtggt	gcctgctcca	300
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ggaccgcttt	gtggccatct	acagcccact	gcgctacaca	accattctga	caattgcctg	420
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gattcttcat	acagtactgg	aaatagcttc	tggagcaggg	cgtggcaggg	actcaacaca	720
tgtgtgtcgc	acatatgtgc	tgtgcttgtg	tactatgtgc	ccatgatcag	cctctcctga	780
tgcaccgctt	tggacggcat	ttacctccac	ttttccagac	tgtcacggcc	aatgcttacc	840
tcttctttcc	tcctgtgggt	aaccccatgt	tctatagtat	caaaatcaaa	gaaattcgca	900
acagcgttgt	tcttacacta	tccaggaaga	ggggtgagtt	ctaattggaga	ccgaagatac	960
cc						962

<210> 787

<211> 872

<212> DNA

<213> Unknown (H38g637 nucleotide)

<220>

<223> Synthetic construct

<400> 787

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cctccatgta	cttcttcttc	tccaacctgt	ccttgctgga	catcggtttc	acctccacca	180
cgggtccccc	gatgactgtg	gacatccagt	ctcgcagcag	agtcactctc	tatgcaggct	240
gcctgactca	gaagctcttc	tttgccattt	ttggaggcac	ggaagagaga	catgctcctg	300
agtgtgatgg	cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatca	ttcagccatc	360
atgaacctgt	gtttctgtgg	cttcctagtt	ttgctgtctt	ttttttttct	cagtctttta	420
gactcccagc	tgtacaactt	gattgcctta	ctaatacact	gcttcaagga	ggtggacatt	480
cctaattttc	tctgtgacct	ttctcaactc	ccccatcttg	ccgttgtgac	accttcatca	540
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gtgttgaggg	gtacctcagt	tcagatgtgt	catcttcccc	cagaaagggt	gcagtggctg	780
cagtgatgta	cacggtgggc	acctccatgc	tcaacccttt	tatctacagc	ctgggaaaca	840
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<210> 788

<211> 646

<212> DNA

<213> Unknown (H38g638 nucleotide)

<220>

<223> Synthetic construct

<400> 788

ctagtggact	tttgttactc	ttcagctgtc	actcccacag	tcatagctgg	gctcggtata	60
ggagacaagg	tcattctctta	caatgcattg	gctgctcaaa	tggtcttttt	tgcagccttt	120
gccactgtgg	aaaatttcct	cttggcctca	atggcctatg	accgctatga	tgcagtgtgc	180
aaacccttac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300
ctgtatgtcc	aatgaagtcc	attgcttttt	ctgtgatgtt	ccaccagtca	tggctctgtc	360
ttgctgtgat	agacatgtga	atgagctagt	tctcatttat	gtagccagtt	tcaatatctt	420
ttctgccatc	ctagtatatc	tgatctccta	cctattcata	tttatcacca	tcctaaagat	480
gcactcagct	tcaggatacc	agaaggcttt	gtccacctgt	gcctcccacc	tactgcagtt	540
catcatcttc	tatgggacta	ttacttctat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgttcta	tactatgatc	atcccc		646

<210> 789
 <211> 648
 <212> DNA
 <213> Unknown (H38g639 nucleotide)

<220>
 <223> Synthetic construct

<400> 789
 ttgtggaca tctgcttctc ctgcaccacc gtccccaaga tgctggccaa tcacatactc 60
 gagactcaga ccatctcctt ctgtggctgt ctcacacaga tgtatttcgt tttcatgttc 120
 gtggacacgg acaatttcct cctagctgtg atggcctatg accactttgt cgccgtgtgc 180
 caccctttac attacacagc aaagatgacc catcagctct gtgccctgct ggttgctgga 240
 ttatgggtgg ttgccaacct gaatgtcctt ctgcacaccc tgctgatggc tccactctca 300
 ttctgtgcag acaatgccat cactcacttc ttctgcatg tgactccctt actgaaactc 360
 tcctgctcag acacacacct caatgaggtc ataatcctta gtgagggtgc cctgggtcatg 420
 atcaccctcat ttctttgcaa cctggcgtct tatatgcaca tcacctgcac tggcctgaag 480
 ggcccatcca caaagggaag gtggaaagcc ttctccacct gtggctctca cctggctgtg 540
 ggtctcctct tctacagcac catcactgct gtgtatttta accctctgtc ctcccactca 600
 gctgcgaaag aactatggc tactgtgttg tatacagtag tgactccc 648

<210> 790
 <211> 471
 <212> DNA
 <213> Unknown (H38g640 nucleotide)

<220>
 <223> Synthetic construct

<400> 790
 atctgcagcc ccttgctgta caatgtcatc atgtcctatc accactgctt ctggctcaca 60
 gtgggagttt acatttttagg catccttgga tctacaattc acaccggctt tatgttgaga 120
 ctctttttgt gcaagactaa tgtgattaac cattattttt gtgactctct ccctctcttg 180
 gggctctcct gctccagcac ctacatcaat gaattactgg ttctgggtctt gagtgcattt 240
 aacatcctga cgctgcctt aaccatcctt gcttcttaca tctttatcat tgccagcatc 300
 ctccgcattc gctccactga gggcaggctc aaagccttca gcacttgag ctcccacatc 360
 ttggctgttg ctggtttctt tgggtctgca gcattcatgt acctgcagcc atcatctgtc 420
 agtcccatgg accaggggaa agtgtcctct gtgttttata ctattgttgt g 471

<210> 791
 <211> 975
 <212> DNA
 <213> Unknown (H38g641 nucleotide)

<220>
 <223> Synthetic construct

<400> 791
 atgaagactt tgtgttcctt tcttcagatc agcagaaata tgcatacaaga aaaccaaaacc 60
 accatcactg aattcattct cctgggactc tccaaccagg ctgaacatca aaacctcctc 120
 tttgtgcttt tcctgagtat gtatgtgggc actgtgggtg ggaacgggct catcattgtg 180
 gctatcagct tggatatata ccttcacacc cccatgtatc tcttccttgc ctacctatcc 240
 tttgctgata tttcctccat ttccaactca gtcccaaaaa tgctggtgaa tattcaaacc 300
 aacagccaat ccatctctta tgagagctgc atcacacaga tgtacttttc tattgtgttt 360
 tcgtcactg acaatttgct tttggggacc atggccttcg accactttgt ggcgatctgc 420
 caccctctga actatacaac tttcatggcg gccagggtcg gcactttgct cacagtcac 480
 tcgtgggtcc tcagtaatat tattgtctct acacacaccc ttctgctcat tcaattgctc 540
 ttctgtgacc acaacactct cccacacttc ttctgtgact tggccctctt gctcaaactg 600
 tcctgttcag atacaatgat caatgagctt gtgttggtta ttgtgggttt atcagttatc 660
 atcttccctt ttgtactcat cttcttctcc tatgtctgca tcatcagagc tgtcctggga 720
 gtatcatcca cacagggaaa gtggaaagcc ttctccactt gtggctctca cctgacaatt 780

gcattactgt	tctacggaac	cactgtaggc	gtgtactttt	tccccctcctc	cactcaccct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gatgaacccc	900
ttcatctaca	gcttgaggaa	taaggatatg	aaagggtgcc	tgagaaagct	catcaataga	960
aaaattttctt	ccctt					975

<210> 792

<211> 943

<212> DNA

<213> Unknown (H38g642 nucleotide)

<220>

<223> Synthetic construct

<400> 792

atgagaccta	ataacagcat	tacagaattt	gtcctcctgg	gattctctca	ggatcctggg	60
atgcaaaaag	aattatttgt	catgttttta	ttcacatacg	ttgtgactgt	gttggggaac	120
cagctcattg	tggtgactat	cattgccagc	ccttccttgg	gctccccaat	gtacttcttc	180
cttgccctgcc	tgtcatttat	agatgctgca	tatttcactg	tcatttctcc	caaattgatt	240
gtggacttac	tctgtgataa	aaagactatt	tccttccaaa	cgttcatggg	ccaactatct	300
atagaccact	tctttgggtg	tgagaggcc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tatgttgcca	tctgtaagac	attgcactat	ttgaccatca	tgactcgaca	ggtttgatc	420
cttgccattgc	tggtggctgc	gacaggcggg	tttgtgcatt	ctgtgtttca	aattgttggt	480
gtgtacagtc	tccctttctg	tggtggccaa	gtcattgatc	atttcagttg	tgacatgtat	540
ccattattgg	aactggcatg	aactgacacc	tactttatag	gcctcactgt	tgttttcagt	600
gggtggagcac	tctgtatggg	catcttcacc	cttctaataa	tttccctatg	ggtcacccca	660
aactccctta	aaacttacac	tcaggaaggg	agcataaagc	cctgtctacc	tgagctccc	720
acatcactgt	gattgtttct	tttttattcc	ctgtatttcc	atatatgtga	gacctgtttc	780
aaacttttct	attgacacat	tcattgactgt	cttttataca	gttatcacac	ccaagttgaa	840
tcctttaata	tacactttca	gaaattcaga	gatgagaaat	gttatagaaa	aactcttggt	900
gaaaaaggta	actatattta	gaataacagg	gtccatcctc	atg		943

<210> 793

<211> 942

<212> DNA

<213> Unknown (H38g643 nucleotide)

<220>

<223> Synthetic construct

<400> 793

atgagacaga	ataaaaaataa	tacagaattt	gtcctcctgg	gcttctctca	ggatcctgat	60
gtgcaaatgc	attatttgtc	atgttttact	cacataattg	gtgacaacag	tggggaacct	120
gtcattgtgt	gtgactatta	ttgccagccc	ttccttgggc	tccccagtg	atttctgact	180
tgccctgtctg	tcattgtatg	atgctgcata	ttccactacc	atttctccca	aactgattgt	240
agagttactc	attgataaaa	agactatttc	cttccgagct	tgcatggggc	agctatttat	300
agaacacttg	tttgggtgga	ctgagatctt	cattctgatg	atgatggcct	gtgatcgcta	360
tggtggacatc	tgtaagccac	tgactatttt	gaccatcatg	aattgacagg	tttgcaccc	420
tctgttgggtg	ttggctgtga	caggagggtt	tgtacattct	atgtttcaaa	ctgttgttgt	480
gtacaatctc	cctttctctg	gccccaatgt	cattgacatt	gaccactttg	tctgtgacat	540
gtaccattta	ttggaactgg	cgttcactga	tacctacttt	ataggcctca	ctgttgttgt	600
caatgggtgga	gcaatgtgta	tggtcatctt	caccattcta	ctaataatcct	acggaatcat	660
cctaaactct	cttaaaactt	atagtcagga	agggagggtg	aaagccctgt	ctacctgcag	720
ccccacata	accgtgggtg	tcctcttttt	tggtccctgt	attttcatat	atgttagacc	780
tggtttcaacc	tttccctattg	ataaattcat	gactgtgttt	tatacagtta	tcacacccat	840
gttgaaatcct	ttaatataca	cgttgagaaa	ttcagagatg	agaaactcta	tagaaaatct	900
cttgtgtaaa	aaagctatct	gtagttagaa	taagagtgtc	cc		942

<210> 794

<211> 945

<212> DNA

<213> Unknown (H38g644 nucleotide)

<220>

<223> Synthetic construct

<400> 794

gagtaaata	gacagaataa	cagtagtaca	gaatttggtc	tcctgggctt	ttctcaggat	60
cctgatgtgc	aaaatgcgct	atttgatcatg	tttttactga	catacattgt	gacaatgggtg	120
gggaacctac	tcattgtggg	gactattatt	gccagccctt	ccttgggctc	cccaatgtac	180
tttttccttg	cccacctgtc	atttatagat	gctgtgtatt	ccaccaccat	ttctcctgta	240
ttgattgtag	acttactctg	tgacaaaag	acgatttcct	tctgagcttg	catggggacaa	300
ctgtttatag	accacttatt	tggtggttct	gagggtcttc	ttctgggtgg	gatggcctgt	360
gatecgtgtg	tggccatctg	taagccactg	cactatttga	ccatcatgaa	tcgacagggtt	420
tgcattcttc	tcttggtgtt	ggctgtgact	ggagggtttg	tgcacccctg	atttcaagtt	480
gttgttgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccactt	tttctgtgac	540
atataccctt	tatttgggaa	tggcatgcac	tgacacctac	tttataggcc	tcactgtggg	600
tttcaatggg	ggagcaatgc	gtatgggtcat	cctcaccctt	ctactagtct	tctatggagt	660
catcctaagc	tcccttaaaa	cttacagtca	ggaaggagg	cataaagccc	tgtctacctg	720
cagctcccat	gttacgtgg	ttatcttgtt	ttttgtcttc	tgtattttca	tatatgttag	780
acctgtttca	aattttctgt	tgataaatc	atgactgtgt	tttatacggg	tatcacaccc	840
atgttgaatc	cttttatatg	catgttgaga	aattcagaga	tgagaaatgc	tatagaaaaa	900
ctcctgtgta	aatgaactg	tagttagaat	aagagtgttc	cttcc		945

<210> 795

<211> 939

<212> DNA

<213> Unknown (H38g645 nucleotide)

<220>

<223> Synthetic construct

<400> 795

atgggactga	gtaacaatgt	tacagaactt	ttcctcctgg	gcctcactca	ggatctcgat	60
gtgcaaaatg	cattatttgt	catgttttta	ctaacataca	ttgtgactat	gggtggggaac	120
ctgctcattg	tggtgactat	tattgccacc	ccatccttgg	gtcctcccaat	gtactttttc	180
cttgccctgcc	tgtcatttat	agatgctgtg	tattccacca	ccatttatcc	caaattgggtt	240
gtagactaac	tccataatta	aaagactatt	ttgttcccaa	cttgcattgg	ccagccactt	300
acagaccact	tatttgggtg	tggtgaggtc	tttttttctg	ttggtgatgg	cctgtgatcg	360
ctatgtggcc	atctgtaagc	cactgcacta	ttttaccatc	atgaatcgac	agggttttcat	420
ccttctgttg	gtagtggctg	tgactggagt	tttgtgcgtt	ctgtgttcca	aattgttgtt	480
gtgtacagtc	tccctttctg	tggccccaat	gtcattgacc	actttttctg	taacatgtac	540
ccattaatgg	aaatggcatg	aactgacacc	tactttatag	gcctcactgt	gggttttcaag	600
gttgaagcaa	tctgtgtggg	catcttcacc	cttctactaa	tctcctctgg	cgtcaccta	660
atctccctta	aaacttacag	tcaggaagg	aggcataaag	ccctgtttac	ctgcagctcc	720
cgcattactg	tagttgtcct	cttttttgtt	ccctgtatct	tcatgtatgt	tagacctgtt	780
tttaacttcc	ccattgataa	atttattatt	gtgttttata	cagttatcac	acccatgctg	840
aatcctttta	tatacatgtt	gagaaattca	tagacgagaa	atgctataga	aaacccttag	900
tgtaaaaaat	taactgtaga	tagaataaga	gtgtacatc			939

<210> 796

<211> 945

<212> DNA

<213> Unknown (H38g646 nucleotide)

<220>

<223> Synthetic construct

<400> 796

atgagacct	ataacagtat	tacagaattt	gtcctcctgg	gcttttcaca	ggatcctgat	60
atgcaaaaca	cattatttgt	catgttttta	ctcacataca	ttgtgacagt	gggtggggaac	120
ctactcgttg	cggtgactat	tattgtcagc	ccttccttga	gtcctcccaat	gtaattcttc	180
cttgcttgcc	tgtcattaat	agatgctgta	ttatccacca	ccatttctcc	catattgatt	240

gtagacctac	tctgtgacaa	aaagactatt	tccttcccag	cttgcatggg	ccagctat	300
acagaccact	tgtttggtgg	aactgagatc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tacgtggcca	tctgtaagcc	actgcactat	tttaaccatca	tgaatcgaca	ggtttccatc	420
cttctgttgg	tggtggccat	gactggagggt	ttccttcatt	ctgtgtttca	aattgctgtt	480
ctgtacagtc	tccttttctg	tggccccaat	gtcattgacc	actttttctg	tgacatgtac	540
ccattattgg	aactggcgtg	cactgacacc	tactctatag	gcctcactgt	agttttcagt	600
ggtggagcaa	tgtgtatgg	catcttcgcc	cttctactaa	tctcctatgg	agtcagccta	660
aactccctta	aaacttatag	tcaggaagggt	aggcgtaaag	ccctgtctac	ctgcagctcg	720
cacatcaccg	tgggtgtcct	cttttttggt	ccctgtat	tcatgtatgt	tagacctgtc	780
tcaaacttcc	ctattgataa	attcggtact	gtgttttata	cagttatcac	acccatgctg	840
aatccctttt	tatacacgtt	gagaaattca	gagatgataa	atgctataaa	acacctgttg	900
tgtaagaagc	taactatagt	tagaataaga	gtgtccctcc	tcatg		945

<210> 797

<211> 967

<212> DNA

<213> Unknown (H38g647 nucleotide)

<220>

<223> Synthetic construct

<400> 797

atgggatcta	gtaacaatgt	tacagaat	gtctctctgg	ccctcactca	ggctcctgat	60
gtgcaaaaag	tattatttgt	aatgttttta	ttcacatata	ttgtgactat	ggtgggcaac	120
ctgctcactg	tggtgaccat	ttttgccctc	cctcttttgg	ctccccagtg	taactcttcc	180
ttgcctgcct	gtcattgatg	gatgccgtat	attccacttc	atcttctcct	aaactgatga	240
tagacttact	ctgcgataaa	aaagactggt	tccttcccgg	cttgcatggg	ccagctat	300
gcggaccacc	tatttggtgg	tgttgagggtc	tttcttttctg	tggggatggc	ctatgatcac	360
tatgtggcca	tctctaagcc	actgcactat	ttgatcatcg	tgaatcgact	ggtttgcatc	420
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catgcgctga	cacctacttt	atagggctca	ctgtgattgc	caatgggtgga	gcaatctgta	660
tggtcatctt	ctgccttcta	ctaacctcct	atggagtcac	cctaaacttc	cttaaaactt	720
atagtcgaaga	agggaggcat	agaacctgtg	ctacctgcag	ctcccacatt	actgtgggtg	780
tcctcttttt	tgttccctgt	attttcatgt	atgtagacc	tgtttcaaac	ttccctattg	840
ataaattcat	tactgagttt	tatacagtta	tcaccccaaa	gttgaatcca	ttaatccaac	900
cactgagaaa	ttgagaaatg	agaattacta	tgaagaaact	ctgggtgtta	acctgaacta	960
tagtttag						967

<210> 798

<211> 930

<212> DNA

<213> Unknown (H38g648 nucleotide)

<220>

<223> Synthetic construct

<400> 798

atgaaaaata	agaacaatgt	gactgaat	atcctcttag	ggctcacaca	gaacctgag	60
gggcaaaaag	ttttatttgt	cacattctta	ctaactctaca	tggtgacgat	aatgggcaac	120
ctgcttatca	tagtgaccat	catggccagc	cagtcctctg	gttcccccat	gtactttttt	180
ctggcttctt	tatcattcat	agataccgtc	tattctactg	catttgctcc	caaaatgatt	240
gttgacttgc	tctctgagaa	aaagaccatt	tcctttcagg	gttgatggc	tcaacttttt	300
atggatcatt	tatttgctgg	tgctgaagtc	attcttctgg	tggtaatggc	ctatgatcga	360
tacatggcca	tctgtaagcc	tcttcatgaa	ttgatcacca	tgaatcgctg	agtcgtgtgt	420
cttatgctgt	tggcggcctg	gattggaggc	tttcttctact	cattggttca	atttctcttt	480
atctatcagc	tccttttctg	tggaccaaat	gtcattgaca	acttctctgtg	tgatttgtat	540
cccttattga	aacttgcttg	caccaatacc	tatgtcactg	ggcttttctat	gatagcta	600
ggaggagcga	ttgtgtctgt	caccttcttc	actatcctgc	tttctctatg	ggcatatta	660
cactctctta	agactcagag	tttggaagggt	aaacgaaaag	ctttctacac	ctgtgcattc	720

cacgtcactg	tggtcatttt	attctttgtc	ccctgtatct	tcttgtatgc	aaggcccaat	780
tctacttttc	ccattgataa	atccatgact	gtagttctaa	cttttataac	tcccatgctg	840
aaccctactaa	tctataccct	gaagaatgca	gaaatgaaaa	gtgccatgag	gaaactttgg	900
agtaaaaaag	taagcttagc	tgggaaatgg				930

<210> 799

<211> 825

<212> DNA

<213> Unknown (H38g649 nucleotide)

<220>

<223> Synthetic construct

<400> 799

atggtgggaa	acctcctcat	ttgggtgact	actattggca	gccccctcct	gggctcccta	60
atgtacttct	tccttgcccta	cttgtcactt	atggatgccca	tatattccac	tgccatgtca	120
cccaaattga	tgatagactt	actctgtgat	aaaatcgcta	tttccttgtc	agcttgcatg	180
ggtcagctct	tcatagaaca	cttactttgt	ggtgcagagg	tcttcctttt	ggtgggtgatg	240
gcctatgatc	gctatgtggc	tatctctaag	ccgctgcact	atgtgaacat	catgaatcga	300
ctggtttgca	tccttctgtt	ggtgggtggc	atgattggag	gttttgtgca	ctctgtgggt	360
caaatgtgct	ttctgtacag	tctaccaatc	tgtggcccca	atgttattga	ccactctgtc	420
tgtgacatgt	acccattgtt	ggaactgttg	tgccttgaca	cctactttat	aggactcact	480
gtggttgcca	atgggtggaat	aatttgtatg	gtcatcttta	cctttctgct	aatctcctgt	540
ggagtcaccc	taaacttcct	taaaacttac	agtcaggaag	agaggcataa	agccctgcct	600
acctgcatct	cccacatcat	tgtggttgcc	ctcgtttttg	ttccctgtat	ttttatgtat	660
gttagaccgg	tttccaactt	tccctttgat	aaattaatga	ctgtgtttta	ttcaattatc	720
acactcatgt	tgaatccttt	aataactcgt	ttgagacaat	cagagatgaa	aaatgctatg	780
aaaaatctct	ggtgtgaaaa	gttaagtata	gttagaaaaa	gagta		825

<210> 800

<211> 654

<212> DNA

<213> Unknown (H38g650 nucleotide)

<220>

<223> Synthetic construct

<400> 800

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cacagcagac	tcattctcta	ggcaggctgc	ctgactccca	tgtctctctt	tgccatcttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatccct	atgaccggtt	tgtagccatc	180
tgtcacccctc	tatatcatte	agccatcatg	aaccggtgtt	tctgtggctt	tctagttttg	240
ttgtcttttt	tttctcagtc	tcttttagac	gccagggtgc	acaacttgat	tgcccttaca	300
atgacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gggaaccttc	tcaactcccc	360
catcttgcat	gttgcgacac	cttcaccaat	aacataatca	tgtattcccc	tgctgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ataagattgt	ttcctccatt	480
ctgagggttt	cttcacacag	tgggaagtat	aaagccctct	ccacctgtgg	gtctcgccctg	540
tcagttgttt	gctgagttta	tgggaacaggc	gttggagagt	acctcggttc	agatgtgtca	600
tcttccccga	gaaagggtgc	agtggcctca	gtgatgtaca	cggtggtcac	cccc	654

<210> 801

<211> 648

<212> DNA

<213> Unknown (H38g651 nucleotide)

<220>

<223> Synthetic construct

<400> 801

tcaatggccc	tcattgtcat	ctgcaccacc	ggacccaaga	ggccttcaac	tacctgtctg	60
gcagcaagtc	ccattttctat	ggctgtttgt	ccacacaaat	tttcttctat	acatcactgc	120

ttggctctga	gtgcttttctt	ttggctgtta	tggtttatga	ccgctacact	gccatttgcc	180
accctctaag	atacaccaat	ctcatgagcc	ctaaaatttg	tggtacttatg	actgcctttt	240
cctggatcct	gggctctacg	gatgyaatta	ttgatgttgt	agcaacattt	tccttctcct	300
actgtgggtc	tcgggaaata	gccactttct	tctgtgactt	ccccctccct	actaatcctc	360
tcatgcagtg	acacatcaat	atttgaaaag	attcttttca	tctgtgtgat	agtaatgatt	420
gttttccttg	ttgcaatcat	cattgcttcc	tatgctcgag	ttatcctggc	tgatcattcac	480
atgggatctg	gagaggggtcg	tcgcaaagct	tttactactt	gttcctctca	cctcttggtg	540
gtgggaatgt	actatggagc	agctttgttc	atgtacatac	ggcccacatc	tgatcgctcc	600
ccaacacagg	acaagatggg	gtctgtattc	tacaccatcc	tcactccc		648

<210> 802

<211> 635

<212> DNA

<213> Unknown (H38g652 nucleotide)

<220>

<223> Synthetic construct

<400> 802

tttgtggaca	ttgcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgctg	agatttttgt	tttgactgtc	atggcttttg	atcgctatgc	tgctatctgc	180
caaccctcc	gttacctgt	catcatgagt	gctaagtctt	atactgtgct	ggcatcactg	240
tcctggttgg	gggcccctgg	tcattccttt	gttcagacct	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaacattac	ttttgtgatg	tccaccagct	cctaaaaactt	360
gcctgtgctg	atacaactct	ggtaaataatg	ttggtggttg	ccaacagtgg	tctcatctcc	420
ctgggggtgtt	tcctcattct	tttggcctcc	tacacagtca	ttctgttttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	caactacttc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	ccccca			635

<210> 803

<211> 670

<212> DNA

<213> Unknown (H38g653 nucleotide)

<220>

<223> Synthetic construct

<400> 803

ttgcctgaca	tcggttttcac	ctccacacgg	tccccaagat	gattgtggac	atccagttctc	60
acagcagagt	catctcctat	gcaggctgcc	tgactcagat	gtctctcttt	gccatttttt	120
gaggcagggg	agagagacat	gtccttgagt	gtgatggcct	acgaccagtt	tgtagccatc	180
tgtcacccctc	catatcggtc	agccatcttg	aaccctgtgt	tctgtggctt	cctagatttg	240
ttgtccttgt	ttttttttct	tttttttttt	tctcagttct	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	tcttctggga	360
acctttctcaa	ctcccccatc	ttgcatgttg	tgacatcttc	accaggaaca	tcaacctgta	420
tttccctgct	gccatatttg	gttttcttcc	catctcgggg	acccttttct	cttactctaa	480
aattgtttcc	tccattctga	gggtttcatc	gtcaggtggg	aggtataaag	ccctctccac	540
ctgtgggtct	cacgtgtcag	ttgtttgctg	agtttatgga	acaggcgttg	gagggtacct	600
cagttcggat	gtgtcatttt	cccccagaaa	gggtgcagtg	gcctcagtga	tgtacgcggg	660
tgtaaccccc						670

<210> 804

<211> 648

<212> DNA

<213> Unknown (H38g654 nucleotide)

<220>

<223> Synthetic construct

<400> 804

ctcctggatc	tttgttacac	cacatgtaca	gtcccacaaa	tgctagtaaa	tttatgcage	60
atcaggaaag	tatcagttta	tcgtggctgt	gtagcccagc	ttttcatatt	tctggccttg	120
ggggctactg	aatatcttct	cctggccgtc	atgtcctttg	ataggtttgt	agctatttgt	180
cggcctctcc	attactcagt	tatcatgcac	cagagactct	gcctccagtt	ggcagctgca	240
tccagggtta	ctgggttttag	taactcagtg	tggttgtcta	ccctgactct	ccagctgcca	300
ctctgtgacc	cctatgtgat	agaccacttt	ctctgtgaag	tccctgcact	gctcaagtta	360
tcttgtgttg	agacaacagc	aaatgaggct	gaactattcc	ttgtcagtga	gctcttccat	420
ctaatacccc	tgacactcat	ccttatatca	tatgtcttta	ttgtccgagc	agtattgagg	480
atacagtctg	ctgaaggctcg	acaaaaagca	tttgggacat	gtggttccca	tctaattgtg	540
gtgtctcttt	ttaatagtac	agccgtctct	gtgtacctgc	aaccaccttc	gccagctcc	600
aaggaccaag	gaaagatggt	ttctctcttc	tatggaatca	ttgcaccc		648

<210> 805

<211> 655

<212> DNA

<213> Unknown (H38g655 nucleotide)

<220>

<223> Synthetic construct

<400> 805

ttgcctgaca	tcggttttcac	ctccaccatt	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tgatctccta	tgaggccgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagacagaca	tgctcctgag	tgtgatggcc	tatgaccggt	tcgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaatccgtgt	ttctgtgggt	tcctactttt	240
gttgtctttt	ttttttctca	gtcttttaga	cgcccagctg	cacaacttga	ttgccttaca	300
aatgacctgc	ttcaaggatg	tggaaattcc	taatttcttc	tgtgaccctt	ctcaactccc	360
ccatcttgca	tgttgtgaca	ccttcaccaa	taacataatc	atgtattttc	ctgctgccat	420
atttggtttt	cttcccatct	cggggaccct	tttctcttac	gataaaattg	tttccctccat	480
tctgagggtt	tcatcatcag	gtgggaagta	taaagccttc	tccacctatg	ggtctcacct	540
gtcagatgtt	tcctgatttt	atggaacagg	cgttggaggg	tacctcagtt	cagatgtgtc	600
atcttccccg	agaaagactg	cagtggcctc	agtgatgtac	acagtggtca	cccc	655

<210> 806

<211> 662

<212> DNA

<213> Unknown (H38g656 nucleotide)

<220>

<223> Synthetic construct

<400> 806

tttcttgaca	tcggttttcac	ctccaccaca	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcatctccta	tgaggctgc	ccgactcaga	tgtctctctt	tgccattttt	120
ggagacacgg	aagagagaca	tgttcctgag	tgtgggtggc	tatgaccggt	ttgtagccat	180
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gttgtccttg	gttttttttt	ttttctcagt	cttttagact	cccagctgca	caacttgatt	300
gccttacaaa	tgacctgctt	caaggatgtg	gaaattccta	atttcttctg	ggaaccttct	360
caactcccc	atcttgcagt	ttgtgacatc	ttcaccagga	acatcaacct	gtatttccct	420
gctgccatat	ttgggttttct	tcccatctcg	gggacgcttt	tctcttgcta	taaaattggt	480
tccttcattc	tgagggtttc	atcatcaggt	gggaagtata	aaccttctcc	gcctgtgggt	540
ctcatctgtc	agttgtttac	tgattttatg	gaacaggctt	tggagggtac	ctcagttcag	600
atgtgtcatc	ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	660
cc						662

<210> 807

<211> 647

<212> DNA

<213> Unknown (H38g657 nucleotide)

<220>

<223> Synthetic construct

<400> 807

gtgctggatg	tgggatgtat	cactgtcact	gttcctgcaa	tgttgggtcg	tctcttgtcc	60
cacaagtcca	caatttccta	tgacgcctgc	ctctcccagc	tcttcttctt	ccactttctg	120
gctgggatgg	actgcttcct	gctgaccgcc	atggcctatg	accgactcct	ggccatctgc	180
cagccctca	cctacagcac	ccgcatgagt	cagacagtcc	agaggatgtt	ggtggctgcy	240
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ttctgtggcc	caaagtgggt	caatcacttc	tactgtgacc	tcccacagct	cttcagctc	360
tcctgtctta	gcacccaact	caatgagctg	ctgctctttg	tagcagcagc	cttcattggct	420
gtggcaccct	tggcttctat	cagtgtgccc	tatgcccattg	tggtagctgc	tgtgctgcaa	480
atcgctccgc	tgagggcaga	aagaaggcct	tctccacatg	tggctcccac	ctcactgtgg	540
tgggcatctt	ctatgggaca	ggtgtcttca	gctacatgag	gctgggttca	gtggaatctt	600
cagacaagga	taaggggggtt	ggggttttca	tgactgtgat	caacccc		647

<210> 808

<211> 635

<212> DNA

<213> Unknown (H38g658 nucleotide)

<220>

<223> Synthetic construct

<400> 808

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gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttggtctg	acatttttgt	tttgactgtc	atggcttttg	atcgctgtgc	tgctatctgc	180
caacccctcc	gttacctgt	catcatgagt	gctaagtctt	atactgtgct	ggcatcactg	240
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gcctgtgctg	atacaactct	ggtaaatatg	ttgggtgggtg	ccaacagtgg	tctcatctcc	420
ctgggggtgtt	tcctcattct	tttggcctcc	tacacagtca	ttctgttttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	ccccca			635

<210> 809

<211> 648

<212> DNA

<213> Unknown (H38g659 nucleotide)

<220>

<223> Synthetic construct

<400> 809

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caggacccat	ccatccccta	tgcggaactgc	ctgacccaaa	tgtacttctt	cctgttattt	120
ggagacctgg	agagcttccct	ccttgtggcc	atggcctatg	accgctatgt	ggccatctgc	180
ttccccctgc	actacaccgc	catcatgagc	cccattgctct	gtctcgccct	ggtggcgctg	240
tcttgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttgtgt	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
gccttctctg	acaactcgagt	taatgaatgg	gtgatattta	tcattggagg	gctcattctt	420
gtcatcccat	tctactcat	ccttgggtcc	tatgcaagag	ttgtctctct	catcctcaag	480
gtcccttctt	ctaagggtat	ctgcaaggcc	ttctctactt	gtggctccca	cctgtctgtg	540
gtgtcactgt	tctatggaac	cgttattgggt	ctctacttat	gctcatcagc	taatagttct	600
actctaaagg	acactgtcat	ggctatgatg	tacactgtgg	tgaccccc		648

<210> 810

<211> 438

<212> DNA

<213> Unknown (H38g660 nucleotide)

<220>

<223> Synthetic construct

<400> 810

actttgcaga	atatcacctc	cacttccatc	attttcctgc	tcactgggtg	tcctgggctg	60
gaagccttcc	acacctggat	ctccattccc	ttctgcttcc	tctctgtaac	tgctctcttg	120
ggaaacagcc	tgatcctctt	cgctaccatc	actcagccca	gcctccacga	accaatgtac	180
tatttcctct	ccatgctgtc	cgccactgac	ctcggcctgt	ccatatccac	tctgggtcacc	240
atgctgagta	tattctgggt	caatgtgagg	gaaatcagct	ttaatgcctg	cttgtcccac	300
atgttcttta	ttaaattctt	cactgtcatg	gaatcctcag	tgctgttggc	catggctttt	360
gacgttttgg	tgccgtctct	atccccttag	tatgccatga	tttaactgac	tcagatagct	420
aaaatgagtg	cagtgtat					438

<210> 811

<211> 1002

<212> DNA

<213> Unknown (H38g661 nucleotide)

<220>

<223> Synthetic construct

<400> 811

gcagggtgtg	aaaacgataa	tacaagttct	ttcgaaggct	tcatectggt	gggcttctct	60
gacgttcccc	acctagagct	gacgttcttt	gtgggtgtcc	tcattcttta	tctgctgact	120
cttcttggca	acatgaccat	tgtcttgctt	tcagctctgg	attcccggct	gcacacacca	180
atgtatttct	ttttggcaaa	cctctcattc	ctggacatgt	gtttcaccac	aggttccatc	240
cctcagatgc	tctacaacct	ttgggggtcca	gataagacca	tcagctatgt	gggttgtgcc	300
atccagctgt	actttgtcct	ggccctggga	gggggtggagt	gtgtctctct	ggctgtcatg	360
gcatatgacc	gctatgctgc	agtctgcaaa	cccctgcaat	acaccatcat	catgcaccca	420
cgtctctgtg	gacagctggc	ttcagtgcca	tggtctgagt	gctttggcaa	ttctctcata	480
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tgtgagatgc	cagcactaat	tggtatggcc	tgtgtagaca	ccatgatgct	tgaggcactg	600
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aacacttgca	gctcgcactc	aattgttgct	tctctcttct	atggtacaat	catatacatg	780
tacctccagc	cagcaaatac	ttattcccag	gaccagggca	agtttcttac	ccttttctac	840
acaattgtca	ctcccagtg	taacccccctg	atctatacac	taagaaacaa	agatgttaaa	900
gaggccatga	agaaggtgct	aggggaagggg	agtgcagaaa	tatagtaagg	ggtgattaaa	960
ctttgggatt	gtattttgac	ccattcttcta	tatatgttgt	ta		1002

<210> 812

<211> 827

<212> DNA

<213> Unknown (H38g662 nucleotide)

<220>

<223> Synthetic construct

<400> 812

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ctggcaggca	cagacctcat	ggtgacattg	accacgatgc	ctactgtaat	gggcatecta	120
tgggtgaatc	acaggggaaga	ttagcagtg	gggctgcttc	ctacaggctt	actttattca	180
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gagtgggatt	gttcctaagg	ggtttggtat	ccatcctgcc	tgtaattttg	cgtctttttc	360
catttccata	tggaataatct	catgttatca	cacgttgctt	tctgcctcca	ccaagaaatc	420
atgagactgg	cttggtgctga	cataacttcc	aataaaacttt	accctgtaat	tttgatctct	480
ttaacaatct	ccctaaactc	tctgatcacc	ccctcctcct	atataccta	ccttaatact	540
gtcataggca	ttgcctctgg	tgaaaaaaaa	ccaaagccct	caatacctgt	atctcccaca	600

taagttgtgt	ccttatctcc	tatgttacgg	tgatgggttt	gacattcatt	tacaaatttg	660
ggaagaatgt	gccaaagggt	gtccacatta	tcataagtta	catctacttc	ctctttcccc	720
ctttaatgaa	ccctgtcatc	tacagcatca	aaaccaagca	aatacaatat	ggcattatc:	780
gccttttatc	taaacaatagg	tttagtaggt	aaactcggat	ctggaaa		827

<210> 813

<211> 657

<212> DNA

<213> Unknown (H38g663 nucleotide)

<220>

<223> Synthetic construct

<400> 813

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cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctgttttt	120
ggaggcatgg	aagaaagaca	tgtccttgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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cttacaaatg	acctgcttca	aggatgtgga	aattccta	ttcttctggg	aaccttctca	360
actctcccat	cttgcatgtt	gtgacacctt	caccaggaac	atcagtattt	ccctgctgcc	420
atatttggtt	ttcttcccat	ctcggggacc	cttttctctt	acgataaaat	tgttttctcc	480
attctgaggg	tttcatcatc	agggtgggaag	cataaggcct	tctccaccag	ggggctctac	540
ctgtcagttg	tttgtctgatt	ttatggaaca	ggcattggag	gtacacctcag	ttcagatgtg	600
tcattctccc	cgagaaaggc	tgcagtggcc	tcagtgatgt	acacgggtggc	catcccc	657

<210> 814

<211> 655

<212> DNA

<213> Unknown (H38g664 nucleotide)

<220>

<223> Synthetic construct

<400> 814

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cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagacaca	tgtccttgaa	tgtgatggcc	tatgtccggt	ttgtagccat	180
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aatgacctgc	atcaaggatg	tggaaattcc	taatttcttc	tgtgacctt	ctcaactccc	360
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atattggttt	cttcttatct	cacggatcat	tttctcttac	tataaaattg	tttctctccat	480
gtgagtggtt	tcattcatcag	gtgggaagta	taaagccttc	tccatctgtg	ggctctccct	540
gtcagttggt	tgcttatttt	atggaaaagt	cgttgggggg	tacctgagtt	cagatgtgtc	600
atcttccccc	agaaaggggtg	cagtggcctc	aatgatgtac	acgggtgatca	cccc	655

<210> 815

<211> 646

<212> DNA

<213> Unknown (H38g665 nucleotide)

<220>

<223> Synthetic construct

<400> 815

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ggagacaagg	tcattctcta	caatgcatgt	gctgctcaaa	tgctcttttt	tgcagccttt	120
gccactgtgg	aaaatttcc	cttggcctcg	atggcctatg	accgccatga	tgcagtgtgc	180
aaaccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtgggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300

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ctgtatgtcc aatgaagtcc attgcttttt ctgtgatgtt ccaccagtca tggtctctgtc 360
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gcactcggct tcaggatacc agaaggcttt gtccacctgt gcctcccacc tcaactgcagt 540
catcatcttc tatgggacta ttatctccat gtacttacag cccagctctg gtcaactccat 600
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<210> 816

<211> 649

<212> DNA

<213> Unknown (H38g666 nucleotide)

<220>

<223> Synthetic construct

<400> 816

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acagcagagt catctcctac gcaggctgcc tgactcagat gtctctcttt gccatttttg 120
gaggcatgga agagagacat gctcctgagt gtgatggcct atgaccgggt tgtagccatc 180
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ttgctgagtt tatggaacag gcgttggagg ttacctcagt tcagatgatg tgatcatctc 600
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<210> 817

<211> 651

<212> DNA

<213> Unknown (H38g667 nucleotide)

<220>

<223> Synthetic construct

<400> 817

```

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aacaagagaa aaacaatctc ctttgtccca tgcacaatgc agaccttttt atacatggct 120
tttgctcaca ctgagtgtct catcttggtg atgatgtcct acgatcggtg catggctatc 180
tgccaccctc tgcaatatc tgtcatcatg agatggggag tgtgcacagt cctggctgtc 240
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<210> 818

<211> 646

<212> DNA

<213> Unknown (H38g668 nucleotide)

<220>

<223> Synthetic construct

<400> 818

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ggagacgagg tcatctctta cagtgcagt gctgctcaaa tgttcttttt tgcagccttt 120
gccactgtgg aaaatttctt cttggcctca atggcctatg accgctatga tgcagtgtgc 180

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aaaccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
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gcactcagct	tcaggatacc	agaaggcttt	gtccaaactgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatcttcat	gtacttacag	cccagctctg	gtcactccat	600
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<210> 819

<211> 933

<212> DNA

<213> Unknown (H38g669 nucleotide)

<220>

<223> Synthetic construct

<400> 819

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gggaacctgg	gcttgataac	cctgataagg	ctcaactctc	acttgacac	ccctatgtac	180
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tgttttctcc	ttttgttggg	tgtctatggg	atgggggttg	ctggggccat	ggccacaca	480
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gtggtgccca	tgtcaaccc	attaatttat	agcctgagga	ataaggacgt	caaagttgct	900
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<210> 820

<211> 927

<212> DNA

<213> Unknown (H38g670 nucleotide)

<220>

<223> Synthetic construct

<400> 820

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ggcaacttgg	gcttgatcac	cttaattggg	ataaatccta	gccttcacac	ccccatgtac	180
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atgctgaatg	actttgtttc	agaaagtatc	atctcttatg	tgggatgtat	gactcagcta	300
tttttcttct	gtttctttgt	caattctgag	tgctatgtgt	tggtatcaat	ggcctatgat	360
cgctatgtgg	ccatctgcaa	ccccctgtct	tacatgggtca	ccatgtcccc	aagggtctgc	420
tttctgctga	tgtttggttc	ctatgtggta	gggtttgtctg	gggccatggc	ccacactgga	480
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<210> 821
 <211> 887
 <212> DNA
 <213> Unknown (H38g671 nucleotide)

<220>
 <223> Synthetic construct

<400> 821
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 cataatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240
 atctcagaga ggaacatcat ctcttttggt ggatggccaa cgtagctata tttcttttgc 300
 atctttgtca aagaacctaa aaatgggggtc attgtgggaa taatgttctc agccaagatg 360
 cttgtagccg agagataatg gactagtcgt tgatgtgaaa ctagaaaatg cacatggccc 420
 tagaaaggtc tgatttttaga atgggataaa caggatctgc taaaaagaa catttaatca 480
 tattcttgta ttacagcgat tatttcagga gatagtggg ctgcagagct ttgggacaag 540
 gttccttagc gaagcaagac acactctcta gaattgcaca tgtactttaa aaagtctgtt 600
 acatattata atatgttttt atatttggaa acagaaaaaa ataagttatt tatatcacia 660
 atcatagaaa atggatcttt acaaaatctt catgttttgt gggttactca caagaaaaat 720
 tttctcgcgc catttctact tctcaaatgg ttcaaggaaa aatgctcctt aaaggatata 780
 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840
 actaccttct gaaaaagttg aaaacactgc tttataagaa cagctat 887

<210> 822
 <211> 939
 <212> DNA
 <213> Unknown (H38g672 nucleotide)

<220>
 <223> Synthetic construct

<400> 822
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 ccagagttcc ggcaaccctt ctttttcctg tttctagtgg tctacattgt caccatggta 120
 ggcaaccttg gcttgatcat tcttttcggt cttaaattctc acctccacac accaatgtac 180
 tatttccctt tcaatctctc cttcattgat ctctgttact cctctgtttt cactcccaa 240
 atgctaatag actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcaggtc 420
 tgttctatgc tcacttttgc tgcttacata atgggattgg ctggagccac ggcccacacc 480
 ggggtgcatgc ttagactcac ctctgcagt gctaatatca tcaaccatta cttgtgtgac 540
 atactcccc tctccagct ttctgcacc agcacctatg tcaacgaggt ggttgttctc 600
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 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780
 aaatattctt ctggatctat ggagcaggga aaagtttctt ctgttttcta cactaatgtg 840
 gtgcccacgc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgcactg 900
 aggaaagctc tgattaaaat tcagagaaga aatatattc 939

<210> 823
 <211> 1071
 <212> DNA
 <213> Unknown (H38g673 nucleotide)

<220>
 <223> Synthetic construct

<400> 823
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ggcaatctga	caataattct	tgtgtcacat	gtggatttca	aactccacac	ccctatgtac	180
ttttttctta	gcaatctctc	actcctggac	ctttgtctata	ccacaagtac	agttccacaa	240
atgctggtaa	acatatgcaa	caccaggaaa	gtaatcagtt	atgggtggctg	tgtggcccag	300
cttttccattt	tccctggcctt	gggttccaca	gaatgtcttc	tccctggccgt	catgtgcttt	360
gataggtttg	tagctatttg	tgggctctct	cattactcaa	ttatcatgca	ccagaggctc	420
tgcttcagtt	tggcagctgc	atcctggatt	agtggcttta	gcaattcagt	attacagtcc	480
acctggacac	ttaagatgcc	actgtgtggt	cacaaagaag	tggatcactt	cttctgtgaa	540
gtccctgctc	tgtcaagtt	gtcctgtgtt	gacacaacag	caaagtgggc	tgaactattc	600
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tttaaaaggt	tggttgcaaa	gagtcttctt	aatcaagaaa	taagaaatat	gcaaattgata	960
agcttttgcta	aagacacagt	gcttacttac	cttactaact	tctccgcaag	ttgtcctatt	1020
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<210> 824

<211> 991

<212> DNA

<213> Unknown (H38g674 nucleotide)

<220>

<223> Synthetic construct

<400> 824

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ccagatctcc	aactccctct	gttcttccctg	tttctagtgt	atggctcactg	cgttgggaaa	120
tttggcttgg	taactctcgt	tgtgctcaat	tcacaccttc	ataccccat	gtactttttc	180
ctctttaact	tgtccttcat	agatctctgt	tattcttctg	tgtttacacc	ccaaatgctg	240
atgaacttca	taacacagaa	ggatattatc	tcccacatgg	ggtgcatgtc	ccagcttttc	300
ttttttcttt	attttttttt	ggtatttctg	aatgctatgt	gtcacctca	atggcctatg	360
atcagcatgt	caccatgatc	accatgtagc	catctgtaac	ccacttttgt	ataatattgc	420
catgtccccc	aaagtgtact	ctcaccttat	gcttggttta	tacttgctag	ccttttctag	480
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tgagctgggtg	gtttccactg	cagcagtcct	tattttccac	tgtcaccata	tttatctctt	660
gtgggttcag	ctcctacatc	atcctccaca	tcaactccaa	ggagggcagg	tccaaagcct	720
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caccaataca	gctcccttga	tgaacccctt	aatctacagt	ttgatgaata	aaatgttcaa	900
ctttctctga	gaaaaaaacc	ctagtaggaa	aaaattttga	ctagaaatag	tatctttctg	960
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<210> 825

<211> 997

<212> DNA

<213> Unknown (H38g675 nucleotide)

<220>

<223> Synthetic construct

<400> 825

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ccagatcttt	aactccctct	gttcttcatg	tttcttgtaa	tgtatgttgt	cactgtgata	120
agaaactttg	tcttggtaat	tctaactatg	cgaaattcac	gtcttcacac	tcccaagtac	180
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cttttctttt	tctttttctg	tttttttttt	tttttaattt	atttctgaat	gttatatgtc	360
gacgtcaatg	gcctatgatt	gctgtgtggc	catctgttac	ccacttcttt	atcacattgc	420

catgtccctt	aaagtgtgtt	tcagccttat	gcttggttcc	tacttccat	ccttttcttg	480
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ttacttccgt	gacatcctcc	ctgtgttcca	gctctccctg	accagcacct	acatcaatga	600
actggtggtt	ttcattgtgg	caggcatcaa	taccattgtg	cccactgtca	cogtctttat	660
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tttttatatg	aacgggcttc	ccatgatgag	ctccttaatc	tacagcttaa	ggaggaaaga	900
tgtaaatttt	gccatgggaa	aatctctgag	taggagaatg	tttttgccat	aaacaacatt	960
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<210> 826

<211> 939

<212> DNA

<213> Unknown (H38g676 nucleotide)

<220>

<223> Synthetic construct

<400> 826

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gggaacattc	tcattcatcat	tgccacagtc	tttactccaa	gtctccatac	ccccatgtat	180
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atggttgagg	gtttgctttt	agaaagaaag	accatttccct	ttgacaactg	catcacacag	300
ctcttcttcc	tacatctctt	tgccctgtgc	gagatctttc	tgctgatcat	tgtggcgtat	360
gatcgttacg	tggctatctg	cactccactc	cactacccca	atgtgatgaa	catgagagtc	420
tgtatacagc	ttgtctttgc	tctctggttg	gggggtactg	ttcactcact	agggcagacc	480
ttcttgacta	ttcgtctacc	ttactgtggc	cccaacatta	ttgacagcta	cttctgtgat	540
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ccagacacca	gcttctccat	tgacaagggt	gtgtctgtct	tctacacagt	ggtcaccctc	840
ttgctgaatc	ccttcattta	caccttgagg	aatgaggagg	taaaaagtgc	catgaagcag	900
ctcaggcaga	gacaagtttt	tttcacgaaa	tcatataca			939

<210> 827

<211> 992

<212> DNA

<213> Unknown (H38g677 nucleotide)

<220>

<223> Synthetic construct

<400> 827

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gggaatttgg	gcttggtaac	tctgattgtg	ttcagttcac	actttcatgc	acccatgtac	180
ttttttcttt	ttagtttagc	ttttatagac	cacttttatt	cttctgtgtt	tattccaaaa	240
atgctgatga	acttcataac	agagaagaat	attatttccct	atgcgggttg	catgtcagct	300
tttttttctt	tctttttttt	tttttttttg	ttatttctga	atgctatggt	ttgacgtcaa	360
tggctcttga	tcactagtgg	ccatggccat	ctgtaacccg	cttctgtata	acattgccat	420
gtcccctaaa	gtgtgttcca	gccatatgct	tggttcctac	ttctggccct	tttctggggc	480
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gttgatgggt	ttcattgcag	caggcatcat	tttactgtg	cccagtatca	ccatctttat	660
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tgtgtcttaa	attatcctca	actgggacta	taaatgaagg	taaaatatct	tctgtctttc	840
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aacttgccctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

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cctctgacc ctcatgggta acacatccat catctgcgct gtgtgggtcaa gccagaaact	180
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ttttactgca cagcaacccc attctttaat cccctgacct acagtctctg gaacaaagat	900
atgacagatg cccttaaaaa agtgctggga gtgccatcaa aagaaatata ttggaacaca	960
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<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

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atagccctca cctcccttac catcaagctg ccctactgtg gtcctgatga gattgacaac	540
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gtgccttaaa caagttagtg gggagaaaag agagaaaaga agaaaaatga aaatgtctac	960
gtccttagga tacgtgggtg tccaaattaa agaagcgcct tgc	1003

<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

<220>

<223> Synth tic construct

<400> 830

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cttactgtgg	cctaacaagg	tgggctatac	ttctgtgata	tcctgcagtg	tacctctagc	120
ctgtaaggac	acatccttag	cccagagggg	aggtttttaca	aatgttgggc	ttttgtctct	180
catttgcttt	tttctcatcc	ttgtttccta	tacttgcatt	gggatttcca	tatcaaaaat	240
ccgctcagca	gagggcaggc	agcgggcctt	ctccacctgc	agcgctcacc	tcactgcaat	300
cctttgtgct	tatgggcccag	tcatcggtat	ctatctacaa	ccaatccca	gtgccttgct	360
tggttccata	attcagatat	tgaataatct	ggtaacccca	atgttgaatc	cactaatcta	420
tagccttagg	aataaggatg	taaaatcaga	tcagccctga	ggaatgtatt	tccaaga	478

<210> 831

<211> 400

<212> DNA

<213> Unknown (H38g681 nucleotide)

<220>

<223> Synthetic construct

<400> 831

ttactatttt	taatgttctt	tattacttcc	ttgggtcata	aattccatct	gatatcattt	60
cccttcagtc	aacaaaccac	ctaacaaaaa	tactttataa	tttttgaagt	atgactctgc	120
tgataacata	cactcacagc	attaatttat	tggtaaatgt	ccttggtcta	gggtatagac	180
ctattttag	ggatatccct	ttagtcccag	agtattgttc	ttatttctag	ggcgtggtcc	240
ttctgggttt	tcattagaaa	gcctaagttt	ttaccgaacc	tctttcactt	ggcagcactt	300
gcatttaaaa	ttctattgcc	ctagttgagg	gtaactgcta	aaatcttttc	tctcagccat	360
ctggctgctg	ttttctactt	actttcttag	agtcttgtct			400

<210> 832

<211> 933

<212> DNA

<213> Unknown (H38g682 nucleotide)

<220>

<223> Synthetic construct

<400> 832

atggctactt	caaaccattc	ttcaggggct	gagtttatcc	tggcaggcct	gacacaacgc	60
ccagaacttc	aactgccact	cttcctcctg	ttccttgga	tatatgtgg	cacagtgggtg	120
gggaacctgg	gcatgatctt	cttaattgct	ctcagttctc	aactttaccc	tccagtgtat	180
tattttctca	gtcatttgtc	tttcattgat	ctctgctact	cctctgtcat	tacccttaag	240
atgctgggtga	actttgttcc	agaggagAAC	attatctcct	ttctgggaatg	cattactcaa	300
ctttattttc	tccttatttt	tgtaattgca	gaaggctacc	ttctgacagc	catggaatat	360
gaccgttatg	ttgctatctg	tcgcccactg	ctttacaata	ttgtcatgtc	ccacagggtc	420
tgttccataa	tgatggctgt	ggatatactca	ctgggttttc	tgtggggccac	agtccatact	480
accgcgatgt	cagtgttgtc	attctgtagg	tctcatacgg	tcagtcatta	tttttgtgat	540
attctccctt	tattgactct	gtcttgctcc	agcaccaca	tcaatgagat	tctgctgttc	600
attattggag	gagttaatac	cttagcaact	acactggcgg	tccttatctc	ttatgctttc	660
attttctcta	gtatccttgg	tattcattcc	actgaggggc	aatccaaagc	ctttggcact	720
tgtagctccc	atctcttggc	tgtgggcate	ttttttgggt	ctataacatt	catgtatttc	780
aagccccctt	ccagcactac	tatggaaaaa	gagaagggtg	cttctgtgtt	ctacatcaca	840
ataatcccca	tgctgaatcc	tctaactctat	agcctgagga	acaaggatgt	gaaaaatgca	900
ctgaagaaga	tgactagggg	aaggcagtca	tcc			933

<210> 833

<211> 948

<212> DNA

<213> Unknown (H38g683 nucleotide)

<220>

<223> Synthetic construct

<400> 833

atggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aatttgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgttttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tcctcctggg	gaacttgtcc	tgtctggaga	tctgggtatac	ctctaacatc	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcatcaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcatctc	tcctgcatgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataccttg	tgcctcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggt	tttgcctt		948

<210> 834

<211> 946

<212> DNA

<213> Unknown (H38g684 nucleotide)

<220>

<223> Synthetic construct

<400> 834

ccagtgagga	ccttggagac	tactaatatc	actggatttg	tgaatgagtt	catcctcttg	60
ggcttcccct	gccgctggga	gatccagatc	ctcctttttg	tggtcttctc	tctcatctac	120
cttctgaccc	tcctaggtaa	cacatccatc	atctgtgctg	tgtgggtcaag	ccagaaactc	180
cacacaccta	tgtacatcct	actggccaat	ttctccttcc	tggagatctg	ctgtgtcagt	240
tctgacgtgc	ccataatggc	agccaatctc	atctcccaga	cacagagcat	ctcctgtgct	300
ggctgctcgc	tcgggttcta	cttcttctcc	atgtgtgctg	cagagtgtct	atttctgtca	360
gtgatgtctt	ttgatagggt	tcctgccatt	tgtagacctt	tgactatcc	caccttaatg	420
acccatcacg	tttgtgtcga	tttttgtgat	cttctgtctg	gtgggtggct	gtctctgggt	480
attgacccct	ttgacactaa	tatctcaggt	gctcttttgt	ggtccaaaca	ctatcgacca	540
ttttttctgt	gatctggcac	ctttgctggc	actgtcttgt	gctccaatac	ctggaattac	600
tctgacttgt	ggtatcatta	gcgctctcat	catctttctt	accttcttgt	atataccttg	660
gacttatttc	tgtgttctaa	gcacagtgtc	acaggtgcct	tcaggcttag	gaaggcataa	720
ggctttctca	acttgtggct	gtcaccttgc	tgtagtgtct	ctcttctatg	gttctcttat	780
ggtgatgtat	gttagcccag	gttctgggga	ctatcatggg	ataaagaaat	ttgcgacctt	840
gttctatact	ttgtcaactc	cattctttaa	tcctctgata	tacagtcttc	ggaacaagga	900
tatgaaagag	gcactaaaga	aatttctgag	gaatcgccac	actgtc		946

<210> 835

<211> 946

<212> DNA

<213> Unknown (H38g685 nucleotide)

<220>

<223> Synthetic construct

<400> 835

cttatagcta	caggaaactg	gacaagaata	agtaagttaa	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatctttc	ctggagattg	gcttcaacct	agtcattgct	240

cccaacatgc	tgtggaccct	gcttgcccag	gacacaacca	tctccttccct	tggtctgtgcc	300
acttagatgt	atttcgtctt	cttcttttgg	gtggctgaat	gcctcctcct	ggctaccatg	360
gcataatgacc	gctatgtggc	catctgagct	ccttgccacta	cccagtcac	atgaaccaa	420
ggactcttgc	caaactggct	gctacctcct	gggtcccagg	cttccctgta	gctactgtgc	480
agaccacatg	gctcttcagt	tttccattct	gtggcaccac	caagggtgaac	cacttcttct	540
gtgacagccc	acctgtgctg	aggctggctt	gtgcagacac	agcactcttt	gagatctacg	600
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ctacatgttc	ctcacacctc	cttgttgtct	ctctttttcta	tatatcatta	agcctcacct	780
acttccggcc	taaatcaa	aattcacctg	agggcaagaa	gctgctatca	ttgtccctaca	840
ctgttatgac	tcccatgttg	aaccccat	tctacagcct	gagaaataac	gaggtgaaga	900
atgccctcag	caggacggct	tctaaggccc	tagccctcag	aaactg		946

<210> 836

<211> 973

<212> DNA

<213> Unknown (H38g686 nucleotide)

<220>

<223> Synthetic construct

<400> 836

atggctgtgg	aaaatgactc	ttcagtgaca	agagtttatt	cttttgggat	taacagacca	60
gcctgagatc	taattgcccc	tgtttttccct	gttcttgggtg	aactatatga	ccaccatggg	120
gggcaacttg	agtttaatta	atctaatttg	cctgaattca	caccttcaca	ctcccatgta	180
ttttttcctt	ttcaatctgt	ccttcattga	tctctgttat	tcatttgtct	ttacccccaa	240
aatgctgatg	agctttatct	cagagaggaa	catcatctcc	tttccaggat	gcgtaactca	300
gctctttttc	ttctgctttt	ttgtccactc	tgagtgtctat	gtgctgacag	ccatggccta	360
tgatcgtat	gtggccatct	gcaaaccctt	tctgtacatg	gtcaccacgt	cccctcagat	420
ctgttctcta	ctgatgcttg	gttcatatgt	gatgggggtt	gctggggcca	tggtccacac	480
agagtgtatg	atgaagctca	tcttttgtga	ctccaacgtc	atcaaccatt	acatgtgtga	540
catcttccca	ctgctccagc	tctcctgcag	cagcacctag	gccaatgagc	tggtgatgtc	600
tgttattgta	ggcacagtgt	ttatagatc	aagcctcatt	atcttaattc	cttatgcttt	660
gattcttttc	aatatccctc	acatgtccctc	agccgagggt	tggttcaaag	ccatcggtac	720
ctgtggctcc	cacataataa	ctgttggcct	attctatgaa	tttgggctga	tcactcatgt	780
taagttatca	tctgattggg	atatgggtca	ggggaagttt	ctctcagtg	tttacacgaa	840
tgaggtaccc	atgctgaacc	ccctcattta	tagcctcagg	aacaaggatg	tcaaacttgc	900
tctaaaggaa	accctaaata	aaattacaaa	ctgagtagag	ccaatgggtg	tgccttagcc	960
cctctccaat	tgc					973

<210> 837

<211> 992

<212> DNA

<213> Unknown (H38g687 nucleotide)

<220>

<223> Synthetic construct

<400> 837

atgagataga	taaatcagac	acaagtgata	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atztatcgta	ttattgggtg	tctacctggg	cactgtgctt	120
ggaaatctgc	ttctaattctc	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgct	tctggctgac	ctctatttct	ctaccaacat	acttcctcag	240
gcactagtcc	acctgcttcc	cataaacaac	ctcattgcat	tcacactttc	tctaactcaa	300
cttctctttt	tctcattttt	tgggtgacct	agtgcgcctt	tattgcagtg	atgtcctata	360
atccctatgt	tgcaatctgc	aatcctctgc	attaccctaa	catcatgacc	tggaaagtgt	420
gtgtccagct	ggcaacagga	tcatggacca	gtggcattct	gggtgtctgtg	gtagacacca	480
ccttcacact	gaggctaccc	taccgaggca	gtaacagcat	tgctcatttc	ttttgtgagg	540
cccctgcact	attgatctta	gcatccacag	acacccatgc	atcagagatg	gccatttata	600
ttacgggggt	tgtgattctc	ctcatacctg	tttttctgat	tctgggtatcc	tatggccgta	660
tcatagtaac	tgtggtcaag	atgaagtcaa	ctgtggggag	tctcaaggca	ttttctacct	720

gtggctccca	cctcatgggtg	gtcatacttt	taaatggatc	agcaatactc	acttgcata	780
cacccaagtc	ttccaaacag	cagtaaaaa	cgggtgtctg	tttctatgca	atagtaactc	840
ccatgcttaa	tcccctcatc	tatagcctga	gaaacaagga	tgtgaaggca	gctctgagg	900
aagtagccac	aaggaatttc	ccatgaaggc	ttggaatctc	acactgacag	tgagctcaga	960
gaaccttttg	gcttcctact	tcaaagactt	gc			992

<210> 838

<211> 549

<212> DNA

<213> Unknown (H38g688 nucleotide)

<220>

<223> Synthetic construct

<400> 838

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgattttctat	cacgtgcacc	cagctcattc	accaacccat	gtattttctc	180
ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgaaccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttggagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttggtg	tactggggga	tttatacatt	ctgccagtca	gtttcttctc	480
accatctctg	taccattttg	tggcccaaat	gatatagatc	actactctcg	cgatgtgtat	540
ccttttgctg						549

<210> 839

<211> 670

<212> DNA

<213> Unknown (H38g689 nucleotide)

<220>

<223> Synthetic construct

<400> 839

ttgcctgaca	tgggtttcac	ctccaccacg	gtccccaaga	tgagcgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	gtgatggcct	atgacctggt	tgtagccatc	180
tgtcaccttc	tatatcggtc	agccatcttg	aaccctgttg	tccgtggctt	cctagatttg	240
ttgtctttgt	tggttggttt	tttttttttc	tctcagtctt	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attccgaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	acaacatgta	420
tttccctget	gccgtatttg	gttttcttcc	catctcgggg	acccttttct	cttactgtaa	480
aattgtttcc	tccattctga	gggtttcatc	atcagggtgg	aagtacaaac	cttctccacc	540
tgtgggtctc	acctgtcagt	tgtttgctga	ttttatggag	caggcgttgg	agggtacctt	600
ggttcagatg	tgcatctttt	cccagaaaag	ggtgcagtgg	cctcagtgc	gtacgtacac	660
ggtggtcacc						670

<210> 840

<211> 645

<212> DNA

<213> Unknown (H38g690 nucleotide)

<220>

<223> Synthetic construct

<400> 840

atggacgtca	ggctcatctg	caccaccgta	cccaagatgg	ccttcaacta	cttgtctggc	60
agcaagtcca	tttctatggc	tggctgtgcc	acacaaattt	tcttctgtgt	atcactgctt	120
ggctctgaat	gctttctgtt	ggctgttatg	tcttatgact	gtacattgc	catttgccac	180
cctctaagat	acaccaatct	catgagaccc	aaaatttgta	gacttatgac	tgcccttctc	240

tggatcctgg	gctctacaga	tggaaatcatt	tatgctgtag	ccacattttc	cttctcctac	300
tgtgggtctc	gggaaatagc	ccacttcttc	tgtgagttac	cttccctact	aatcctctca	360
tgcaatgaca	cgtcaatatt	tgaaaagggt	attttcattt	gctctatagt	aatgcttggt	420
ttccctgttg	caatcatcat	tgttctctat	gctggagtta	ttctggctgt	cattcacatg	480
ggatctggag	agggctgctg	caaagctttc	acgacctgtt	cctctcacct	catgggtggtg	540
ggaatgttct	atggagcagg	tttgttcatg	tacatacagc	ccacatctga	tgcctcccca	600
acgcaggaca	agctgggtgc	tgtattctac	accatcctca	ctccc		645

<210> 841

<211> 380

<212> DNA

<213> Unknown (H38g691 nucleotide)

<220>

<223> Synthetic construct

<400> 841

aatctcctcc	ccgtgtggac	ccctggaagc	aggtgtccct	tcattgatcac	aaattttctgt	60
ctccgagaag	caaggcatgt	cctttcccaa	gaaacttttc	cagaatcaca	aacttttcct	120
actcttttga	gggatgaatg	tatttctgca	gactgtgatg	gcctatgacc	actttgtggc	180
catctgtcac	cccctgcact	acagggtcat	catgaatcct	gggatctttg	gactgtgggt	240
tctggtgtcc	tggagcatga	gtgccctgaa	ttcctcactg	caaagcagaa	tgtgttgtag	300
ctgtccttct	gcacaaactt	ggaaatcccc	ccattttttt	ctgtgaactt	aatcagttga	360
tctgtcttgc	ctgttctaac					380

<210> 842

<211> 648

<212> DNA

<213> Unknown (H38g692 nucleotide)

<220>

<223> Synthetic construct

<400> 842

tttgttgatt	tctgttatcc	caccacgatt	acacccaaac	tgctggagaa	cttgggtgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	atcatgcagt	tattctttgt	ctgcataatt	120
gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtggctacg	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
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tcttggtctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcggcc	tggatgatcat	tctcactccc	tatgctttca	tttttatcac	tgtcatgaag	480
acgccttcca	ctggggggcg	caagaaagcg	ttctccacgt	ctgcctccca	cttgacggcc	540
attaccattt	tccatgggac	tatccttttc	ctctactgtg	ttcctaactc	caaaagttag	600
tggctcatgg	tcaagggtgg	ctctgtcctt	tacacagtgg	tcattccc		648

<210> 843

<211> 643

<212> DNA

<213> Unknown (H38g693 nucleotide)

<220>

<223> Synthetic construct

<400> 843

ttgccagaca	ttggttttcac	cttggccacg	gtccccaaga	tgattgtaga	catgcaatca	60
catagcagaa	tcattctccca	tgcaggctgt	ctgacacaga	tacctttctt	tgtccttttt	120
gtatgtatag	atgacatgct	cctgactgtg	atggcctatg	actgatttgt	ggccatctgt	180
cacccctctc	actacccagt	catcatgaat	cctcacctct	gtgtcttctt	agtgttgatg	240
tctttttcct	tagcctgttg	gattccttag	tgcacaactg	gattgtttaca	attcacctgc	300
ttcaagaatg	tggaaatctc	taattttttc	tgtgactgat	ctcaacttct	caaccttgcc	360

tggtctgact	gtcatcagta	acatattcat	acgttttagat	agtactatat	ttggctttct	420
tcccatttca	gggatccctt	tgtcttacta	taaaattgtg	ccctccattc	taagaattcc	480
attgtcagat	gggaagtata	aagccttctc	cacctgcggc	tctcacctgg	caattgtttg	540
cttattttat	ggaacaggca	ttggcatgta	cctgacttca	gctgtgtcac	cagccccag	600
gaatgggtg	gtggcatcag	tggtgtacgc	tatggtcacc	ccc		643

<210> 844

<211> 652

<212> DNA

<213> Unknown (H38g694 nucleotide)

<220>

<223> Synthetic construct

<400> 844

ttgcctgaca	tcggtttcac	ccccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcatctatgc	aggctgcctg	actgtgatgt	ctctctttgc	catttttggga	120
ggcatggaag	agacacatgc	tcttgaatgt	gatggcctat	gtccggtttg	tagccatctg	180
tcaccctcta	tatcattcag	ccatcatgaa	ccgtgtttc	tggtggcttct	tacttttgtt	240
gtcttttttt	tttctcggtc	tttttagacgc	ccagctgcac	aacatgattg	ccttacaaat	300
gacctgtctc	aaggatgtgg	aaattcctaa	tttcttctgt	gacccttctc	aactccccca	360
tcttgcatgt	tgtgacacct	tcaccaataa	cataatcatg	tattttcctg	ctgccatatt	420
tggttttctt	cccatctcgg	ggaccctttt	ctcttactat	gaaattgttt	cctccattct	480
gagggtttca	tcataagggtg	ggaagtataa	ggccttcgcc	acctgtgggt	ctcacctgtc	540
agtcgtttgc	tgattttatg	gaacaggcgt	tggagggtac	ctcagttcag	atgtgtcatc	600
ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtgggtcacc	cc	652

<210> 845

<211> 692

<212> DNA

<213> Unknown (H38g695 nucleotide)

<220>

<223> Synthetic construct

<400> 845

ttgcctgaca	tcggtttcac	ctccaccaca	gtcgccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgtccttgag	tgtgatggcc	tatgaccggt	ttgtagccat	180
ctgtcaccct	ctatatcggt	cagccatctt	gagcccgtga	ttctgtgcct	tcctagattt	240
gttgtctttg	ttttgttttg	ttttgttttg	ttttgttttg	ttttgttttg	ctcagtcctt	300
tagactccca	gctgcacaac	ttgattgcct	tacaaatgac	ctgcttcaaa	gatgtggaaa	360
ttcctaattt	cctctgggaa	ccttctcaac	tccccatct	tgcattgtgt	gacaccttca	420
ccaggaacat	caacatgtat	ttccctgctg	ctgtatttgg	ttttcttccc	atctcgggga	480
ccttttctct	tacaatggag	taaaattgtt	tcctccactc	tgagggtttc	atcatcaggt	540
gggaagtata	aaccttctcc	acctgtgggt	ctcacctgtc	agttgtttgc	tgattttgtg	600
gaacaggcgt	tggagggtac	ctcggttcag	atgtgtcatc	ttccccgaga	aagagtgcag	660
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<210> 846

<211> 939

<212> DNA

<213> Unknown (H38g696 nucleotide)

<220>

<223> Synthetic construct

<400> 846

atgctggcta	gaaacaactc	cttagtgact	gaatttatct	ttgctggatt	aacagatcgt	60
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ggcaaccttg	gcttgatcac	tcttttcggt	ctaaattctc	acctccacac	accaatgtac	180

tatttcctct	tcaatctctc	cttcattgat	ctctgttact	cctctgtttt	caactccaaa	240
atgctaata	actttgtgtc	aaaaaagaat	attatctcca	atgttgggtg	catgactcgg	300
ctgtttttct	ttctcttttt	cgatcatctc	gaatgttaca	tgttgacctc	aatggcatac	360
gatcgctatg	tggccatctg	taatccattg	ctgtataagg	tcaccatgtc	ccatcaggtc	420
tgttctatgc	tcaacttttg	tgtttacata	atgggattgg	ctggagccac	ggcccacacc	480
gggtgcatgc	ttagactcac	cttctgcagt	gctaatatca	tcaaccatta	cttgtgtgac	540
atactcccc	tcctccagct	ttcctgcacc	agcacctatg	tcaacgaggt	ggttgttcac	600
attgttgtgg	gtactaatat	cacggtaccc	agttgtacca	tcctcatttc	ttatgttttc	660
attgtcacta	gcattcttca	tatcaaatcc	actcaaggaa	gatcaaaagc	cttcagtact	720
tgtagctctc	atgtcattgc	tctgtctctg	ttttttgggt	cagcggcatt	catgtatatt	780
aaatattctt	ctggatctat	ggagcagggg	aaagtttctt	ctgttttcta	cactaatgtg	840
gtgcccacgc	tcaatcccc	catctacagt	ttgaggaaaca	aggatgtcaa	agttgcactg	900
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<210> 847

<211> 924

<212> DNA

<213> Unknown (H38g697 nucleotide)

<220>

<223> Synthetic construct

<400> 847

atgaccatgg	aaaattattc	tatggcagct	cagtttgtct	tagatgggtt	aacacagcaa	60
gcagagctcc	agctgcccc	cttccctcctg	ttcctgggaa	tctatgtggg	cacagtagtg	120
ggcaacctgg	gcattgattct	cctgattgca	gtcagccctc	tacttcacac	ccccatgtac	180
tatttccctca	gcagcttgctc	cttcgtcgat	ttctgctatt	cctctgtcat	tactcccaaa	240
atgctgggtga	acttcctagg	aaagaagaat	acaatccctt	actctgagtg	catgggtccag	300
ctctttttct	ttgtgggtct	tgtgggtggct	gagggttacc	tcctgactgc	catggcatat	360
gatcgctatg	ttgccatctg	tagcccaactg	ctttataatg	cgatcatgtc	ctcatgggtc	420
tgtcactcgc	tagtgctggc	tgccttcttc	ttgggctttc	tctctgcctt	gactcataca	480
agtgccatga	tgaactgtc	cttttgcaaa	tcccacatta	tcaaccatta	cttctgtgat	540
gttcttcccc	tcctcaatct	ctcctgctcc	aacacacacc	tcaatgagct	tctacttttt	600
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aagccccctt	caagtaactc	cctggaccag	gagaagggtgt	cctctgtatt	ctacaccacg	840
gtgatcccca	tgctgaacct	tttaatatat	agtctgagga	ataaggatgt	gaagaaagca	900
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<210> 848

<211> 984

<212> DNA

<213> Unknown (H38g698 nucleotide)

<220>

<223> Synthetic construct

<400> 848

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
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ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttccctc	tttaacttgc	cttcatagat	ctctgttatt	cttctgtgtt	tacacccaaa	240
atgctaata	actttatttc	agagaagaat	attatctcct	tcaaggggtg	catgacccaa	300
cttttctttt	tctgtttttt	ttggtcattt	ctgaatgtta	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	taaccacatt	ctgtatcaca	ttgccatgtc	tcctacagt	420
tgtccagacc	ttatgttttg	ttcctatttg	atggcctttt	ctgggtccat	ggcccacact	480
ggatgcatgc	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
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actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatgggttc	660
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tgcagttccc	atataattgc	tgttttctctg	ttctttggat	caggtgcatt	tatgtatctc	780
aacctatctt	ctgctgggtc	catggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtggttccc	tggtgaaccc	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960
agtcacaaga	cagggatatt	ctgt				984

<210> 849

<211> 940

<212> DNA

<213> Unknown (H38g699 nucleotide)

<220>

<223> Synthetic construct

<400> 849

atgaaaccag	ggaatgagac	acaaatttca	caattccttc	tcctgggact	ttcagaggaa	60
ccagaattgc	agcccttcct	ctttgggcta	tttctgtcca	tgtacctggt	caccgtgctc	120
gggaacctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	ctttgcagac	atctgttttg	tgtctaccac	tgtcccaaag	240
atgctggtga	acatccagac	acagagcaga	gtcatcacct	atgcagactg	catcacccag	300
atgtgctttt	ttatactctt	tgtagtggtg	gacagcttac	tcctgactgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccccctg	cactacacag	tcattatgaa	ctcctggctc	420
tgtggactgc	tggttctggt	gtcctggatc	gtgagcatcc	tatattctct	gttaciaaagc	480
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tgcatactac	ctctcagttg	tctccttatt	ttattgtaca	ggcgtaggtg	tgtaccttag	780
ttctgctgca	accataaact	cactctcaaa	tgctgcagcc	tcgggtgatgt	acactgtggt	840
cacctccatg	ctgaacccct	tcatactacag	cctgaggaat	aaagacataa	acagagctct	900
gaatcgattc	ttcagagagc	agaaacagga	gggccatttt			940

<210> 850

<211> 971

<212> DNA

<213> Unknown (H38g700 nucleotide)

<220>

<223> Synthetic construct

<400> 850

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gatccagaac	tgcagtcggt	cctcgctttg	ctgtccctgt	ccctgtccct	gaatctgggc	120
acggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccatgtact	tcttctcttc	caacctgtgc	tgggctgaca	tcgggtctcac	ctcggccacg	240
gttcccaagg	tgattctgga	tatgcagtcg	catagcagag	tcatactctca	tgtgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	gctgctttgt	agccatctgt	cgccctctgc	actacccagt	catagtgaat	420
cctcacctct	gtgtcttctt	cgttttgggt	tcctttttcc	ttaacctggt	ggattcccag	480
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ttctgtgacc	cctctcagct	tctcaacctt	gcctgttctg	acagcgctcat	caatagcata	600
ttcatatatt	tcgatagtag	tatgtttggt	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	ttgtcccttc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaagcc	720
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taggctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcgagggtc	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
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<210> 851

<211> 1014

<212> DNA

<213> Unknown (H38g701 nucleotide)

<220>

<223> Synthetic construct

<400> 851

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gtcccaagag ctgagcttgg tcttatttct tttcttattt tttgtgtact cagcaactgt      120
gctgggtaac ctctcatca tggctgtggt gacctgtgag tctcgcttc acacccccac      180
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gaaggtgcta atagaccttt caagcagaaa gaccatctcc ttcaatgggt gcatgacaca      300
gatgtttttt ttccacctcc tcggtgggac agacgttttt tctctctttg tgatggcggt      360
tgaccaatac atggccatct tcaagccctt gcactgtgtg accatcgtga gtaggggaca      420
gtgctccctt acatcgtgag tagggggcgt gagtgaggcg caggcctcat catggcttcc      480
tggtgtgggg gtttgtccac tccattgtgc aggtatttct gttgtctcca ctcccttctg      540
tggaatcat atgattgatg gtttctactg tgatgtcccc caggctctca aacttgctg      600
caccacacac tttgtctctg aggtcttaat gatttccaat aatggcttga tctctatgct      660
gtggttcate ttctctctca tatcttacac ggtcatcttg atgatgttga ggtctcacac      720
tgaggaaggc aggagaaag ccacgcccac ctgcacctcc cacatcactg tggtgaccct      780
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gctgtctcca tcacctttac agtcattatt cctgtcctga accccatgat ctacaccctg      900
aggaaccagg agatgaagtc agccttgagg aggcggaaga aaagaccttc tggaaaggga      960
tagatgctac gaagtccaga ttggaaaatc agaactgaaa agtatttctt cata      1014

```

<210> 852

<211> 1004

<212> DNA

<213> Unknown (H38g702 nucleotide)

<220>

<223> Synthetic construct

<400> 852

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tctacatacc cgcagaatth aacagatgtc tctttattcc tcttcctaga agctcagagg      60
atccagaaca gcagcctgtc ctgctggggc tgttctctgc catgtgcctg gtcacgggtgc      120
tggggaacct gctcatcatc ctggccgtca gccctgactc ccacctccac acccccatgt      180
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agatgattgt ggacatctaa tctcacagca gactcatctc ctaggcaggc tgcctgactc      300
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tgcacaactt gattgcctta caaatgacct gcttcaagga tgtggaaatt cctaatttct      540
tctgggaacc ttctcaactc ccccatcttg catgttgcca cacttcacc aataacataa      600
tcatgtattc ccctgctgcc atatttggtt ttcttcccat ctgggggacc cttttctctt      660
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gtccacactg tgggtctcac ctgtcagttg ttgtctgatt ttatggaaca ggcttttggg      780
ggtacctcag ttcagatgtg tcatcttccc cgggaaaggc tgcagtggcc tcagtgatgt      840
acacgggtgt caccacctg ccgaacctt tcatctacag cctgagaaac agggatatta      900
aaagcgtctt gcggcgccg cagggcagca cagtctaata tcaatatctc cttatctgtt      960
ccatgccttt ttagtgtgtg gtaaaaaaag gcagcaaggt caaa      1004

```

<210> 853

<211> 945

<212> DNA

<213> Unknown (H38g703 nucleotide)

<220>

<223> Synthetic construct

<400> 853

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acaagattgg	tcctatttct	tttctactc	ttgggtgtaca	tgacgactct	gctgggaaac	120
ctectcatca	tgggtactgt	cacctgtgaa	tcttgccctc	acatgcccac	gtattttttg	180
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ctcttccacc	ttattggagg	ggtggatgca	ttttctctat	cagtgatggc	attggatcaa	360
tatgtggcca	tttccaagtc	cctgcactat	gcgaccatca	tgagtagaga	ccgttgccatt	420
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caggttctca	aactcgccca	tacagacatt	ttcatacttg	agctgttgat	gatttccaac	600
aatggactgc	tcaccacact	gtggtttttc	ctgctcctgg	tgctctacat	ggatcatatta	660
tcattactca	agtctcaggc	aggatagggc	aggaggaaag	tcattctccac	ctgcacctcc	720
cacatcactg	tggtgaccct	gcattttgtg	ccctgcactc	atgtctatgc	ccggcctttc	780
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aacctttgat	ctacactctg	agaaaccatg	agatgaagtc	aaccatgaag	agactgaaga	900
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<210> 854

<211> 962

<212> DNA

<213> Unknown (H38g704 nucleotide)

<220>

<223> Synthetic construct

<400> 854

cacacagagc	cacggaatct	cacagggtgc	tgaaaagtgc	tcctgggact	ctctctgaga	60
ggatccagaa	ctgcagccca	tcctcgctgg	gctgtccctg	tcctatgtatc	tggtcacggg	120
gctgaggaac	gtgctcatca	tcctggctgt	cagctctgac	tcctacctcc	acacccccat	180
gtacttcttc	ctctccagcc	tgtgctgggc	tgacatcggt	ttcacctcgg	ccactgttcc	240
caagatgact	gtggacatgc	agtcgcatag	cagagtcatc	tccttatgtga	gctgcctgac	300
acagatatct	ttcttggtcc	tttttgcatg	tatggaagac	atgctcctgt	gatggcctat	360
gacagagttg	tggccatctg	tcacccccctg	cactatccag	tcattcatgaa	tcctcacctt	420
cgtgtcttct	tagttttgct	gtcctttttc	cttagcttgt	tggtattccca	gctgcacagt	480
tggatttgtg	tacaattcac	cttattcaag	aatgtggaaa	actctagtgt	tgtctgtgac	540
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ctgcggaggc	tgcgcagcag	aacagtcgaa	tctcatgatc	tggtcccatcc	tttttcttgt	960
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<210> 855

<211> 952

<212> DNA

<213> Unknown (H38g705 nucleotide)

<220>

<223> Synthetic construct

<400> 855

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ggtggcaacg	tcaccatcat	caccatcacc	catgcggata	ggtcccgcga	cactcccacg	180
taccacttcc	tgggtgtgct	gtccctctcg	gagacctgct	atacacgctg	gtcaccatcc	240
ccagcatgct	ggctcatctg	ctgatggaga	ccaggccatc	tcctatccctg	gctgtcaggc	300
tcagatgttt	ttcttccctg	gtctgggatg	cagccactgc	ttcctcctta	ccctgatggg	360
ttatgaccgc	tatgtggcca	tctgccaccc	cctgcgctac	tctatgggtca	tgagaccac	420
cgtttgccctc	tgcctgggag	ccctgggtttt	ctgctctggg	ttctcggtgg	ccttgatcga	480

gaccagcatg	atctttctcat	cgcccttttg	cgggcggagac	cacgtggagc	acttcttctg	540
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ggtggtgatg	ccactgctga	accctgtggt	gtgcactctg	tggaacaagg	aggtgagagt	900
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<210> 856

<211> 339

<212> DNA

<213> Unknown (H38g706 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(339)

<223> n = A,T,C or G

<400> 856

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gccgtcatcc	tggcctccta	cgggtgccgtg	gcccagactg	tctgttgcat	gcgggttcagc	180
ggaggccgga	gggaggggcg	tgggcacgtg	ttgggtccca	cctgacagcc	gtctgcctgt	240
tctacggctc	ggccatctac	acctacctgc	agcccgcgca	gcgctacaac	cagcacgggn	300
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<210> 857

<211> 939

<212> DNA

<213> Unknown (H38g707 nucleotide)

<220>

<223> Synthetic construct

<400> 857

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cgagaactga	gccaggtctt	atttaccttc	ctgtttttgg	tgtacatgac	aactctaata	120
ggaaacttcc	tcatcatggt	tacagttacc	tgtgaatctc	accttcatac	gcccattgtac	180
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acctcccaca	tcaccgtggt	gacctgcat	ttcgtgccct	gcattctatg	ctatgcccgg	780
cccttcaactg	ccctccccac	agacactgcc	atctctgtca	ccttcaactg	catctcccct	840
ttgctcaatc	ctataattta	cacgctgagg	aatcaggaaa	tgaagttggc	catgaggaaa	900
ctgaagagac	ggctaggaca	atcagaaagg	attttaatt			939

<210> 858

<211> 486

<212> DNA

<213> Unknown (H38g708 nucleotide)

<220>

<223> Synthetic construct

<400> 858

gtagccatat	gtaatccctt	gctttatcca	gtgatgatgt	ccaacaaact	cagcgctcag	60
ttgctaagta	tttcatatgt	aattggtttc	ctgcaccttc	tggttcatgt	gagtttacta	120
ttgcgactaa	ctttctgcag	gtttaacata	atacattatt	tctactgtga	aattttacaa	180
ctgttcaaaa	tttcatgcaa	tgggccatct	attaacgcac	taataatatt	tatttttggg	240
gcttttatac	aaatacccac	tttaatgact	atcataatct	cttataactcg	tgtgctcttt	300
gatattctga	aaaaaaagtc	tgaaaagggc	agaagcaaag	ccttctccac	atgcggcgcc	360
catctgcttt	ctgtctcatt	gtactacgga	actctgatct	tcatgtatgt	gcgtcctgca	420
tctggcttag	ctgaagacca	agacaaaagt	tattctctgt	tttacacgat	tataattccc	480
ctgcta						486

<210> 859

<211> 774

<212> DNA

<213> Unknown (H38g709 nucleotide)

<220>

<223> Synthetic construct

<400> 859

atgtactact	tcctctgcca	cctggccttg	gtagacgcgg	gcttcactac	tagcgtgggtg	60
ccgccgctgc	tggccaacct	gcgcggacca	gcgtcttggc	tgccgcgcag	ccactgcacg	120
gcccagctgt	gcgcacgcgt	ggctctgggt	tcggccgaat	gcgtcctcct	ggcgggtgatg	180
gctctggacc	gcgcggcgcc	agtgtgcgc	ccgtctgcgt	atgcgggggt	cgtctccccg	240
cgcctatgtc	gcacgctggc	cagcgcctcc	tggctaagcg	gcctcaccac	ctcgggttgcg	300
caaaccgcgc	tcctggctga	gcggccgcgt	tgcgcgcccc	gcctgtgtga	ccacttcate	360
tgtgagctgc	cggcggttgc	caagctggcc	tgcggaggcg	acggagacac	taccgagaac	420
cagatgttcg	ccgcccgcgt	ggctacccctg	ctgctgcctg	ttgccgtcat	cctggcctcc	480
tacggtgccg	tggcccagac	tgtctgttgc	atgcggttca	gcggaggccg	gaggaggggcg	540
gtgggcacgt	gtgggtccca	cctgacagcc	gtctgcctgt	tctacggctc	ggccatctac	600
acctacctgc	agcccgcgca	gcgtacaaac	caggcacggg	gcaagtctgt	atcgtctctt	660
tacaccgtgg	tcacacctgc	tctcaaccgc	ctcatctaca	ccctcaggaa	taagaaagtg	720
aagggggcag	cgaggaggct	gctgcggagt	ctggggagag	gccaggctgg	gcag	774

<210> 860

<211> 948

<212> DNA

<213> Unknown (H38g710 nucleotide)

<220>

<223> Synthetic construct

<400> 860

atgcagagag	ccaatcactc	cacagtgacc	caattcatcc	tcgtcggctt	ctctgtcttc	60
ccccacctcc	agctgatgct	cttctgtctg	ttcctgtctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcacatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctgt	gcgcctctc	cgtctccgag	atcctctaca	ccgtggccat	catcccgcgc	240
atgctggcgg	acctgctgtc	caccagcgcc	tccatcgctt	tcctggcctg	tgccagtcag	300
atgttctctt	ccttcagctt	cggcttcacc	cactccttcc	tgtccaccgt	catgggctac	360
gaccgctacg	tggccatctg	ccacccccctg	cgctacaacg	tgtctatgag	cccgcggggc	420
tgcgcctgcc	tgggtgggctg	ctcctgggct	ggtggcttgg	tcatggggat	ggtgggtgacc	480
tcggccattt	tccacctcgc	cttctgttga	cacaaggaga	tccaccattt	tgcttgccat	540
gtgccacctc	tgttgaagtt	ggcctgttga	gacgatgtgc	tgggtgggtggc	caaaggcgtg	600
ggcttgggtg	gtatcacggc	cctgctgggc	tgttttctcc	tcactcctct	ctcctatgcc	660
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acctgtgcct	ctcacctcac	tgtggtggtc	gtgcactatg	gctttgcctc	cgctatttac	780
ctgaagccca	aaagtcccca	gtctctggaa	ggagacacct	tgatgggcat	cacctacacg	840
gtcctcacac	ccttctctcag	ccccatcatc	ttcagcctca	ggaacaagga	gctgaagggtc	900
gccatgaaga	agaccttctt	cagtaaaactc	taccagaaaa	aaaatgta		948

<210> 861
 <211> 674
 <212> DNA
 <213> Unknown (H38g711 nucleotide)

<220>
 <223> Synthetic construct

<400> 861
 ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga catccagtct 60
 cacagcagag tcctctccta tgcgggctgc ctgatcagat gtctctcttt gccacttttg 120
 gaagcatgga agagaggcat gtccttgagt gtgatggcat atgaccgggt tgtagccatc 180
 tgtcaccctc tatatcggtc agccatcttg aaccctgat tctgtggctt cctagatttg 240
 ttgtctttgt tttttttgt ttgtttggtt tgtttttctc agtcttctag actcccagct 300
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360
 ctgggaacct tctcarctcc cccatcttgc atgttgtgac accttcacca ggaacatcaa 420
 catgtatttc cctgctgccc tatttgggtt tcttcccatc tcagggaacct tttctcttac 480
 tgtaaaattc tttcctccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540
 ccacctgtgg gtctcacctg tcagttggtt gctgatttta tggaacaggc gttggagggt 600
 acctcggttc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660
 ygggtggtcac cccc 674

<210> 862
 <211> 653
 <212> DNA
 <213> Unknown (H38g712 nucleotide)

<220>
 <223> Synthetic construct

<400> 862
 ttgcctgaca tcggtttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60
 acagcagagt catctcctat gcaggccgcc tgactcagat gtctctcttt gccatttttg 120
 gaggcagatgga agagagacat gtccttgagt gtgatggcct atgaccgggt tgtagccatc 180
 tgtcaccctc tatgtcattc agccatcacg aaccctggtt tctgtggctt tctagttttg 240
 ttgtcttttt tttttctcag tccttttagac gccagctgc acaacttgat tgccttacia 300
 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360
 gtcttgcattg ttgtggcacc ttcaccaata acataatcat gtatttcctt gctgccatat 420
 ttggttttct tcccattctg gggacccttt tctcttacga taaaattggt tctctcattc 480
 tgagggtttc atcatcaggt gggaagcata aggccttctc caccaggggg tctcacctgt 540
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcggttca gatgtgtcat 600
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863
 <211> 648
 <212> DNA
 <213> Unknown (H38g713 nucleotide)

<220>
 <223> Synthetic construct

<400> 863
 ctgggtggact ttggatactc ctacagctgtc actcccaagg tcatggctgg gttccttata 60
 gaagacaagg tcattctctta caatgcatgt gctgctcaaa tgtatattt ttagctttt 120
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180
 aaacccttac attacaccac aaccatgaca acaactgtgt gtgctcgtct ggccataggc 240
 tcctacctct gtggtttcct gaatgcctcc atccacactg gggacacatt tagtctctct 300
 ttctgttaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catggttctc 360
 tcttgctctg atagacatat tagcgagctt gttcttattt atgttgtgag cttcaatata 420
 tttatagctc tcctgggttat cttgatatcc tacacattca tttttatcac catcctaaa 480

atgcactcag	cttcagtata	ccagaagcct	ttgtccacct	gtgcctctca	tttcattgca	540
gtcggcatct	tctatgggac	tattatcttc	atgtacttac	aaccagctc	cagtcactcc	600
atggacacag	acaaaatggc	acctgtgttc	tatacaatgg	tcatcccc		648

<210> 864

<211> 645

<212> DNA

<213> Unknown (H38g714 nucleotide)

<220>

<223> Synthetic construct

<400> 864

attgttgaca	tatcctatgc	ttccaactat	gtccccaaga	tgctgacgaa	tcttatgaac	60
caggaaagca	ccatctcctt	ttttccatgc	ataatgcaga	cattcttgta	tttggtttt	120
gtcacgtag	agtgtctgat	tttggtggtg	atgtcctatg	atcgctatgc	ggacatctgc	180
cacccttac	gttacaatat	cctcatgagc	tggagagtgt	gcactgtcct	ggctgtggct	240
tcctgggtgt	tcagcttcct	cctgggtctg	gtccctttag	ttctcatcct	gaggctgccc	300
ttctgcgggc	ctcatgaaat	caaccacttc	tgtgaaatcc	tgtctgtcct	caagttggcc	360
tgtgtgaca	cctgggtcaa	ccagggtggtc	atctttgcag	cctgctgtgt	catcctgggtg	420
gggccactct	gcctgggtgct	ggctccttac	ttgcgcaccc	tggccgccat	cttgaggatc	480
cagtctgggg	agggccgcag	aaaggccttc	tccacctgct	cctccacact	ttgcgtgggtg	540
ggactcttct	ttggcagcgc	cattgtcacg	tacatggccc	ccaagtcccg	ccatcctgag	600
gagcagcaga	aagttctttc	cctgtttttac	agccttttca	atcca		645

<210> 865

<211> 486

<212> DNA

<213> Unknown (H38g715 nucleotide)

<220>

<223> Synthetic construct

<400> 865

gtggccatct	gtaaaccct	tcattatgtg	gtcatcatga	acaacagggt	gtgtacctta	60
ttagttctct	gctgttggtg	ggctggcttg	atgatcattg	ttccaccact	tagcttaggc	120
ctccagctcg	aattctgtga	ctccaatgcc	attgatcatt	ttagctgtga	tgcaggctcct	180
ctcctaaaga	tctcatgctc	agatacatgg	gtaatagaac	agatgggttat	acttatggct	240
gtatttgcac	tcattatcac	cccagtttgt	gtgattctgt	cctacttgta	catagtcaga	300
acaattctga	agttcccttc	tgttcagcaa	aggaaaaagg	ccttttctac	ctgttcaccc	360
cacatgattg	tggtttccat	tgccatgga	agctgcatct	tcatttatat	caagccctct	420
gcaaaagatg	agggtggccat	aaataaagga	gtttcagttc	ttactacttc	tgtcgcaccc	480
ttgttg						486

<210> 866

<211> 670

<212> DNA

<213> Unknown (H38g716 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 866

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cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	cgtgatggcc	tacgaccagt	ttgtagccat	180
ctgtcacct	ccatctcgtt	cagccatctt	gaaccctgtg	ttctgtggct	tccaagattt	240

gttgctccttg	tntttttttt	tttttttttt	tttttccctca	ggctttttaga	ctcccagctg	300
cataacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaatttc	taatgtcttc	360
tgggaacctt	ctcaactctc	ccatcttgca	tgttgtaga	ccctcaccag	gaacatcagt	420
atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttcc	tcttactgta	480
aaattgtttc	ctccattctg	agggtttcat	catcagggtg	gaagtataaa	ccttctccac	540
ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acagggtgtg	gagggtacct	600
cagttcagat	gtgtcatctt	ccctgagaaa	ggctgcagtg	gctcagtgta	tgtacaagat	660
gttcaccccc						670

<210> 867

<211> 654

<212> DNA

<213> Unknown (H38g717 nucleotide)

<220>

<223> Synthetic construct

<400> 867

ttggctgaca	tcggtttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgtgtttttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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catcttgcat	gttgtgacac	cttcaccatt	aacatagtca	tgtatttccc	tgccgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttcctccatt	480
ctgagggttt	catcatcagg	tgggaagtat	aaagccttct	ccacctgtgg	gtctcacctg	540
tcagttgttt	gctgagttta	tggaaacaggc	gttggaggtt	acctcagttc	agatgtgtca	600
tcttccctga	gaaaggctgc	agtggcctca	gtgatgtaca	cgggtggtcac	cccc	654

<210> 868

<211> 882

<212> DNA

<213> Unknown (H38g718 nucleotide)

<220>

<223> Synthetic construct

<400> 868

ttgattttct	tcttaatcta	tccgcttata	ctgggtgggta	atgaccagat	cctgggtgggt	60
gtgatggcag	aggccagcct	tcacaagcct	gtgtacttct	tcctgataaa	cctctcagcc	120
ctagacatcc	tctccactac	agtcactgtc	cccaagacgc	tgccctgtgt	cttgcttggg	180
gaccacttcc	tcagcttccc	tgcttgcttc	ctacagatgt	acctgttcca	cagcttctcc	240
tgctcagaag	ccttcatcct	ggtggtcatg	gcctatgacc	gctatgtagc	tatctgccac	300
ccactgcaat	accctgttct	catgaacca	cagaccaatg	ctgtcttggc	aaccgggtgcc	360
tggtcactg	ccctcctcct	gcccattcca	gcagtagtac	agacctccca	gatggcattt	420
gacagcattg	ctgacatcta	ccactgcttc	tgtgatcatc	tggctgtggg	ccaggcctcc	480
tgtcttgata	ccacccccag	accttcatgg	gtttctgcat	cgccatgggtg	gtgtccttcc	540
tcccccttct	cctgggtgctt	ctctcctatg	cccacatctt	gacctcggtg	cttcgcatta	600
actcccaaga	aggacgctcc	aaagccttct	ccacctgcag	ctcccatctc	ccggtagtgg	660
gcacctacta	ctcatccatt	gccatagcct	atgtggccta	cagcgtgac	ctgcccctcg	720
acttccacgt	catgggcaat	gttgtacatg	tcttcttctt	cctcttcttc	ttcttcttcc	780
tcttctctct	cttctctctc	ctcttcgtct	tcttcttctt	cttcttctcc	ttctccttcc	840
tcttctctct	cttctccttc	tccttcttct	tctttcttct	tt		882

<210> 869

<211> 934

<212> DNA

<213> Unknown (H38g719 nucleotide)

<220>

<223> Synthetic construct

<400> 869

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cggaagtga	gcttagtctt	atttctttt	ctactcttg	tgtatgtgac	aactttgctg	120
ggaaacctcc	tcatcatggt	cactgttacc	tgtgaatctc	gccttcacac	gcccattgat	180
tttttgctcc	ataatttatc	tattgccgat	atctgcttct	cttccatcac	agtgcccaag	240
gttctgggtg	accttctgtc	tgaaagaaa	accatctcct	tcaatcattg	cttcactcag	300
atgtttctat	tccaccttat	tggaggggtg	gatgtatttt	ctctttcggg	gatggcattg	360
gatcgatatg	tggccatctc	caagcccctg	cactatgcga	ctatcatgag	tagagaccaa	420
tgcattgggc	tcacagtggc	tgccctggtg	gggggctttg	tccactccat	cgtgcagatt	480
tccttgttgc	tcccactccc	tttctgcgga	cccaatgttc	ttgacacttt	ctactgtgat	540
gtccaccggg	tectcaaact	ggcccataca	gacattttca	tacttgaact	actaatgatt	600
tccaacaatg	gactgtcac	cacactgtgg	tttttctctg	tcttgggtgc	ctacatagtc	660
atattatcat	tacccaaagt	tcaggcagga	gagggcagga	ggaaagccat	ctccacctgc	720
acctcccaca	tactgtggt	gacctgcac	ttctgtgccc	tgcattctatg	tctatgcccg	780
gcccttcaact	gccctcccca	tggataaggc	catctctgtc	accttcaactg	tcatctcccc	840
tctgtctaac	cccttgatct	acactctgag	gaaccatgag	atgaagtcag	ccatgaggag	900
actgaagaga	agacttgtgc	cttctgatag	aaaa			934

<210> 870

<211> 898

<212> DNA

<213> Unknown (H38g720 nucleotide)

<220>

<223> Synthetic construct

<400> 870

acaatgcagc	aaaataacag	tgtgcctgaa	ttcatactgt	taggattaac	acaggatccc	60
ttgaggcaga	aaatagtgtt	tgtaatcttc	ttaattttct	atatgggaac	tgtgggtggg	120
aatatgtcca	ttattgtgac	catcaagtc	agccggacac	taggaagccc	catgtacttc	180
tttctatatt	atttgtcctt	tgcagattct	tgcttttcaa	cttccacagc	ccctagatta	240
attgtggatg	ctctctctga	aaagaaaatt	ataacctaca	atgagtgcac	gacacaagtc	300
tttgcactac	atttatttgg	ctgcatggag	atctttgtcc	tcattctcat	ggctgttgat	360
cgctatgtgg	ccatctgtaa	gcccttgctg	tacccaacca	tcattgagcca	gcaggctctgc	420
atcatcctga	ttgttcttgc	ctggataggg	tctttaatac	actctacagc	tcagattatc	480
ctggccttaa	gattgccttt	ctgtggaccc	tatttgattg	atcattattg	ctgtgatttg	540
cagcccttgt	tgaaacttgc	ctgcatggac	acttacatga	tcaacctgct	gttgggtgtct	600
aacagtgggg	caatttgcct	aagtagtttc	atgattttga	taatttcata	tattgtcatc	660
ttgcattcac	tgagaaacca	cagtgcacaa	gggaagaaaa	aggctctctc	cgcttgcaag	720
tctcacataa	ttgtagtcat	cttattcttt	ggcccatgta	tattcatata	tacacgcccc	780
ccgaccactt	tccccatgga	caagatgggt	gcagtatatt	atactatttg	aacacccttt	840
ctcaatccac	tcattctacac	atctgaggaa	tgcagaagtg	aaaaatgcca	tgagaaag	898

<210> 871

<211> 943

<212> DNA

<213> Unknown (H38g721 nucleotide)

<220>

<223> Synthetic construct

<400> 871

atggagttgg	gaaatgtcac	cagagtaaaa	gaatttatat	ttctgggact	tactcaatcc	60
caagaccaga	gtttgggtctt	gtttcttttt	ttatgtcttg	tgtacatgac	gactctgctg	120
ggaaacctcc	tcatcatggt	caccgtgacc	tgtgagtctc	gccttcacac	ccccatgtac	180
ttcctgtctc	gcaatctagc	catccttgac	atctgcttct	cctccacaac	tgctcctaaa	240
gtcttggctg	accttctgtc	aaagaaaaag	accatatcct	atacaagctg	catgacacag	300
atatttctct	tccacctctc	tgggggggca	gacatttttt	ctctctctgt	gatggcgctt	360
gactgctaca	tggccatctc	caagcccctg	cactatgtga	ccatcatgag	tagagggcaa	420

tgcaactgccc	tcatctctgc	ctcttgggatg	gggggctttg	tccactccat	cgtgcagatc	480
tccctgttgc	tgccctctccc	tttctgtgga	cccaatgttc	ttgacacttt	ctactgcgat	540
gtcccccagg	tccctcaaat	cacttgcaact	gacacttttg	ctcttgagtt	cttgatgatt	600
tccaacaatg	gcctgggtcac	tacctgtgg	tttatcttcc	tgcttggtgc	ctacacagtc	660
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acctccccac	atcactgtgg	tgaccctgca	ttttgtgccc	tgcatctatg	tctatgcccc	780
gcccttcaact	gccctcccca	cagaaaaggc	catctctgtc	accttcaactg	tcatctccc	840
tctgtctgaac	cctttgatct	acactctgag	gaaccaggaa	atgaagtcag	ccatgagaag	900
actgaagaga	agactcgtgc	cttctgaaa	ggaatagaaa	aca		943

<210> 872

<211> 942

<212> DNA

<213> Unknown (H38g722 nucleotide)

<220>

<223> Synthetic construct

<400> 872

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ccccacctcc	aactgatgct	cttctgtctg	ttctgtctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcatcatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctctg	gcgtcctctc	agtctccgag	atcctctaca	ccgtggccat	catcccgcgc	240
atgctggcgc	acctgctgtc	caccagcgc	tccatcgctt	tctggcctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggttcacc	cactccttcc	tgctcaccgt	catgggctac	360
gaccgctacg	tgcccatctg	ccacccctg	cgctacaacg	tgctcatgag	cccacggggc	420
tgcgcctgcc	tggtgggctg	ctcctgggct	gggtggctcg	tcatggggat	gggtgggacc	480
tgggccattt	tccaactgac	tttctgtgga	tcccatgaga	tccagcattt	tttatgtcat	540
gtgccacctc	tgttgaagtt	ggcctgtgga	aataatgtac	cagctgtggc	cctgggcgtg	600
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acctgtgcct	ctcaccttat	tgtggctcatt	gtgcactatg	gctttgcctc	tgtcatctac	780
ctcaagccca	aaggctccca	ctctcaggag	gggtgacacc	tgatggccac	cacctacgca	840
gtcctcacgc	ccttctctcag	ccccatcatc	ttcagcctca	ggaacaaaaga	actgaaggtt	900
gccatgaaga	ggaccttctt	cagcacactc	tattcctcag	gc		942

<210> 873

<211> 948

<212> DNA

<213> Unknown (H38g723 nucleotide)

<220>

<223> Synthetic construct

<400> 873

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ccccagcagc	tctgtcctgt	cttgttccctg	ctgtacctcc	tgatgttccct	gttcacattg	120
cttggcaacc	ttcttatcat	ggccacagtt	tggattgaac	gcagactcca	cacacccatg	180
tacctcttct	tgtgtgccct	ctccatctct	gagattctgt	tactgtttgc	catcacccct	240
cgcattgctg	ctgatctgct	cttcacccat	cgttccatca	cctttgtggc	ttgtgccatt	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcat	ggtcatgggc	360
tatgatcact	acgtgaccat	ctgccaccca	ctgcattaca	acatgctaata	gagtccccgt	420
ggctgtgccc	atcttgtggc	ctggacctgg	gctgggtggc	cggtcatggg	gatgatgggtg	480
acaatgatgg	tttttccact	cactttctgt	gggtctaata	tgatccacca	ttttctctgt	540
catgtgcttt	ccctcttgaa	gttggcctgt	gggagcaaga	catcatctgt	catcatgggt	600
gtgatgctgg	tgtgtgtcac	agccctgata	ggctgtttgt	tcctcatcat	cctctccttt	660
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tccacttgtg	tatccacact	cactgtgggtg	gtcatgcact	atagttttgc	ctcccttctc	780
tacctcaaac	ccaagggcct	ccattctatg	tacagtgtatg	ccttgatggc	caccacctat	840
actgtcttca	cccccttctt	cagcccaatc	attttcagtc	taagggaacaa	ggagctgaag	900
aatgccataa	ataaaaaactt	ttgcagaagg	ttctgccttc	taagctcc		948

<210> 874
 <211> 484
 <212> DNA
 <213> Unknown (H38g724 nucleotide)

<220>
 <223> Synthetic construct

<400> 874
 ggatggaaat acaagcacct tcaacatctc ctgcaccaag ttcttcctgg tgggtttccc 60
 tggacttcga gagtgggtgg cccttcttgt cctgcctctt gtcttcctct ttgtgaccat 120
 catctctgcc aatgccctgg tcatccacac agtgggtggc cggcaaaatc tgcacagcc 180
 tacgtgtatg ctcatcactg tgctcctggc tgtaaatatt cgtgctgcca cagccgtgat 240
 gcctaaaatg ctggagggtt ttgtatatta tgctaaccac atatcgctgc atggccgcct 300
 ggcctagggt ttcttttatct acttcaccct cctcctggac tacaacttcc tctggccctg 360
 gccctggact gggtactttg ccactctgcca cccactctgc ttttctgacc tgatgacctc 420
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgacccgcg 480
 ccct 484

<210> 875
 <211> 595
 <212> DNA
 <213> Unknown (H38g725 nucleotide)

<220>
 <223> Synthetic construct

<400> 875
 gtagccatct ggccaccctc tctgttttca aactgaatga cttcccagct ggctgggatt 60
 gctggccatt cttgccttga cacagagctg gggagtgaac gtgccttttg tagtactaac 120
 tgcaaaagcc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcatgtc 180
 actgctgagc atagcttgtg gagacctgac cttcaacaac tggctggggc tggctatgtg 240
 tttggtcact gtaatctctg atatggccct gctggggacc tcctacaccc acatcatcta 300
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360
 ccacctactg gtcacctctt ccactctacg tctgtgtctt tccacttcca tcaccttctg 420
 agtagccaag actgtgtccc agaattgtcca gaattacttc agtgccatat acttgctgct 480
 tccaggagcc ttgaatcctg tcatttatgg ggtgaggact agggagatcc agcaacatgt 540
 agaaaagatg ctctgtgaaa aggaaacagc ccagaaggct ggggagaagc caaag 595

<210> 876
 <211> 944
 <212> DNA
 <213> Unknown (H38g726 nucleotide)

<220>
 <223> Synthetic construct

<400> 876
 ttcagtcaga acttgctgat ctctgggtct gggtcctttg tcctgctggg gatgccggga 60
 ctggaggctc tgcattgctg gctctctgtg cctgtgtgcc tgctctacat ggcagctttg 120
 gtagggaaat cccttctagt ggggctgggt ggtcgtgac aaggcactct gggcacccat 180
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240
 caaagctctg gctgtacttt ggggcttgct tagtgagata tcatttggag gctgcttggc 300
 tcaactcttt gttgcccatg tgtcaatcat tgccacattg ctgagtcctc agtgctgctg 360
 tccacggccg tagactgcca gcctttgcgc tatggggcgt tgctggccca gtttgtggta 420
 ggtctagtgg cctgactac catgaccctg gatgtctgtg tcatgtacac cctgtgatec 480
 tgttcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgcgaacaca 540
 tgggtgtggc ttgcctggca tgtggagata cgtgcccat catcagggtat ggactggcca 600
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcctat gccctcattt 660
 tccgtgctgt ctgccgtctg ccaccccatg ttgcctgcca caaggctctg ggtaactgcg 720

ggacctatgc	tagcatcatt	ggtctcttct	acacacctgc	cctcttctcc	ttccttgctc	780
actgttttgg	gtgtcacaca	gtgcccacc	atattcacat	cctactggct	aacctctacg	840
cagtgggtgt	cccagcttcc	aatcctgtgg	tctatggagt	gcagactcag	cagagctcag	900
aggctcagga	acttgcttca	acttttctgg	gcaggagcag	tgaa		944

<210> 877

<211> 939

<212> DNA

<213> Unknown (H38g727 nucleotide)

<220>

<223> Synthetic construct

<400> 877

atgaattggg	aaaatgagag	ctccccaaaa	gagtttatac	tacttggctt	ctcagatagg	60
gcttggctac	aaatgcccct	ttttgtggtc	ctgttaatat	catacacaaat	caccatattt	120
ggcaatgtgt	ccatcatgat	ggtgtgcatt	ctggatccca	aacttcatac	tcccatgtat	180
ttctttctca	ctaattctct	catcttagat	ctctgtctata	ccacaactac	agtcacctcat	240
atgttggttaa	atattgggtg	caacaaaaag	accatcagct	atgctggctg	tgtggccac	300
ctcatcatct	tcctggccct	agggtgtaca	gagtgctctc	ttctggctgt	tatgtccttt	360
gacagatatg	tggctgtttg	cagaccctc	cactatgtag	tcatcatgaa	ttattgggtc	420
tgccctaagga	tggcagccct	ctcatggctc	attggtttcg	gcaactcagt	gctgcagtct	480
tccttgactc	ttaacatgcc	acgctgtggt	caccaggaag	tggaccactt	tttctgtgag	540
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ttcttttagtg	tactaattct	tctaattcca	gtgacattga	tcctcatctc	ctatggcttc	660
atagctcaag	cagtattaaa	aatcagggtca	gcagaaggac	ggcaaaaagc	atttgggaca	720
tgtgggtccc	acatgattgt	ggtgtccctc	ttttatggaa	cagccattta	tatgtatctt	780
caaccacctt	catccacctc	taaggactgg	ggaaagatgg	tttccctctt	ctatggaatc	840
atcacatcca	tgttgaactc	cctcatctac	agccttagaa	ataaagatat	gaaggaggcc	900
ttcaagaggc	tgatgccaag	aatctttttc	tgtaagaaa			939

<210> 878

<211> 968

<212> DNA

<213> Unknown (H38g728 nucleotide)

<220>

<223> Synthetic construct

<400> 878

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ctggagtggg	tctgcatctg	gatgggaatt	ctctccctta	ccagttacct	tgtctccctt	120
gcagggaatg	tcactcttct	ctaccttata	actgtggaac	acaacctcca	taaaccatg	180
ttttcccttc	tctctatacc	ggcctctgca	aacctcatat	tatgcattac	atatttcccc	240
aaaacatttg	ggatattcta	gctgaaagct	cagaaaaata	tatttctctg	atgcttcacc	300
aggttttttt	tttttgggtc	acttcacttt	agcttttttt	ctggacttgg	ccatcttggt	360
gggtctggca	tttgatcatt	acatgacctt	tggtttcctt	ctgagataca	ccagtggctt	420
gacacctcaa	cacttggaac	gattgtgggt	agcattgatt	gaaggtttaa	taacattttg	480
cccattgatt	tcctggggaa	gcatttgccc	ttctgcagaa	cacacattaa	ttctaacaca	540
tactgtgagc	acataggtgt	ggccctgctt	tcctatgctg	atatctccat	caatatctgg	600
tatgacttta	ctatattggt	aatgactatt	atctcagatc	tgatcctcac	tgatatttcc	660
tacaccttca	cccttcatgc	tgttttccac	cttccatcca	gtgatgccct	tctgaaggcc	720
ctaagcacct	gtggttctca	tgtcagtgtc	attctcatgt	tgtacacacc	aacctatgct	780
tctgccctta	ctcacactt	tggccagagt	atctcttgca	ctttttacat	tatgtttgtg	840
ggcctctata	gggcaatccc	tcctgtactc	aattccataa	ttatggagta	aaaacaaagc	900
agattggaaa	caaggctcata	cttttattct	ttcttaaagg	gatgcagtga	tatgaggatg	960
agaatatg						968

<210> 879

<211> 1011

<212> DNA

<213> Unknown (H38g729 nucleotide)

<220>

<223> Synthetic construct

<400> 879

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catctggaag	tagttctctt	tgtggttatc	ttgatcttct	acttgataac	actgatagga	120
aacctgttca	tcatcatcct	gtcatacctg	gactcccac	tccacactcc	catgtacttc	180
ttcctttcaa	atctctcatt	tctggatctc	tgctacacca	ccagctctat	ccctcagttg	240
ctggtgaatc	tctggggccc	ggaaaagacc	atctcttatg	ctggttgtag	agttcaactt	300
tactttgttc	tgcactggg	aaccgcagag	tgtgtcctac	tgggtggtgat	gtcctatgat	360
cgttatgcag	ctgtgtgtag	acctttgcat	tacactgtcc	tcatgcaccc	tcgtttctgc	420
cgcttggttg	ctgcggcttc	ttgggtaagt	ggttttacaa	cctcagcact	tcattcctcc	480
tttactttct	ggataccctt	atgtagacat	cgcctagtgg	atcacttctt	ctgtgaagct	540
ccagcacttc	tgcgattatc	atgtgttgat	acctaggcaa	atgagctgac	cctcatggtc	600
atgagctcca	tttttgttct	catacctctc	atcctcatcc	tcacttecta	tggtgccatt	660
gccccggctg	tactgagcat	gcaatcaacc	actgggcttc	agaaagtgtc	taggacatgt	720
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ccaccatcag	aaaattctca	agatcaaggc	aagttcattg	ccctctttta	cactgttgct	840
acacctagtc	ttaaccctct	aatctacact	ttcagaaaca	aggatgtaag	aggggcagtg	900
aagagactaa	tgggggtgga	atgggggatg	tgacagggaa	atcatgttgg	ctgttgtttt	960
tcctagggtc	ttatccattt	tgaagggttg	tttccttgct	tctttgtgat	t	1011

<210> 880

<211> 956

<212> DNA

<213> Unknown (H38g730 nucleotide)

<220>

<223> Synthetic construct

<400> 880

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ggacttgagc	agtaccacgt	ctggatcagc	atcccattct	gcttaatacta	tctcatggct	120
gtcgtggcca	agagtatcct	tctctacctc	attgtggtag	agcacagtct	tcatgcaccc	180
atgttctttt	tcctttccat	gctggccatt	actgatctca	tattgtccac	cacatgtgtc	240
cccaaaacac	ttagcatctt	ctggtttggt	cccaaaacag	tttcctctggc	tgtctcacc	300
aattattctt	tctgcactat	agctttgtgt	tggactcagc	tatactgctg	gccatggcat	360
ttgaccgcta	tatggccatt	tgctcacctc	tgagatacac	tactattctg	actcccaaaa	420
ccattgtcaa	aattgtctgt	ggaatatggt	tccgaagttt	ctgtgttttt	gtcccgtgtg	480
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ttgcccacgc	ctttgggcac	aatgtccctc	atacctttca	tattatgttt	gccaaccttt	840
atgtaatcat	tccacctgct	ctcaacccta	ttgtctacag	aataaagacc	aagcaaattcc	900
agaacagaat	ccttttgctc	tttcccaagg	ggtcccagtg	ataggtgcct	gagctc	956

<210> 881

<211> 933

<212> DNA

<213> Unknown (H38g731 nucleotide)

<220>

<223> Synthetic construct

<400> 881

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tctaattggc	ctcatctgga	agtagttatc	tttgtgggtg	tcttgatctt	ctacttgatg	120

acactgatag	gaaacctggt	catcatcatc	ctgtcatacc	tggactccca	tctgcacaca	180
ccaatgtact	tcttcctttc	aaacctctca	ttctctggatc	tctgtctacac	caccagctct	240
atccctcagt	tgctgggtcaa	tctctggggc	ccggaaaaga	ccatctctta	tgctgggtgc	300
atgattcaac	tttactttgt	tctcgcactg	ggaaccacag	agtgtgtcct	actggtgggtg	360
atgtcctatg	accgtttatg	agctgtgtgt	agacctttgc	attacactgt	cctcatgcac	420
cctcgttttt	gccacctget	ggctgtgggt	tcttgggttaa	gtgggttttac	caactcagca	480
cttcatcctt	ccttcacctt	ctgggtacct	ctgtgtggac	accgccaagt	agatcacttt	540
ttctgtgaag	ttccagcact	tctgcgatta	tctgtgtgtg	ataccatgt	caatgagctg	600
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tatgggtgcca	tcgtccgagc	tgtactgagg	atgcagtcaa	ccactggggt	tcagaaagtg	720
tttggaaacat	gtggagctca	tcttatgggt	gtatctctct	ttttcattcc	ggccatgtgc	780
atatactccc	agccaccatc	aggaaattct	caagatcaag	gcaagttcat	tgccctcttt	840
tatactgttg	tcacacctag	tcttaaccct	ctaacttaca	ccctcagaaa	caaagttgta	900
agagggggcag	tgaagagact	aatgggggtg	gaa			933

<210> 882

<211> 264

<212> DNA

<213> Unknown (H38g732 nucleotide)

<220>

<223> Synthetic construct

<400> 882

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tatgtggcca	tatgccaccc	actgtgccat	gctgaagtgc	tcaacagtac	agtaacagcc	120
catattggca	tcgtagctgg	ggtacgggga	tccctctttt	tttccccact	ggctctgctg	180
ataaagacgc	tgggcttatg	ccactcctat	gtgctctcgc	actcctattc	gctccaccag	240
gatgtagcga	acttgtccta	tgcg				264

<210> 883

<211> 477

<212> DNA

<213> Unknown (H38g733 nucleotide)

<220>

<223> Synthetic construct

<400> 883

gttgccatct	gtaacccttt	gcgtacactt	acagtcata	acccccagct	atgccttttg	60
ttggttcttg	cctgctgggt	tgggggtttt	atccactcta	tcatgcaggt	catactagtc	120
atccagctgc	ctttctgtgg	gccaatgaa	ctggacaact	tctactgtga	tgctctacaa	180
atcatcaagc	tgccctgcat	ggacacctat	gtggtagagg	tgctgggtgat	agccaacagt	240
ggtctgctgt	ctcttgtctg	cttcttggtc	ttactattct	cttatgctat	catectgac	300
accctgagaa	cacgcttctg	ccagggccag	aacaagggtc	tctctacctg	tgcttctcac	360
ctgacagtgg	tcagcctgat	cttcgtgcca	tgcgtattca	tctatttgag	gcctttctgc	420
agcttctctg	tggataagat	attctccttg	ttttacacag	tgattacacc	tatgttg	477

<210> 884

<211> 948

<212> DNA

<213> Unknown (H38g734 nucleotide)

<220>

<223> Synthetic construct

<400> 884

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gtgtcaggaa	atgggtctct	tgtctgtgtg	gtggcagtg	agcacagtct	tcatgaacct	180
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cccaaagcct	tgagcatttt	ctggtttgat	gatgtggaca	tctcctttgg	tggtgtgtgc	300
actcagctct	tttttatgca	ttttgccttt	gtagcggagt	caggcattct	cttgaccatg	360
gctttcgacc	gctatgtggc	catctgctac	ccattgaggt	atagcaccat	acttagccac	420
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ctctatgttc	ttgttccccc	catgatgaac	ccaattatct	atggagtaaa	gactaaacag	900
attcagaaaag	gggttgccct	tgtgttttct	ccaaaaggaa	aatgttgc		948

<210> 885

<211> 1087

<212> DNA

<213> Unknown (H38g735 nucleotide)

<220>

<223> Synthetic construct

<400> 885

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ccttggctag	agcttctct	gttccactag	cttcttataa	tgtaccctat	agccgtgatg	120
ggaaacatca	caatcattct	catgtccagg	ttagactctc	gtcttcatag	ccccatgtac	180
tttttcccca	ccaacctctc	ctttttggac	atgtgttata	ccacaagcat	tgtccctcag	240
atgctgttta	acctgggaag	ctctaagaag	accatcagct	atatgggggtg	tgccggttcag	300
ctttattttct	ttcacataat	gggggggaaca	gaatgtttgc	ttttggctat	tatgtccttt	360
gacgcctatg	tggccatctg	cagacctctt	cactacaccc	tcacatgaa	tcagcgcgtc	420
tgtatccctta	gtttccaccg	tgtggctaata	tgggaataatc	tatgctgtct	cagaggccac	480
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cctgttctga	taaagattgc	ctgtggtgaa	aagggttcta	acgagctcac	actctctgtg	600
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ggaagtgtctg	tatttaagat	caaactcttc	aagggaagga	aaaaggcctt	tgggacatgc	720
tcctcccatc	ttattgtagt	tttcttattt	tatggcccag	ccatcagcat	gtaccttcag	780
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attgaacagt	tagagtaggt	tgtatgggtt	ttatctaaca	aattcttgtc	tcataatcaa	1020
atatcgcttt	acatgttctt	gcaaaatatg	ttatgtctcc	gagactcttt	gtaaacaatgt	1080
tcagcaa						1087

<210> 886

<211> 498

<212> DNA

<213> Unknown (H38g736 nucleotide)

<220>

<223> Synthetic construct

<400> 886

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tatgtggcca	tctgccaccc	actgcgccat	gctgcagtg	tcaacaatac	agtaacagcc	120
cagattggca	tctgtggtgt	ggctccggga	tccctctttt	ttttcccaact	gcctctgctg	180
atcaagcggc	tggccttctg	ccactccaat	gtgctctcgc	actcctattg	tgtccaccag	240
gatgtactga	agttggccta	tgcagacact	ttgcccaatg	tggtatatgg	tcttactgcc	300
attctgctgg	ccatgggcgt	ggacgcaatg	ttcatctect	tgtcctattt	tctgataata	360
cgaacggttc	tgcaactgcc	ttccaagtca	tagcggggcca	aggcctttgg	aacctgtgta	420
gtacacattg	gtgtgggtact	cggcttgtat	gtgccactta	ttggcacttc	aagtgggtcac	480
cggtttggga	acaaactt					498

<210> 887
 <211> 936
 <212> DNA
 <213> Unknown (H38g737 nucleotide)

<220>
 <223> Synthetic construct

<400> 887
 atgatgatta aaaaaaatgc aagttcggaa gacttcttta ttctacttgg attttctaata 60
 tggcctcage tgggaagtagt tctctttgtg gttatcttga tcttctacct gatgacactg 120
 acaggaaacc tgttcatcat catcctgtca tacgtggact cccatctcca cacaccaatg 180
 tacttcttcc tttaaaccct ctcatctctg gatctctgcc acaccaccag ctctatccct 240
 cagttgctgg tgaatctccg gggcccgaa aagaccatct cgtatgctgg ttgcatgggt 300
 caactttact ttgttcttgc actgggaatc gcagagtgtg tctactgggt ggtgatgtcg 360
 tatgatcgtt atgtagctgt gtgtagacct ttgcattaca ctgtcctcat gcaccctcgt 420
 ttctgccact tgttggctgc ggcttcttgg gtaattgggt ttactatctc agcacttcat 480
 tctctcttta ctttctgggt accccttctg ggacatcgcc tagtggatca cttcttctgt 540
 gaagtccag cacttctgcg tttatcatgt gttgacaccc atgcaaata gctgaccctc 600
 atggtcatga gctccatttt tgttctcata cctctcatte tgattctcac tgcctatgggt 660
 gccattgccc gggctgtact gagcatgcaa tcaaccactg ggcttcagaa agtggttagg 720
 acatgtggag cccatcttat ggttgtatct ctctttttca ttccagtcac gtgcatgtat 780
 ctccagccac catcagaaaa ttctcctgat cagggcaagt tcattgccct cttttatact 840
 gttgtcacac cgagtcttaa tctctaatc tacactctca gaaacaagca tgtaaaaggg 900
 gcagcgaaga gactattggg gtgggagtgg gggaag 936

<210> 888
 <211> 453
 <212> DNA
 <213> Unknown (H38g738 nucleotide)

<220>
 <223> Synthetic construct

<400> 888
 cggcgcgtgt gcgcgccccg cctgctggac cacttcatct gtgagctgcc ggcgttgctc 60
 aagctggcct gcggaggcga cggagacact accgagaacc agatgttcgc cgcccgctg 120
 gtcacctctc tgcggggggt tgccgtcatc ctggcctcct acggtgccgt ggcccgagct 180
 gtctgttgca tgcggttcaa cggaggccgg aggagggcgg tgggcacgtg tgggtcccac 240
 ctgacagccg tctgcctggt ctacggctcg gccatctaca cctacctgca gcccgcgag 300
 cgctacaacc aggcacgggg caagttcgtg tcgctcttct acaccgtggt cacactgct 360
 cttaaccgct tcatctacac cctcaggaat aagaaaatga aaggggcacc gaggaggctg 420
 ctgcggagtc ttgggagagg ccaggctggg cag 453

<210> 889
 <211> 1014
 <212> DNA
 <213> Unknown (H38g739 nucleotide)

<220>
 <223> Synthetic construct

<400> 889
 aaagtcaatg ctagctctga ggggtacttt atttttagttg gattttctaa ttggccttat 60
 ctggaagtag ttctctttgt gggtattttg atcttctgct tgatgacact gataggaaac 120
 ctgttcatca tcatcctgac gtacctggac tcccatctcc atactccctt gtatttcttc 180
 ctttcaaate tctcatttct ggatctctgc tacaccacca gctctatccc tcagttgctg 240
 gtcagtctct ggggtgtgga aaagaccatt tcttatgctg gttgcatgggt tcaactttac 300
 ttttttctca cactgggaac cacagagtgt gtccactctg tgggtgatgtc ctatgaccgt 360
 tatgcagctg tgtgtagacc tttgcattac actgtcctca tgcactctcg tttctgccac 420
 ttgttggtct tggcttcttg ggtaagtggg tttaaaaacc cagcacttca ttctctcttc 480

accttctggg	tacctctgtg	tggacaccgc	caaataagatc	actttttctg	tgaagttccg	540
gcacttttat	gattatcatt	tgtcaatacc	cgtgaaaata	aactgaccct	catgatcaca	600
agctccattt	ttgttctgct	acttctcacc	ctcattttca	cttcctatgg	tgctattgcc	660
caggctgtac	tgaggatgca	gtcaaccact	gggcttcaga	aagtatttgg	aacatgtgga	720
gctcatcata	tggttgtatc	tctcttttcc	attccggcca	tgtgcatgta	tctccagcca	780
ccatcaggga	attctcaaga	tcaaggcaag	ttcattgctc	tctttttatac	tggtgttaca	840
cctagtctta	accctctaata	ctacaccctc	agaaacaaag	atgtaagagg	ggtagtgaag	900
agactaaggg	gggtgggagt	agcctgtgtt	tgtgtgatata	taacaatata	atggagtctt	960
tcctcacaat	gattcatcca	tctgttcatt	tatcaaccat	tctttttattc	actc	1014

<210> 890

<211> 656

<212> DNA

<213> Unknown (H38g740 nucleotide)

<220>

<223> Synthetic construct

<400> 890

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagacagaca	tactcctgag	tgtgatggcc	tatgaccagt	ttgtagccaa	180
atgtcaccct	ctatatcatt	cagccatcat	gaacccgtgt	tctgtggctt	tctacttttg	240
ttgtcttttt	tttttccctc	agtcttttag	atgccagct	gtacaatttg	attgccttac	300
aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctt	ctgtgaccct	tctcaactcc	360
cccattctgc	atgttgtgac	accttcaaca	ataacataat	cctgtatttc	cctgatgccca	420
tatttggttt	tcttcccatc	tcggggacac	ttttctctta	cgataaaaatt	gtttcctcca	480
ttctgagggt	ttcatcgta	gggtgggagg	ataaagccct	ctccacctgt	gggtctcagc	540
tgctcagttg	ttgctgagtt	tatggaacag	gcgttgagg	gtacctcagt	tgggatgtgt	600
cattttcccc	cagaaagggt	gcagtggcct	cagtgatgta	cgcggttgtc	accccc	656

<210> 891

<211> 971

<212> DNA

<213> Unknown (H38g741 nucleotide)

<220>

<223> Synthetic construct

<400> 891

atgattataa	tttgcaatga	cagccacagt	gatttcatcc	ttctgggctt	ctctaacaag	60
ccacatttgg	agaagatact	ttttggatca	tttttatttt	ttattttttg	actcttgcag	120
gaaatatggt	catagttctt	gtgtccttga	aggatccaaa	actccacatc	cctatgtatt	180
tctttctttc	caacctttcc	ttggtagacc	tctgtttgac	cagcagctgt	gttccacaga	240
tggtgattaa	cttctggggc	ccagaaaaga	ccatcagcta	cattggctgt	gccattcaac	300
tctatgtttt	tttgtggctt	ggggccacgg	aatatgtcct	tcttgttgte	atggctgtgg	360
attgttatgt	agcagtgtgt	catccactgc	aaaataccat	gatcatgcac	ccaaaacttt	420
gtctgcagct	ggctatcttg	gcatggggga	ctggcttggc	ccagtctctg	atccagtcct	480
ctgccaccct	ccggttaccc	ttctgtctcc	agcggatggg	ggatgatgtt	gtttgtgaag	540
tcccagctct	gattcagctc	tccagtactg	atactacctc	cagtgaat	cagatgtcta	600
tgcagctgt	tgtctctctg	gtgatgccct	tgatcattat	cctttctctc	tctgggtgta	660
ttgctaaggc	tgtgctgaga	attaagtcaa	ctgcaggaca	gaagaaagca	tttggcacct	720
gcactctctc	ccttcttctg	gtttctctct	tttatggcac	tgtcacaggt	gtctaccttc	780
aacaaaaaaa	tactatctct	catgaatggg	gcaaatttct	cactcttttc	tacactgtag	840
taacccccac	tcttaatccc	ctcatctaca	ctctaaggaa	caaggaggta	aaggagacac	900
taataagatt	ggggaggagg	acctgggatt	cccagaataa	ctaacaaggt	taacatatgt	960
ttacctttgc	t					971

<210> 892

<211> 651

<212> DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

ttgcctgaca ttggtttcac cttggccacg gtcaccaaga tgatggagac atgcaatcac	60
atagcagagt catctcccat gcaggctgtc tgacacagat acctttcttt gtcctttttg	120
tatgtataga tgacatgctc ctgactgtga tggcctataa ctgattttgtg gccatctgtc	180
acccctgca ctaccagtc atcatgaatc ctcacctctg tgtcttctta gttttgggtg	240
cctttttcct tagcctgttg gattccacg tgcacagctg gattgtgtta cacaactcac	300
cttcttcaag aatgtggaaa tctataattt tttttctgtg acctatctca acttctcaac	360
cttgctgtt ctgacagcat catcaataac atattatgta ttttagatat ccctataattt	420
ggtttttctt ccatttcagg gatccttttg tcttactata aaattgtctc ctccattcca	480
agaattccat cgtcagatgg gaagtataaa gccttctcca cctgtggctc tcacctggca	540
gttgtttgct tattttatgg aacagggctt gtagggtagc tcagttcagc tgtgttacca	600
tccccagga agagtatggg ggcttcagtg atgtacactg tggtcacccc c	651

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

ttctctcttt aggccaaactt acagcgcaga ggagcgcttt ctctgctgg gtttctccga	60
ctggccttcc ctgcagccgg tctctctcgc ccttgctctc ctgtgctacc tctgacctt	120
gacgggcaat tcgggcgctg gtgctgcttg gcngngnngg acctacgcct gcanacncac	180
gatgtatgna ctacttctc tgccacctgg ccttggtaga cgcgggcttc actactagcg	240
tggtgccgcc gctgtggcc aacctgcgcg gaccagcgt gctntgncgc gcagccactg	300
cacggcccga gctgtgcgca tcgctggctc tgggttcggc cgaatgcgtc ctctggcggt	360
gatggctctg gan	373

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

atattagaaa tttcgttcac aaccgtcagt atacccaagt ttctgggtaa cattatttca	60
ggagataaaa ccatttcctt taataattgc atagttcagt tatttttctt cattctcttg	120
ggagtcacag agttttacct tctggctgcc atgtcctatg accgctatgt ggccatctgc	180
aagcctctgc attacttgag tatcatgaat cgaagagtct gcacactgct tgtttttact	240
tcttggtctg tttcattctt aatcatattc ccagcactca tgttgctttt aaagcttgat	300
tactgtagg taaatattat tgaccatttt acctgtgatt attttccact gctgcaactt	360
gctgttccag acacaaaatt cttagaggtg atgggatttt cttgtgctgc gtttactcta	420
atgttctact tggcattaat atttctgtcc tacatatata ttatcagaac aattttgaga	480
attccttcta ctagtcagag gacaaaggcc ttttccacat gttcttccca catgggtgtt	540
atctccatct cttatggcag ctgcattttt atgtacatta aaccctcagc aaaagataga	600
gtgtccttga gcaagggagt ggcaatacta aacacctcag tagccccc	648

<210> 895

<211> 659
 <212> DNA
 <213> Unknown (H38g745 nucleotide)

<220>
 <223> Synthetic construct

<400> 895
 tttcttgaca tcggtttcac ctccaccaca gtccccaaga tgattgtgga catccagtct 60
 cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccattttt 120
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatgaccggt ttgtagccat 180
 ctgtcaccct ctatatcgct cagccatctt gaacccggtt ttctgtggct tcctagattt 240
 gttgtctttt ttttttttcc ctccagtctt tagactccca gctgcacaac ttgattgcct 300
 tacaaatgac ctgcttcaag gatgtggaaa ttcctaattt cttctgtgac ctttctcaac 360
 tcccccatct tgcattgtgt gacaccttca ccaataacat aatcatgtat ttccctgctg 420
 ccatatttgg ttttcttcag atctcgggga cccttttctc ttactataaa attgtttcct 480
 ccattctgag ggtttcatca tcagggtggga actataaagc cttctccacc tgtgggtctc 540
 acctgtcagt tgtttgctga ttttatggaa caggcggttg agggtagctc agttcagatg 600
 tgtcatcttc cctgagaaag gctgcagtgg cctcagtgat gtacatggtg gtcacaccc 659

<210> 896
 <211> 804
 <212> DNA
 <213> Unknown (H38g746 nucleotide)

<220>
 <223> Synthetic construct

<400> 896
 atgatggcac tcatcttcac agactcccat ctccaaagcc caatgtattt cttcctcaat 60
 gtccctctcg tttcttgatat ttgttactct tctgtgggtca cacctaagct cttgggtcaac 120
 ttccctggct ctgacaagtc catctctttt gagggtctgt tgggtccagct cgccttcttt 180
 gtagtgcatg tgacagctga gagcttcctg ctggcctcca tggcctatga ccgcttctta 240
 gccatctgtc aacccctcca ttatggttct atcatgacca gggggacctg tctccagctg 300
 gtactgtgt cctatgcatt tgggtggagcc aactccgcta tccagactgg aaatgtcttt 360
 gccctgcctt tctgtgggccc caaccagcta acacactact actgtgacat accacccctt 420
 ctccacatgg cttgtgcccac cacagccaca gcaagagtgg tccctctatgt cttttctgct 480
 ctggtcaccc ttctgcctgc tgcagtcatt ctccacctct actgcttggg cttgggtggcc 540
 attgggagga tgcgctcagt agcagggagg gagaaggacc tctccacttg tgcctcccac 600
 tttctggcca ttgccatttt ctatggcacc gtgggttttca cctatgttca gccccatgga 660
 tctactaaca ataccaatgg ccaagtagtg tccgtcttct acaccatcat aattcccatg 720
 ctcaatccct tcatctatag cctccgcaac aaggaggtga agggcgctct gcagaggaag 780
 cttcagggtca acatctttcc cggc 804

<210> 897
 <211> 949
 <212> DNA
 <213> Unknown (H38g747 nucleotide)

<220>
 <223> Synthetic construct

<400> 897
 atggacttgg gaaatcaaac aagagtttca gaattttttac tcttgggatt ttcccaagac 60
 ctagaggatc aacagttgct ctttgcactg tttctgtcca tgtacctggt caccgttctg 120
 gggaacctgc tcatcatcct ggccatcagc tctgactccc acctccacac ccccaggtag 180
 ttcttctctt ccaatctgtc cctggctgac atcggtttca cctccaccgc agtccccaaag 240
 atgctggtga acatccaggt gcagagcaat gccatcagct atgcagactg catcgcccag 300
 atgtatgttt ttcatgtttt ttggaggcat ggacacattt ctccctaccg tgatggccta 360
 tgaccggtat gtggccatct gtcacccctt gtactactgt gtcaccagga accctgcct 420
 ctgtggcctg ctgggttctt tgtcctgggt cctcagcttg tcatactccc tgatccagag 480

tctgttgggtg	ctgcgggtgt	ccttctgcac	cagttgagtc	attcagcact	tttactgtga	540
gcttgctcag	gtcctcaggc	ttacctgctc	agacacacat	gtcaattaca	tcctgctcta	600
cgtgggtggcc	ggccttcttg	actttgtgcc	cttctcaggg	atccttttct	cctacaccra	660
aattgtctcc	tacatcctga	gaatctcatc	cacagatggg	aaacacaaag	ccttttctac	720
ctgtggatct	catctgtttg	tggtttcttt	attctatggg	acaggccttg	gtgtgtatct	780
tagttccaat	gcacgtcct	cttcctgggtg	gggcatgggtg	gcctcgggtca	tgtacactgt	840
ggtcaccccc	atgctgaacc	ccttcactcta	ttgcttgctg	aacaggggaca	tcaagaggaa	900
cctagaaaca	ctgcttggga	gaatgctgta	tgctcaatga	cggggacat		949

<210> 898

<211> 927

<212> DNA

<213> Unknown (H38g748 nucleotide)

<220>

<223> Synthetic construct

<400> 898

atggagaatt	gtacggaagt	gacaaagttc	attcttctag	gactaaccag	tgtcccagaa	60
ctacagatcc	ccctctttat	cttgttcacc	ttcatctacc	tcctcactct	gtgtgggaac	120
ctggggatga	tgttgctgat	cctgatggac	tcttgtctcc	acacccccat	gtactttttc	180
ctcagtaacc	tgtctctggg	ggactttgga	tactcctcag	ctgtcactcc	caagggtcatg	240
gctgggttcc	ttagaggaga	caagggtcatc	tcctacaatg	catgtgctgt	tcagatgttc	300
ttctttgtag	ccttggccac	gggtgaaaat	tacttgttgg	cctcaatggc	ctatgaccgc	360
tatgcagcag	tgtgcaaacc	cctacactac	accaccacca	tgacggccag	tgtagggtgcc	420
tgtctggccc	taggtccta	tgtctgtggc	ttcctaaatg	cctcattcca	cattgggggc	480
atattcagtc	tctctttctg	taaatccaat	ctggtacatc	actttttctg	tgatgttcca	540
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tctcatttca	ctgcagtctc	cgtcttctat	gggacagtaa	tcttcactta	cttgagcccc	780
agctccagcc	actccatgga	cacagacaaa	atggcatctg	tgttctatgc	tatgatcatc	840
cccattgctga	accctgtggg	ctacagcctg	aggaacagag	aagtccagaa	tgcattcaag	900
aaagtgttga	gaaggcaaaa	atttcta				927

<210> 899

<211> 938

<212> DNA

<213> Unknown (H38g749 nucleotide)

<220>

<223> Synthetic construct

<400> 899

atgcacacca	tgggtggagaa	ccacacccaa	gtcacctggg	tccgcctgct	gggacttaca	60
gagcaggagg	agctcagagg	catcctcttt	gtgctcttcc	tgctcatgca	ttcagtcact	120
gttatgggca	acctgggaat	gatcactctg	atccatgcag	acccacagct	ccacaccccc	180
atgtatttct	tcctgagcgt	cctatccttc	atagactcct	cgttttccac	agtggacacc	240
cccaggctgc	tggagagctt	cctcatctca	agccaatcca	tctcctttgc	aggctgtatg	300
gtccagatgg	ccctcatgat	cctccatggg	actgctgagt	gtctgctcct	ggccatcatg	360
gcctatgacc	gattcaccgc	catctgccac	cctctcctct	atcacactat	tatatcccaa	420
tgtctgtgtg	ccctgctggg	ggtagcctgc	tatactgttt	ctgttgccaa	ttcagctttg	480
ctgactgggt	gcacttttaa	gctgccctac	tgtggcccca	atgtcattaa	ccactatttc	540
tgtgacatcc	cccctgtgct	ccaacttgcc	gggtgcagata	ctacgagggt	gagaccatta	600
tcttctcatt	gtgtgccttg	ctcatcctct	ttaccatcac	cattatccca	gtctcctatg	660
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ctgtgggtcat	ccgcaggctg	aaccctctga	tctacagcct	gaggaataaa	gatgtaaaat	900
atgcttttga	gaggagatgc	ctgtgcaagc	tgtcttca			938

<210> 900
 <211> 942
 <212> DNA
 <213> Unknown (H38g750 nucleotide)

<220>
 <223> Synthetic construct

<400> 900
 atggaata agacagaagt aacacaattc attcttctag gactaaccaa tgactcagaa 60
 ctgcagggtc ccctctttat aacgttcccc ttcattctata ttatcactct ggttggaac 120
 ctgggaatta ttgtattgat attctgggat tcctgtctcc acaatcccat gtactttttt 180
 ctgagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgtcatg 240
 gctggattcc ttatagaaga caaggtcac tcttacaatg catgtgctgc tcaaagtgtat 300
 atctttgtag cttttgccac tgtggaaaat tacctcttgg cctcaatggc ctatgaccgc 360
 tatgcagcag tgtgcaaacc cctacattac accacaacca tgacaacaac tgtgtgtgct 420
 cgtctggcca taggtctcta cctctgtggt ttcctgaatg cctccatcca cactggggac 480
 acatttagtc tctctttctg taagtccaat gaagtccatc actttttctg tgatattcca 540
 gcagtcattg ttctctcttg ctctgataga catattagcg agcttgttct tatttatgtt 600
 gtgagcttca atatctttat agctctcctg gttatcttga tctctacac attcattttt 660
 atcaccatcc taaagatgca ctgagcttca gtataccaga agcctttgtc cactgtgccc 720
 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcattga cttacaaccc 780
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatggctatc 840
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900
 aaagttgttg agaaggcaaa attgtctgta ggatggtcag tt 942

<210> 901
 <211> 936
 <212> DNA
 <213> Unknown (H38g751 nucleotide)

<220>
 <223> Synthetic construct

<400> 901
 atgaacaact ctgacactcg catagcaggc tgccttctca ctggcatccc tgggctggag 60
 caactacata tctggctgtc catcccttc tgcattcatgt acatcgtgc cctggaaggc 120
 aatggcatcc taatttgtgt catcctctcc caggcaatcc tgcattgagcc catgtacata 180
 ttcttatcta tgcctggccag tgcctgatgc ttgctctcta ccaccaccat gcctaaggcc 240
 ctggccaatt tgtggctagg ttatagccac atttcccttg atggctgcct cactcaaaag 300
 ttcttcattc acttctctt cattcactct gctgtcctgc tggccatggc ctttgaccgc 360
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 aagatcgcca ctgccaccct gagccgcagc ttcattcata tgtttccatc catctttctc 480
 cttgagcacc tgcactattg ccagatcaac atcattgcac acacattttg tgagcacatg 540
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 gctcttctct ccacaggcct ggacatcatg cttattactg tttcctacat ccacatcctc 660
 caagcagtct tccgcctcct ttctcaagat gcccgctcca aggccctgag tacctgtgga 720
 tcccatatct gtgtcatcct actcttctat gtccttgccc ttttttctgt ctttgccctac 780
 aggtttggtg ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840
 gtcattctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902
 <211> 994
 <212> DNA
 <213> Unknown (H38g752 nucleotide)

<220>
 <223> Synthetic construct

<400> 902

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agcattcttt tcctttatctt ctcattgctg caggcatcct ctgattttct aataacattg      60
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ctacaagtcc cctcctctat catgttccact ctcataatcc ttgtcaatgt ggttggaaac      180
ctggggatga ttgttttaat tgtttgggac attcatctcc acactcccat gtattttttc      240
ctcagtcacc tgtctctagt ggacttttgt tactcttcag ctgtcactcc cacagtcata      300
gctgggctcg ttataggaga caaggtcac tcttacaatg catgtgctgc tcaaattgtc      360
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tatgatgcag tgtgcaaacc cctacattac accaccacca tgacaacaag tgtgtgtgca      480
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cagtttcaat atctttctgt ccctcctagt tatcttgatc tctacctat tcatatttat      720
caccatccta aagatgcact cagcttcagg ataccagaag gctttgtcca cctgtgtctc      780
ccacctcact gcagtcacat tcttctatgg gactattatc ttcatgtact tacagcccag      840
ctctggtcac tccatggaca cagacaaact ggcactctgt ttctatacta tgatcatccc      900
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<210> 903

<211> 954

<212> DNA

<213> Unknown (H38g753 nucleotide)

<220>

<223> Synthetic construct

<400> 903

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gcactgggtg gaaatgctgc cctcatcctg gtcattgcca tggacaatgc tcttcatgca      180
cctatgtacc tcttctctct ccttctctca ctcacagacc tggctctcag ttctaccact      240
gtgcccaga tgctggccat tttgtggctc catgctgggt agatttcctt tgggtggatgc      300
ctggcccaga tgttttgtgt ccattctatc tatgctctgg agtcctcgat tctacttgcc      360
atggcctttg ataggtatgt ggctatctgt aaccatttaa ggtacacaac cattctcaac      420
catgctgtca taggcagaat tggctttgtt gggctattcc gtagtgtggc tattgtctcc      480
cccttcatct tcttgctgag gcgactcccc tactgtgggt accgtgtcat gacacacaca      540
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gctaattctc atgtgctggg gcctcctgta ctcaatccta ttctctatgg agctgaacc      900
aaggagattc ggagtcgact tctaaaactg cttcacctgg ggaagacttc aata                                     954

```

<210> 904

<211> 989

<212> DNA

<213> Unknown (H38g754 nucleotide)

<220>

<223> Synthetic construct

<400> 904

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cacatagaac cagggaaatga tacacagatt tcagaatttc ttcttctggg acttttcagat      60
aaaccagaat tgcagccctt cctctttggg ctgttcttct ccatgtacct ggctactgtg      120
cttgggaatc tgetcatcat cctggccaca atctcagact cccacctcca caccctatgt      180
acttcttctc ctccaacctg tcttttgcgg acatctgttt catctctact acaatcccaa      240
agatgctcgt aaacatccag acacagagca gagtcacac ttatgcaggc tgcacacccc      300
agatgtgctt ttttgtactc ttagaagcac tggacagctt actcctgacc gtgatggcct      360
atgaccagtt tgtggccatc tgtcaccccc tgcactacat ggtcatcatg agccctgggt      420
tctgtggact gctggttctg gcacccctgga tcatcatgag cccctggctc tgtggactgc      480

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tggttctggc	atcctggatt	atcagtgatc	tggattcctc	attacatagc	ttgatgggtgc	540
tgtcactgcc	cttctgcaca	gatttccaaa	ttccacattt	tgtctatgaa	cttaatcagg	600
tcattcgcc	tgccggttct	gataccttcc	ttaatgacat	ggcgatgat	tttgacagtag	660
ggccactggg	tggagttccc	ctcgtctggg	tcctgtactt	gtactgtaag	atagttttct	720
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tgctgaaccc	cttcactctgc	agtctgagga	ataaagacat	aaagagagct	ctgaatcaat	960
tcactcagggt	agtgccattc	ttcaggaag				989

<210> 905

<211> 932

<212> DNA

<213> Unknown (H38g755 nucleotide)

<220>

<223> Synthetic construct

<400> 905

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gccccagaac	tacaggtcca	cctctttgtc	ttattttaact	tcactctacct	cttcactctg	120
agtgggaacc	tggggatgat	gctgctgctc	ctgctggact	ctcgtctcca	cacttccatg	180
tactttttcc	tcagtaacct	gtctctgggtg	gacttttgct	actcagaaac	tgtcactcca	240
aagatgatgg	ctgggttgct	gatagctcac	aaggctcatct	cctacaatgt	atgtgctgct	300
cagatgttct	tttttgacgt	ctttgctact	gtggaaagtt	acttcttgac	ttcagtgggc	360
tatgattgct	acagagtaat	gtgtaaacc	ctacattaca	ccaccaccat	gacaacaaat	420
gtgtgtgctt	ctctggccat	acatgcatgt	cttaggttta	ctgactgctg	ctgttgacat	480
tggagacatt	ttatgtccaa	tgagatccat	cactttttct	gtgatattct	ggcagtcattg	540
actctgactt	gctctaataa	acataattaat	gagttgatcc	ttgttccctac	ttcaagctat	600
atttttttacc	ctcctagtta	tcttgatttc	ctgcttggtt	gtatttgat	ttgtcaccat	660
tttaaagatg	ctctctttta	gtatacaaga	agggtttatc	tacctatggg	tctcacctca	720
ctgcagttcc	tttattttat	gagactgtcc	tcacacata	tgtgcagcca	agttctatca	780
tttcatgaac	acagaaaaaa	ttgtatctgt	gtttcatatt	atgggttatcc	ccatgctaatt	840
ccctgtgggt	tatagcctga	gaaacaacga	gggtcaagagt	gcattcaaga	ctggttggtg	900
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<210> 906

<211> 945

<212> DNA

<213> Unknown (H38g756 nucleotide)

<220>

<223> Synthetic construct

<400> 906

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gagatgaagg	gtctggagca	ctggctggct	gcccttctgc	tgctgctttg	tgctatttcc	120
ttcctgggca	acatcctcat	cctctttatc	ataaaggaag	agcagagctt	gcaccagcca	180
atgtactact	tcctgtctct	ttttctgtt	aatgacctgg	gtgtgtcctt	ttctacattg	240
cccactgtac	tggctgctgt	gtgttttcat	gccccagaga	caacttttga	tgccctgctg	300
gcccagacgt	tcttcatcca	cttttctcc	tggacagagt	ttggcatcct	actggccatg	360
agttttgacc	actatgtggc	catctgtaac	ccgctgcgct	atgccacagt	gctcactgat	420
gtccgtgtgg	cccacaatgg	catatccatt	gtcatccgca	gcttctgcat	ggtattccca	480
cttcccttcc	tcctgaagag	actgccttcc	tgtaaggcca	gtgtgggtact	ggcccatccc	540
tactgtctgc	atgcagacct	gattcggctg	ccctgtggag	acactaccat	caacagcatg	600
tatggcctgt	tcattgtcat	ctctgccttt	ggtgtagatt	cactgctcat	cctcctctcc	660
tatgtgctca	ttctacattc	tgtgtgcgca	ttgcctccag	gggtgagagg	cttaagacac	720
tcgaacacat	gtgtgtcaca	tatctatgca	gtgctgatct	tctatgtgcc	tatggttagt	780
gtgtccatgg	ttcatcgatt	tgggaggcat	gctcctgaat	atgtgcacaa	gttcattgct	840
ctttgtacct	gccaatgtct	taccgcaatt	atctattcca	tcaagactaa	ggagattcgc	900
aggagactac	acaagatggt	attgggagct	aagttctgat	cgaag		945

<210> 907
 <211> 989
 <212> DNA
 <213> Unknown (H38g757 nucleotide)

<220>
 <223> Synthetic construct

<400> 907
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 gtatttgga acttgcttat catcctgggt atcattttat gctcccacct ccacacctcc 180
 atgtacttct ttctctccaa cctgtccttt gtagacatct gttttgcctc caccagggtc 240
 ccaaagatgc tgggtgaatat ccaggcacag agcaaagtca tcacctctgc aggctgcac 300
 acccagatgt actttttcat acatttttga ggattggaca gcttcctcct gactgtgatg 360
 gcctatgacc ggtttgtggc catctgtcac cccctgtact acacgggcat catgaaccct 420
 caactctgtg gattgcttgt tctggatcc tggatcaca gtgtcttgca ttccttatta 480
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 ctctaagaca gtttctccca tatgtgcaat ctcatcagct caaggggaagt ataaggcatt 720
 ttccacctgt ccactcacc tctcagttgt ctcttgttt tactgtacaa gcctaggagt 780
 gtaccttagc tgggtgtcat cccacaactc acactcaggt gcaatagcct cagtgtatgta 840
 cactgtgtgc acccccattg tgaacccctt catctacagc ctgaggaata aggacataaa 900
 gagggctctg aagaattctt tgggaggga actagaaaag ggccagttgt cctagggctg 960
 aagctatata catgattgca aggtcaaa 989

<210> 908
 <211> 960
 <212> DNA
 <213> Unknown (H38g758 nucleotide)

<220>
 <223> Synthetic construct

<400> 908
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 ggaaacctgc tcatcatcct gaccatcagt tcagactccc acctccacac ccccatgtac 180
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 atattttttt tcattgcatt tggatgcctg gacaatttgc tctgacctat gacggcctat 360
 gaccgcttcg tggccatctg ttacccctg cactacacgg tcatcatgaa ccccggtc 420
 tgtggactgc tggttctggg gtcctgggtc atcagtgtca tgggttcctt gcttgagacc 480
 ttgaccattt tgaggctgtc ctctgcaca aatatggaaa ttccgcactt tttttgtgat 540
 ccttcgaag tcctgaagct ggctgttct gacaccttca tcaataacat cgtgatgtgt 600
 tttgtgacca ttgtcctggg tgtttttcct ctctgtggaa tctattctc ttattctcag 660
 attttctcct ccgtcctaag agtatcatct gccagaggcc agcacaaagc ctttaccacc 720
 tgtggttccc acctctcagt ggtcagcttg ttctatggca ctggccttgg ggtctatctc 780
 agttctgcag ttacaccacc ttctaggaca agtctggcag cctcgggtgat gcacaccatg 840
 gtcaccccca tgctgaaccc ctcatctac agcctgagga acaaggacat gaaggggtca 900
 ctggggagac tctcctcag ggcaacgtct ctcaaagagg ggaccattgc taagctctca 960

<210> 909
 <211> 981
 <212> DNA
 <213> Unknown (H38g759 nucleotide)

<220>
 <223> Synthetic construct

<400> 909

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gacccagcac	tgcagctggg	cgctactggg	ctgtgcctgt	gtgcctgggc	acgggtgctgt	120
ggaaactgct	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcttctctctg	caacctgtcc	ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcctctccta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaaccctgtg	420
ttctgtgggt	tcctgggtttt	gttgtctttt	ttttctcag	tcttttagac	tcccagctgc	480
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tgtatttccc	tttggttttc	ttcccatctc	ggggaccctt	ttctcttact		660
ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggagctat	aaagccttcg	720
ccacctgtgg	atctcacctg	tcagttgttt	gctgatttta	tggaacaggc	gttggagggt	780
acctcagttc	agatgtgtcg	tcttccctga	gaaagcgtgc	agtggcctca	gtgatgtaca	840
cagtggtcac	ccccatgctg	aatcccttga	tctacagcct	gagaaacagg	gatattaaag	900
gtgtcctgtg	gcagccgtgc	agccgcacgg	cagcacagtc	tcattctaat	atcttatctg	960
ttccattcct	tttgcaggat	g				981

<210> 910

<211> 628

<212> DNA

<213> Unknown (H38g760 nucleotide)

<220>

<223> Synthetic construct

<400> 910

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ttgggaaata	gtgctattat	tctgggtctt	caactagatt	cccaacttca	tagtccctatg	180
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caaagtctgt	tcaatttagg	gggcccaca	agaacatcac	ttaaataggc	tgtatggccc	300
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tagactgcta	tgtggctgtc	tgtaagcctc	caaggtagac	tataatcata	gaccataagg	420
tctgcctgca	cctgtccagc	actgcttggc	taattgggtc	ggccaattca	ctgctgcagt	480
caacaatcac	aattcagttg	cccctgtaga	ggtgtatagc	tcagatcttc	ctttagtttag	540
agtctgtcac	ctaacagtct	ctaactgtaa	caacctttga	gatctgctac	agcattctat	600
ctgaggccaa	cttcatgctg	gggagctc				628

<210> 911

<211> 945

<212> DNA

<213> Unknown (H38g761 nucleotide)

<220>

<223> Synthetic construct

<400> 911

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ggaaatgccc	tcattatcct	ggccatcatc	acggactctc	acctccacac	acccatgtac	180
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atgctagcga	acatccagge	tcagagcaga	gccatccctt	ttgtgggctg	cctcaccag	300
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tgtggcttac	acctcactgt	ggtgtcactg	tccatggga	ccatctttgc	tgtgtactta	780
cagccacat	ccccagctc	ctcccagaag	gacaaggcag	ccgcccta	gtgtggggtg	840
ttcatccca	tgtcaaccc	ctttatctac	agcatacgga	acaaggatat	gaaggcagcc	900
ctggggaagc	tcacggcaa	agtggcgcgc	ccctgtccta	ggcca		945

<210> 912

<211> 949

<212> DNA

<213> Unknown (H38g762 nucleotide)

<220>

<223> Synthetic construct

<400> 912

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agcaacctga	gcatgggtgc	gctgggtgaga	tccgacgggg	ccctcgcctc	ccccatgtat	180
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tgcgcctcgc	tggtgcgtgc	gtcgtgggccc	gtgacgcacc	tgcactcgtc	gctgcacacg	480
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tcacgccgac	cttgaacctt	ttcatcaaca	gccttcgcaa	caaagaggtc	aagggcgccc	900
tgaaaagggg	gctcagatgg	agggctgcac	cccaagaggc	gtgagggca		949

<210> 913

<211> 936

<212> DNA

<213> Unknown (H38g763 nucleotide)

<220>

<223> Synthetic construct

<400> 913

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ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
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atcctgttta	ctgtttggaa	acattcctca	ggtgggttcac	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggc	ccttttggtc	tttggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtagtcaaac	agctagtgtat	ttacaagagg	atctca			936

<210> 914

<211> 954

<212> DNA

<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

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ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttcctgctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaac	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaaccagg	300
cacttctctt	atgtgtgtct	aggtgggtgt	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcatccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggtgtgcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcaacttcc	tttctgtggg	cctcggaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagtt	ggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
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cttcaaagtg	tcattcagat	gcgctcatct	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacggtggt	ttctcttttg	tttgggtgct	gcactctctc	ctacatgaga	780
cccagggtccc	agtgcactct	attgcagaac	aaagttgggt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tggtatcacc	cagtgcattc	aacgactgca	attg	954

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

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ctggcccgcg	gagcatcgga	gacactaccg	agaaccagat	gttcgccgcc	cgctgtgtca	120
tctgtgtgct	gccgtttgcc	gtcatcctgg	cctcctacgg	tgccgtggcc	gagctgtctg	180
ttgtatgcgg	ttcagcggag	gccggagagg	gcggtgggca	cgtgtgggtc	ccactgacag	240
ccgtctgcct	gttctacggc	tcggcatcta	cacctacctg	cagcccgcgc	agctaacaac	300
caggcacgg						309

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

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attggcatcg	tggtgtgggt	ccgcggatcc	ctcttttttt	tcccactgcc	tctgtgtgat	180
aagcggctgg	ccttcttgcca	ctccaatgtc	ctctcgact	cctatttgtt	ccaccaggat	240
gtaatgaagt	tggcctatgc	aagacanttt	gcccgaatgtg	gtatatggtc	ttaactgncc	300

atttttggttg gtc

313

<210> 917

<211> 960

<212> DNA

<213> Unknown (H38g767 nucleotide)

<220>

<223> Synthetic construct

<400> 917

atggaaacag	gaaatcaaac	acatgcccaa	gaatttctcc	tcctgggatt	ttcagcaacg	60
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gggaacctgc	tcatacatcct	ggccatatgc	tcagactccc	acctccacac	ccccatgtac	180
ttcttcctct	ccaacctgtc	ttttgctgac	ctctgtttta	cctccacgac	tgtcccaaag	240
atgttactga	atatactgac	acagaacaaa	ttcataacat	atgcaggctg	tctcagtcag	300
attttttttt	tcacttcatt	tggatgcctg	gacaatttac	tcttgaccgt	gatggcctat	360
gaccgcttcg	tggccgtctg	tcacccctg	cactatacgg	tcatcatgaa	ccccagetc	420
tgtggactgc	tggttctggg	gtcctggtgc	atcagtgtca	tgggttcctt	gctcgagacc	480
ttgactgttt	tgaggctgtc	cttctgcacc	aaaatggaaa	ttccacactt	tttttgat	540
ctacttgaag	tcctgaagct	cgcctgttct	gacaccttca	ttaataacgt	ggtgatatac	600
tttgcaactg	gcgtcctggg	tgtgatttcc	ttcactggaa	tatttttctc	ttactataaa	660
attgttttct	ctatactgag	gatttcctca	gctgggagaa	agcacaagc	gttttccacc	720
tgtggttccc	acctctcagt	ggtcaccttg	ttctatggca	cgggctttgg	ggtctatctc	780
agttctgcag	ccacaccatc	ttctaggaca	agtctggtgg	cctcagtgat	gtacaccatg	840
gtcaccccca	tgctgaaccc	cttcatctac	agcctgagga	acacggacat	gaagagggcc	900
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<210> 918

<211> 937

<212> DNA

<213> Unknown (H38g768 nucleotide)

<220>

<223> Synthetic construct

<400> 918

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gagatggaag	tgctcctctt	ctggatcttc	tcctgttat	atctcttcag	cctgctggca	120
aatggcatga	tcttggggct	catctgtctg	gatccagac	tggcaccctc	catgtacttc	180
ttcctgtcac	acttggccgt	cattgacata	tactatgctt	ccagcaattt	gctcaacatg	240
ctggaaaacc	tagtgaaaca	caaaaaaac	tatctcgttc	atctcttgca	ttatgcagat	300
ggctttgtat	ttgacttttg	ctgctgcagt	gtgcatgatt	ttggtggtga	tgtcctatga	360
cagattttgtg	gcgatctgcc	atcccctgca	ttacactgtc	atcatgaact	ggagagtgtg	420
cacagtactg	gctattactt	cctgggcatg	tggattttcc	ctggccctca	taaatactaat	480
tctccttcta	aggctgccct	tctgtgggcc	ccaggagggtg	aaccacttct	tcggtgaaat	540
tctgtctgtc	ctcaaaactgg	cctgtgcaga	cacctggatt	aatgaaattt	ttgtctttgc	600
tgggtggtgtg	tttgtcttag	tcgggcccct	ttccttgatg	ctgatctcct	acatgcgcat	660
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ctcctccac	ctctgtgtgg	ttgggcttta	ctttggcatg	gccatggtgg	tttacctggt	780
cccagacaac	agtcaacgac	agaagcagca	gaaaattctc	accctgtttt	acagcctttt	840
caaccatttg	ctgaaccccc	tcactctacag	cctgcggaat	gctcaagtga	agggtgcctt	900
atacagagca	ctgcagaaaa	agaggaccat	gtgaatg			937

<210> 919

<211> 957

<212> DNA

<213> Unknown (H38g769 nucleotide)

<220>

<223> Synthetic construct

<400> 919

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cctggactgc	aacccttcc	ctttgggctg	ttcctgtcca	tgtacctggt	cactgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttcctct	ccaacctgtc	ctttgctgac	atttgtgta	cttcaccac	cattccaaaa	240
atgctgatga	acatccagac	acagaacaaa	gtcatcacct	acatagcctg	cctcatgcag	300
atgtattttt	tcatactctt	tgctggattt	gaaaacttcc	tcctgtccgt	gatggcctat	360
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tgtggactgc	tggttctagc	atcctggacc	atgagtgtc	tgtattcctt	gctacaaatc	480
ttaatggtag	tacggctgtc	cttctgcaca	gccttagaaa	ttccccactt	tttctgtgaa	540
cttaatcagg	tcatccaact	tgcttgttct	gatagctttc	ttaatcacat	gggtgatatat	600
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tgtgcatctc	acctctcagt	tgtctcctta	ttttatgggtg	caatcctagg	gggtgtacctt	780
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gtcaccacca	tgtgaaccc	ctttatctat	agtctgagga	ataaagacat	aaagagggtc	900
ctgggaatac	atttgttgtg	gggaacaatg	aaagggaat	ttttcaagaa	gtgccca	957

<210> 920

<211> 222

<212> DNA

<213> Unknown (H38g770 nucleotide)

<220>

<223> Synthetic construct

<400> 920

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gacgtcatac	tggcctccta	aggtgccgtg	gcccagagctg	tctgttgcac	gcggttcagc	120
ggaggaccga	ggagggcgct	gggcacgtgt	gggtcccacc	cgacagccgt	ctggctgttc	180
taaggctcgg	gcaataaac	ctatctgcaa	gccgcgcagc	ta		222

<210> 921

<211> 927

<212> DNA

<213> Unknown (H38g771 nucleotide)

<220>

<223> Synthetic construct

<400> 921

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ccagaattgc	aggccttcc	ctttgggctg	ttcctgtcca	tgtacctggt	cactgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
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atgctgggtga	acatccagac	acacaacaaa	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	tcttactctt	tgtaggattg	gataacttcc	ttctgaccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctctg	cactacatgg	tcattatgaa	ccctcaactc	420
tgtggactgc	tggttctggc	atcctggatc	atgagtgttc	tgaattccat	gttacaaagc	480
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tgtgcatctc	acctctcagt	tgtctcctta	ttttatggta	catgcttagg	gggtgtacctt	780
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gtcaccacca	tgtgaaccc	cttcatctac	agtctgagga	ataaacacat	aaagggtgct	900
atgaaaacat	tcttcagagg	aaagcaa				927

<210> 922

<211> 246

<212> DNA

<213> Unknown (H38g772 nucleotide)

<220>

<223> Synthetic construct

<400> 922

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cttgggctct tctccctgtt ctatgtcttc accccgctgg ggaatgggac catccccggg	120
ctcatctcac tggactccag actccacacc cccatgtact tcttctcttc acacctggcc	180
gtcgtcaaca tcgctatgc ctgcaacaca gtgccccaga tgctgggtgaa cctcctgcat	240
ccagcc	246

<210> 923

<211> 648

<212> DNA

<213> Unknown (H38g773 nucleotide)

<220>

<223> Synthetic construct

<400> 923

ctcatggacc tcaagctcat ctgcaccacc gtacccaaga tggccttcaa ctacctgtct	60
ggcagcaagt ccatttctat ggctgggtgt gtcacacaaa ttttcttcta tatatcactg	120
tctggctctg aatgttttct tttggctgtt atggcttatg accgtatat tgctatttgc	180
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gtgggaatgt actatggagc agctttgttc atgtacatac ggcccacatc tgatcactcc	600
ccaacgcagg acaagatggt gtctgtattc tacaccatcc tcaactccc	648

<210> 924

<211> 916

<212> DNA

<213> Unknown (H38g774 nucleotide)

<220>

<223> Synthetic construct

<400> 924

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gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac	180
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gatcggtttg tggccatctg tcatcctctg tactacacaa tcatcatgaa cctcagttc	420
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agttgtctcc ttgttttatg gtacaagcct aggaatgtac cttagtctct ctgcaaccca	780
caactcacc tcaagtgcaa cagcctcagt gatgtacact gtggtcaccc ccatgctgaa	840
cccctttatc tacagtctga ggaataaaga cctaaaggat gctctgaaac gcttcttcag	900
aaggaagcaa taaaag	916

<210> 925

<211> 360
 <212> DNA
 <213> Unknown (H38g775 nucleotide)

<220>
 <223> Synthetic construct

<400> 925
 ttttccctct cacacctggc ggttggtgac attgcctacg cctgcaacac ggtgccccgg 60
 atgctggtga acctcctgca tccagccaag cccatctcct ttgcgggccc catgatgcag 120
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<210> 926
 <211> 643
 <212> DNA
 <213> Unknown (H38g776 nucleotide)

<220>
 <223> Synthetic construct

<400> 926
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 gagaaagact gcagtggcct cagtgatgta cgcagtggtc acc 643

<210> 927
 <211> 498
 <212> DNA
 <213> Unknown (H38g777 nucleotide)

<220>
 <223> Synthetic construct

<400> 927
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 atctctgcca tcactttcat gtacatgtgg ttctttctg tcttggtcca tgtaagcctc 480
 atactaagac tgcctttt 498

<210> 928
 <211> 276
 <212> DNA
 <213> Unknown (H38g778 nucleotide)

<220>

<223> Synthetic construct

<400> 928

caaagtgaagt	tggttgtaatt	ctttgcctct	ggctgaatgc	aatttggttta	aactcgcact	60
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tctaagaggc	cattatcttt	ttcttggttag	caggatgcta	ccttggtggg	ttagttaaag	180
tggtcactgt	gacaacttcc	atcacacaac	tatcgctttg	tcaaccatgt	gtcacctgc	240
cttctctgtg	acattccctc	attttgtagc	tattcg			276

<210> 929

<211> 645

<212> DNA

<213> Unknown (H38g779 nucleotide)

<220>

<223> Synthetic construct

<400> 929

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caagtaccaa	cgatataccta	tgagatttgc	ctgacacagc	tgtacttctt	tatgggtttt	120
ggagatatgg	agagcttctt	tcttggtggtc	atggcctatg	accgctatgt	ggccatctgc	180
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gtgaccttgt	tttatgggac	aattattggg	ctctacttat	gtccatcagg	caataattct	600
actgtgaatg	agatttccat	ggccatgatg	tacacagtgg	tggt		645

<210> 930

<211> 657

<212> DNA

<213> Unknown (H38g780 nucleotide)

<220>

<223> Synthetic construct

<400> 930

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actaggttgt	ctttctgtga	aaacaatgtg	atccccatt	ttttctgtga	tctgtctgcc	360
ctgctgaagc	tgccctgtct	tgatattcac	attaatgaat	tggtgatatt	gatcatagga	420
gggcttggtg	ttatacttcc	atttctactc	atcacagtgt	cttatgcacg	catcatctcc	480
tccattctca	aggctccctc	aactcaaggc	atccacaagg	tcttctccac	ttgtggttct	540
cacctgtctg	tggtgtcact	gttctatggg	acaattattg	gcctctactt	atgtccatct	600
gctaataact	ctactctaaa	ggacactgtc	atgtctatga	tgtacaccgt	ggtaact	657

<210> 931

<211> 942

<212> DNA

<213> Unknown (H38g781 nucleotide)

<220>

<223> Synthetic construct

<400> 931

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ctgcagatcc cactcttcat agtcttccctt ttcattctacc tcatcactct ggttgggaac 120
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cccattgtga atccactggt ctacagcctg aggaacaaag aggttaagag tgcctttaa 900
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<210> 932

<211> 562

<212> DNA

<213> Unknown (H38g782 nucleotide)

<220>

<223> Synthetic construct

<400> 932

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acctggcctt gattgctcta attggctgaa attcatacct tcccaccccc aagctctgtt 180
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gacttttgta tcaaagaaaa acatcttcta tgtcagggtg atgactcagc tgtcgcagct 300
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gagagagaga gagagtggat ttgctggaac cactcccaca cagggcacat acttaggccg 480
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<210> 933

<211> 933

<212> DNA

<213> Unknown (H38g783 nucleotide)

<220>

<223> Synthetic construct

<400> 933

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gcctggaaac tctccctcat tgttttaata aggatggatt cccacctcca tacacccatg 180
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gccttaaaga gggtgcaaaa gagaaagtgc tgc 933

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<210> 934
 <211> 935
 <212> DNA
 <213> Unknown (H38g784 nucleotide)

<220>
 <223> Synthetic construct

<400> 934
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 tcttggaaca taaacctcat cacccttate aggacgactc ccatctgcat acacctatgt 180
 actttttcct tagtaatctg tcgtttctgg acatctgcta tgtttccact atagccccc 240
 agatgctctc agactttctc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300
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 atgategata tgctgccatt tgcaaccctc tgctctacag ggccatcatg tttcccaccc 420
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 tctgtgcctt gcttcagctc catttctgtg ggccaaatgt catcaaccat ttcttctgtg 540
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 ttacaatccc catgttaaatt ccagtgatct acagcctgag gaacaaggaa atcaaagatg 900
 ctctaaacag atggaagaag agaattctct cctgg 935

<210> 935
 <211> 1330
 <212> DNA
 <213> Unknown (H38g785 nucleotide)

<220>
 <223> Synthetic construct

<400> 935
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 tcttgaaacg ttagtctcat cgcccttate aggacggact cccatctaca tgcacctgtg 180
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 aagatgccct cagacttttt caagaagcat aaattcattt cctttatggg gtgcacctgtg 300
 cagtacttct cttagcctgaa tgtgactgag tgctgtcttc ttacagccat ggcttatgat 360
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 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgcc 540
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 tctcttctat tgctcaagaa tctttgtcta tatgtgctct cactctgatg cttctctgag 1200
 tagaaacaag gtggattcta ttgtatacac tgtgggtgat cccagggttg atccattgat 1260
 ctacagcctg agtgacaagt aaatcaaaga tgccttaaag agatggacga agagaatatt 1320
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<210> 936

<211> 930
 <212> DNA
 <213> Unknown (H38g786 nucleotide)

<220>
 <223> Synthetic construct

<400> 936
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 aggattcaga tgctcctctt tgggtctctt tccctgttct atatcttcac cctgctgggg 120
 aacggggcca tcctggggct catctcactg gactccagac tccacacccc catgtacttc 180
 ttccctctac acctggctgt cgtcgacatc gcctacaccc gcaacacggt gccccagatg 240
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 tttctctgtt tgagtttttg acacagcgaa tgtctcctgc tgggtgctgat gtcctacgat 360
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 gcctgctgtt tcttctctgt ggggccaccc agcctgggtc ttgtctccta ctgcacatc 660
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 tctctccacc tctgcgtggt gggactcttc tttggcagtg ccatcatcat gtacatggcc 780
 cccaagtccc gccatcctga ggagcagcaa aaggctcttt ttctatttta cagttttttc 840
 aaccaaacac ttaacccctt gatttacagc ctgaggaacg gagaggtcaa gggtgccctg 900
 aggagagcac tgggcaagga aagtcattcc 930

<210> 937
 <211> 942
 <212> DNA
 <213> Unknown (H38g787 nucleotide)

<220>
 <223> Synthetic construct

<400> 937
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 cctgagctcc aggggcagct ctttgtggct ttccctgggtta tttatctggt gaccctgata 120
 ggaaatgcca ttattatagt catcgtctcc ctagaccaga gcctccacgt tcccatgtac 180
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 atgctgggtg tcctctctac tgaaaaaact acaatttctt ttgggggctg ttttgacag 300
 atgtatttca tccttctttt tgggtggggct gaattgtttt ttctggggagc aatggcttat 360
 gaccgatttg ctgcaatttg ccctcctctc aactaccaa tgattatgaa taaaggagtt 420
 tttatgaaat taattatatt ttcattgggc ttaggtttta tgtaggtac tgttcaaca 480
 tcatgggtat ctagttttcc cttttgtggc cttaatgaaa ttaaccatat atcttgtaga 540
 accccagcag tgtagaact tgcattgtga gacacgtttt tgtttgaaat ctatgcattc 600
 acaggcacct ttttgattat tttggttctt ttcttgttga tactcttgtc ttacattcga 660
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 caaccctaat ctggctactc accggaaacc aagaaagtga tgtcattgtc ttactcactt 840
 ctgacaccac tgctgaatct gcttatctac agtttgcgaa atagtgaat gaagagggt 900
 ttgatgaaat tatggcgaag gcgagtgggt ttacacacaa tc 942

<210> 938
 <211> 993
 <212> DNA
 <213> Unknown (H38g788 nucleotide)

<220>
 <223> Synthetic construct

<400> 938
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ctcatctcac	tggactccag	actccacacc	cccattgtact	tcttcctctc	acacctggcc	180
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gcacatactg	aatgcctcct	gttgggtgctg	atgtcctacg	atcggtacgt	ggccatctgc	360
carcctctcc	gatatttcat	catcatgacc	tggaagtct	gcatcactct	ggccatcact	420
tcctggacat	gtggctccct	cctggctatg	gtccatgtga	gcctcatcct	aagactgccc	480
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gaaagtcatt	cctaagagggt	gtgacatttg	aactgccagc	ctcagttgtc	acgtggactc	960
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<210> 939

<211> 930

<212> DNA

<213> Unknown (H38g789 nucleotide)

<220>

<223> Synthetic construct

<400> 939

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aggattcaga	tgctcctctt	tgggctcttc	tcctgtttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgacgcccc	catgtacttc	180
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tttctgtttt	ccacttttgc	tgctcacaga	tgctcctcc	tggtgggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttgccca	tcattgacctg	gagagtctgc	420
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ttggctgttc	tcaaacttgc	ctgtgcagat	accacatca	atgagaacat	ggtcttggcc	600
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cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	cgctgtttca	cagcctcttt	840
aatcccatgc	tcaatccctt	tatctgtagt	cttaggaact	cagaagtgaa	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtctta				930

<210> 940

<211> 942

<212> DNA

<213> Unknown (H38g790 nucleotide)

<220>

<223> Synthetic construct

<400> 940

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ggaaatgcca	tcattacagt	catcatctcc	ttaaaccaga	gcctccacgt	tcccatgtac	180
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gaccgatttg	ctgcaatttg	ccatcctctg	aactaccag	tgattatgaa	cagaggggtt	420
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acttgggtat	ttagtcttcc	attttgtggc	cccaatgaaa	ttaatcatct	cttctgtgag	540

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gttctgtttg	ccatcctyaa	gatgccatca	actactggga	gacaaaaggc	cttttccacc	720
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caacccaaat	ctgggtactc	accgaaaacc	aagaaactga	tctcattggc	ttacacgttg	840
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<210> 941

<211> 936

<212> DNA

<213> Unknown (H38g791 nucleotide)

<220>

<223> Synthetic construct

<400> 941

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gacctccagg	gcttgctctt	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatttctca	ttgtggtgct	ggtctccact	gatgctgccc	tccagtcccc	tatgtacttc	180
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cgctatgcag	ccatctgtga	acccctccgc	tacccactgc	tgtgagcca	ccgggtgtgt	420
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cagcctgtcc	tgcagctggt	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
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acccccatcc	tcaaccccat	catctacagc	ctgcggaaca	cagagggtcaa	agctgcctta	900
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<210> 942

<211> 828

<212> DNA

<213> Unknown (H38g792 nucleotide)

<220>

<223> Synthetic construct

<400> 942

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gcctccacca	tggtcccaaa	gatgttggtg	aacatccaga	cacagagcaa	agtcattacc	180
tatgcagggt	gcatcaccca	gatgtgcttt	tttgtactct	ttatagtgtt	ggacagctta	240
ctcctgaccg	tgatggccta	tgaccagttt	gtggccatct	gtcaccctct	gcactacacg	300
gtcatcatga	gccctcagct	ctgtggactg	ctggttctgg	tgtcctggat	catgagtgtc	360
ctaaactcca	tgttacaaag	cttagtgaca	ttgcagttgt	ccttctgcac	agacttgga	420
atccctcact	ttttctgtga	acttaatgag	atgatccacc	ttgcctgttc	tgacaccttt	480
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gcctcgggtga	tgtacactgt	ggtcaccccc	atgctcaacc	ccttcattta	cagtctgagg	780
aataaagaca	taaagggggc	tctgacacaa	ttcttcagag	ggaaacaa		828

<210> 943

<211> 950

<212> DNA

<213> Unknown (H38g793 nucleotide)

<220>

<223> Synthetic construct

<400> 943

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actgggaaca	ttctcattgt	gggtgccatt	cacacagaaa	cctgtctatg	cacatccatg	180
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<210> 944

<211> 927

<212> DNA

<213> Unknown (H38g794 nucleotide)

<220>

<223> Synthetic construct

<400> 944

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gggaatctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttcctct	ccaacctgtc	ctttgcagac	atctgtttca	tctccactac	aatcccaaag	240
atgtctatta	acatccagac	acagagcaga	gtcatcacct	atgcaggctg	catcaccag	300
atgtgctttt	ttgtactttt	tggagggtta	gacagcttac	tcctgggtgt	gatggcctat	360
gatcggtttg	tggccatctg	tcactcctctg	cactacacag	tcatactgaa	ccctcggttc	420
tgtggactcc	tggttctggc	atcctggatg	attgtgtccc	tgaattcctt	gtcacaaagc	480
ttaatggtat	tgtggtgtgc	cttctgcaca	gacttggaag	tccccactt	ttctgtgtaa	540
cttaatcagg	tcataccact	tgcctgttct	gacacctttc	ttaatgacat	ggggatgtat	600
tttgcagcag	ggctgtctggc	tgggtgtccc	cttgtgggga	tcctttgttc	ttactctaag	660
atagtttcct	ccatactgtc	aatctcatca	gctcagggga	agtacaaggc	atcttccacc	720
tgtgcatcac	acctctcagt	tgtctcttta	ttttgttgta	cgggcctagg	tgtgtacctt	780
acttctgtctg	caaccacaaa	ctcacacaca	agtgaacag	cctcagtgat	gtacactgtg	840
gccaccccca	tgtgtgaacc	ctttatctac	agtctgagga	ataaagacat	aaagagggtc	900
ctgaaaatgt	ccttcagagg	aaagcaa				927

<210> 945

<211> 942

<212> DNA

<213> Unknown (H38g795 nucleotide)

<220>

<223> Synthetic construct

<400> 945

atggagaata	atacagaggt	gagtgaattc	atcctgcttg	gtctaaccac	tgccccagaa	60
ctacagggtc	ccctctttat	catgtttacc	ctcatctacc	tcatactctt	gactgggaac	120
ctggggatga	tcataatta	cctgtctggc	tctcatctcc	acactcccat	gtactttttt	180

ctcagtaacc	tgtctcttgc	aggcattggt	tactcctcag	ctgtcactcc	aaagggttta	240
actgggttgc	ttatagaaga	caaagccatc	tcttacagt	cctgtgctgc	tcagatgttc	300
ttttgtgcag	tctttgccac	tgtggaaaat	tacctcttgt	cctcaatggc	ctatgaccgc	360
tacgcagcag	tgtgtaaccc	cctacattat	accaccacca	tgacaacacg	tgtgtgtgct	420
tgtctggcta	taggctgtta	tgtcattggt	ttcttgaatg	cttctatcca	aattggagat	480
acatttcgcc	tctctttctg	catgtccaat	gtgattcatc	actttttctg	tgacaaacca	540
gcagtcatta	ctctgacctg	ctctgagaaa	cacattagtg	agttgattct	tgttcttata	600
tcaagtttta	atgtcttttt	tgcacttctt	gttaccttga	tttcttatct	gttcatattg	660
atcaccattc	ttaagaggca	cacaggtaag	ggataccaga	agcctttatc	tacctgtggt	720
tctcacctca	ttgccatttt	cttattttat	ataactgtca	tcatcatgta	catacgacca	780
agttccagtc	attccatgga	cacagacaaa	attgcatctg	tgttctacac	tatgatcatc	840
cccattgtca	gtcctatagt	ctataccctg	aggaacaaag	acgtgaagaa	tgcattcatg	900
aaggttgttg	agaaggcaaa	atattctcta	gattcagtct	tt		942

<210> 946

<211> 946

<212> DNA

<213> Unknown (H38g796 nucleotide)

<220>

<223> Synthetic construct

<400> 946

atgtaaaata	actcaaagtt	tactgatttc	atcctggtag	gtctaaccaa	tgccacagaa	60
cttcagatcc	ccctctttat	cttgttcatc	ctcatccacc	tcctcattct	gactaggaac	120
ctggagatca	tactgttgat	cctgctggac	tcttgtctcc	aattcccatg	tactttttcc	180
tcagtaacct	gtctctgctt	ggatacttaa	ctgtcactcc	cagggtcacg	gctagcaggg	240
ctaggttact	tagagggtag	gaggctaagt	tcctcgtaca	atgcttgtgc	tgctcagatg	300
ttcttttttg	tagccttggc	cacagtggaa	aatatcgctg	ttgacatcaa	tgccctatga	360
ccactatata	gcagtgtgca	aacccttaca	ctacactacc	accacgatag	ccagtgtatg	420
tgctcatctg	gtcataggct	cctatgtctg	tggttttcta	aatgcctccc	tccgcattgg	480
ggacatatcc	agtctctctt	tctgtaagtc	caatcttgtc	catcaccttt	tctgtgatgt	540
tccaccagtc	atggctgtgt	cttgctctgg	taaacacatt	agcaagaaga	ttctgggttt	600
tatgtcaagc	ttcaatgtct	ttttggctct	tctagttatc	ttgacctcct	acctgttcat	660
attcatcacc	atcttgaaga	tgcactcagc	tcagggacac	ttaaaagctt	tgtccacctg	720
tgccctctac	ctcattgcag	tctccatctt	ctatggaaact	actatcttta	tgcacttaca	780
gcctagctcc	agccattcca	tggacacaga	tgaatggca	tccttgttct	atgctgtgtt	840
catctccatg	ctgaaccttg	tgttctacag	cctgaggagc	aaagaagtca	agaatgcatt	900
caaaaaggcg	gttgagaagg	caaaattttt	cttagaactg	tgattt		946

<210> 947

<211> 942

<212> DNA

<213> Unknown (H38g797 nucleotide)

<220>

<223> Synthetic construct

<400> 947

atggacaaca	gcaactggac	cagtgtgtcc	cattttgttc	tcttgggcat	ttccaccac	60
ccagaagagc	aaatcccact	cttccttgtt	ttctcactca	tgtagcgaat	caatatttct	120
ggcaacttgg	ccatcatcac	actgattctc	tctgtctcac	gcctccacat	ccccatgtac	180
atcttctca	gtaacttggc	cttgacagac	atctgttcca	cctccaccac	ggcccccaag	240
atgctgcaga	ttattttctc	ccctacaaag	gtaatttcct	acacaggctg	tttagcccaa	300
acttatttct	tcatttgcct	cgccgtcatg	gaaaacttca	tcctggctgt	gatggcctat	360
gacaggtaca	ttgccatctg	ccaccctttc	cactacacta	tgatcctgac	tagaatgctg	420
tgtgtgaaga	tggtgggtcat	gtgccatgct	ctctcccacc	ttcatgccat	gctgcatacc	480
tttctcatgg	gccaaactaat	cttctgtgca	gataacagaa	tccccactt	cttctgtgac	540
ctctacgctc	tgatgaagat	ctcctgcacc	agcacctacc	tcaacacctt	tatgattcac	600
acagaagggtg	ctgttgtaat	cagtggagct	ctggccttca	ttactgcctc	ctatgcctgc	660
atcatcctgg	tggtcctccg	gatccccctca	gccaagggca	ggtaggaaac	cttttctacc	720

tgcggtcccc	acctcactgt	ggtggccata	ttctatggca	ccctcagttg	ggtctacttc	780
cggccccctt	ccagctattc	agtgaccaag	ggtcgcatta	taacagtcgt	gtacacagtg	840
gtgactccca	tgctgaacce	cttcactctac	agcctgagga	atggggatgt	caagggagggc	900
ttcatgaaat	ggatgagcag	aatgcagact	ttttctctta	ga		942

<210> 948

<211> 948

<212> DNA

<213> Unknown (H38g798 nucleotide)

<220>

<223> Synthetic construct

<400> 948

atgggttaacc	aaagctcccc	catgggcttc	ctccttctgg	gcttctctga	acacccagca	60
ctggaaagga	ctctctttgt	ggttgtcttc	acttcctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tctgtctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttgtgtccc	ccagatgctg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttctctg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctcctga	cagtgatggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccg	cctgtgtctg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctggttcaat	cgatagtcca	gacaccatcc	480
accctccact	tgcccttctg	tccccaccag	cagatagatg	actttttatg	tgagggtccca	540
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agtgtcatct	tcgtgggtgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtgc	tgaggattaa	ctctgccaca	gcatggagaa	aggcctttgg	gacctgtctc	720
tcccactctc	ctgtggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gagggggcaag	ttctttgggc	tcttctatgc	agtgggcact	840
ccttcactta	accctctcgt	atacaccttg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

<210> 949

<211> 971

<212> DNA

<213> Unknown (H38g799 nucleotide)

<220>

<223> Synthetic construct

<400> 949

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gatccagaac	tgacgccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatatggtc	120
acgggtgctg	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	gctccacacc	180
cccattgtgt	tcttctcttc	caaactgtgc	tgagctgaca	tcggtttcac	cttggccatg	240
gttcccaaga	tgattgtgaa	catgcagtcg	catagcagag	tcattctctta	tgagggtctg	300
ctgacacgga	tgtctttctt	tgtccttttt	gcatgtatgg	aagacatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actacccagt	catcgtgaat	420
cctcacctct	gtgtcttctt	cgtcttgggt	tcctttttcc	ttagcccgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	actattcacc	atcatcaaga	atgtggaaat	cactaatttt	540
gtctgtgaac	cctctcaact	tctcaacctt	gcttgttctg	acagcgtcat	caataacata	600
ttcataatatt	tcgatagtac	tatgtttggg	tttcttccca	tttcagggat	ccttttgtct	660
tactataaaa	ttgtcccttc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaggc	720
ttctccacct	gtggctctta	cctggcagtt	gtttgctgat	ttgatggaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaatg	gtgtgggtggc	gtcagtgatg	840
tatgctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctaggaaa	gagggatata	900
caaagtgtcc	tgcgagggtc	gtgcagcaga	acagtcgaat	ctcatgatat	gttccatcct	960
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<210> 950

<211> 474

<212> DNA

<213> Unknown (H38g800 nucleotide)

<220>

<223> Synthetic construct

<400> 950

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ccagaattgc	agcccggtat	gtttggactc	ttcctctcca	tgtatctgac	aactgtgttt	120
ggaaacctgc	tcatcatcct	ggccatctgc	tctgggtccc	acctccacac	ccccatgtac	180
ttcttctct	ctaacctgtc	ctttgtagac	atctgtgtta	cctccaccac	agtcccaaag	240
acactgtcaa	acatccggac	acagagtaaa	gtcatcacct	atgcagggtg	catcaccag	300
atgtactttt	ttgtactctt	tatagtgttg	gacagettac	tcttgaccgt	gatggcctat	360
gaccagtttg	tggccatctg	tcacccctg	cactacacgg	tcatcgtgaa	ccctcggctc	420
tgtggactgc	tggttctggc	gtcctggatc	atgagtggcc	tgaattcctt	gata	474

<210> 951

<211> 954

<212> DNA

<213> Unknown (H38g801 nucleotide)

<220>

<223> Synthetic construct

<400> 951

atgatgagct	ttgccctaa	tgttccacac	tctccggttt	ttttgctcct	tgggttctcg	60
agagctaaca	tctcctacac	tctcctcttc	ttcctgttcc	tggctattta	cctgaccacc	120
atactgggga	atgtgacact	ggtgctgctc	atctcctggg	actccagact	gcactcacc	180
atgtattatc	tgttctgttg	cctctctgtg	atagacatgg	ggctatccac	agttacactg	240
ccccagttgc	tggcccatct	ggctctctcat	tacccaacca	ttcctgctgc	ccgctgcttg	300
gctcagttct	ttttcttcta	tgcatttggg	gttacagata	cacttgtcat	tgctgtcatg	360
gctctggatc	gctatgtggc	catctgtgac	cccctgcact	atgctttggg	aatgaatcac	420
caacggtgtg	cctgcttact	agccttgagc	tgggtgggtg	ccatactgca	caccatgttg	480
cgtgtgggac	tcgtcctgcc	tctttgctgg	actgggggatg	ctgggggcaa	cgtaaaccct	540
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aatgagctgg	ccatattctt	tgagggtggc	ttccttatgc	tgggcccctg	tgccctcatt	660
gtactctctt	atgtccgaat	tggggccgct	attctacgtt	tgccctcagc	tgctggctgc	720
cgccgagcag	tctccacctg	tggatcccac	ctcaccatgg	ttggtttctt	ctacggcacc	780
atcatttgtg	tctacttcca	gcctcccttc	cagaactctc	agtatcagga	catggtggct	840
tcagtaatgt	atactgccat	tacacctttg	gccaaacctat	ttgtgtatag	cctccacaat	900
aaggatgtca	agggtgcact	ctgcaggctg	cttgaatggg	tgaaggtaga	cccc	954

<210> 952

<211> 921

<212> DNA

<213> Unknown (H38g802 nucleotide)

<220>

<223> Synthetic construct

<400> 952

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ggagccgttc	tgatgattgt	catctccgat	cctagactcc	attcccttat	gtatttcttc	180
ctgggaaacc	tgctctacct	ggatatctgt	tactctacgg	tgacactgcc	aaaaatgctg	240
cagaactttc	tctctacaca	caaagcaatt	tctttcttgg	gatgcataag	ccagcttcat	300
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tctgtggcta	tctgcaagcc	acttcgctac	actgtcatca	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	ggtcattggg	tttttccatg	ccctgctgca	ctccgtaatg	480
acttctctgt	tgaacttctg	tggttccaac	cgtatccatc	attttctctg	tgatattaag	540
ccattgctaa	agctggcctg	tgggaacact	gagcttaatc	agtggctact	cagtactgtc	600
acggggacaa	ttgccatggg	ccccttcttt	ctgacacttc	tctcctattt	ctacattatc	660

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gcctcccact	tcattgtagt	tattcttttc	tatgcacctg	ttctttttcac	ctatatccat	780
cctgcgttag	agagcttcat	ggaccaggac	cggattgttg	ccatcatgta	cactgtgtgc	840
actcctgtac	taaaccctact	gatctatact	ttgaggaaca	aggaagtga	gggggccttg	900
ggtagagtga	tcagaaggct	t				921

<210> 953

<211> 959

<212> DNA

<213> Unknown (H38g803 nucleotide)

<220>

<223> Synthetic construct

<400> 953

cagccacgga	atctcacaga	tgtctgagaa	ttcctcctca	tgggactctc	agaggatcca	60
gaactgcagc	ccgtcctcgc	tgggctgtcc	ctgtccatgt	atctggtcac	gggtgctgagg	120
aacctgtcca	gcattcctggc	tgtcagctct	gactcccacc	tccacacccc	catgtacttc	180
ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cggccacggg	tcccaagata	240
attgtggaca	tgcagtcgca	tagcagagtc	atctcttatg	tgggctgcct	gacacggatg	300
tcttttttgg	tcctttttgc	atgtatagaa	gacatgcttc	tgactgtgat	ggcctatgac	360
tgctttgtag	ccatctgtcg	ccctctacac	taccagtc	tcgtgaatgc	tcacctccgt	420
gtcttcttag	ttttggtgtc	ctttttcctt	agcctgttgg	attcccagct	gcacagttag	480
attgtgttac	aattcacctt	cttcaagaat	gtggaaatct	ctaattttgt	ctgtgagcca	540
tctcaacttc	tcaagcttgc	ctgttctgac	agcatcatca	atagcatatt	catatatattc	600
gatagtacta	tgtttggttt	tcttcccatt	tcagggatcc	ttttgtctta	ctgtaaaatt	660
gttccctcca	ttctaaggat	ttcaacatca	gatgggaaat	ataaagcctt	ctccacctgt	720
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tcagctgtgt	caccaccccc	caggaatggg	gtgggtgtgt	cagtgatgta	cactgtgggc	840
acccccatgc	tgaacccttt	catctacagc	ctgagaaaca	gggacattca	aagcaccctg	900
cggaggctgc	tcagcagaac	agtcgaatct	catgatctgt	tccatccttt	ttcttgtgt	959

<210> 954

<211> 984

<212> DNA

<213> Unknown (H38g804 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(984)

<223> n = A,T,C or G

<400> 954

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ccagatctcc	agtcccctct	gttcttctgt	tttctagtaa	tctatgtggg	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctt	ttaacttgtc	cttcatagat	ctctgttatt	cttctgtgtt	tatacccaaa	240
atgctaata	actttatttc	agagaagaat	attatgtcct	tcaaggggtg	catgacccaa	300
ctttcctttt	nctgattttt	ttggtcattt	ctgaagggtt	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	tacccactt	ctgtatcaca	ttgccatgtc	tcctacagt	420
tgctccagcc	ttatgtttgg	ttcctatttg	atgccttttt	ctgggtgcat	ggccacact	480
ggatgcatac	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
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actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatggtttc	660
atcctctcca	gcatacctcca	tatcagttcc	aaggagggtg	gggtccaaagc	tttcagcact	720
tgcagttccc	atataattgc	tgtttctctg	ttctttggat	caggtgcatt	tatgtatctc	780
aacccatctt	ctgctgggtc	catggataag	agaaaattat	cttctgtcct	ttatacaaat	840
gtgggttccc	tgttgaaccc	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960

agtcacaaga cagggatatt ctgt

984

<210> 955

<211> 930

<212> DNA

<213> Unknown (H38g805 nucleotide)

<220>

<223> Synthetic construct

<400> 955

atgggaagaa	ataacctaac	aagaccctct	gaattcatcc	tccttggact	ctcctctcga	60
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ggaaacctgc	ttatcatcct	ggccatccgc	tcagacactc	gtctccagac	gcccattgtac	180
ttctttctaa	gcatectgtc	ttttgttgac	atttgctatg	tgacagtcac	tatccctaag	240
atgctggtga	acttcttate	agagacaaag	accatctctt	acagtgaagt	tctgacccag	300
atgtactttt	tcttagcctt	tggaaacaca	gacagttacc	tgctagcagc	catggccatt	360
gaccgctatg	tggccatatt	taatcccttc	cactacatca	ccattatgag	tcacagatgc	420
tgtgtcctgc	ttctggttct	ctccttctgc	attccacatt	ttcactccct	cctgcacatt	480
cttctgacta	atcagctcat	cttctgtgac	tcaaagtgtc	tccatcactt	tttctgcgat	540
gatcaaccag	tgctaaaatt	gtcctgttcc	tcccattttg	tcaaagaaat	cacagtaatg	600
acagaaggct	tggctgtcat	aatgaccccc	ttttcatgca	tcacatcttc	ttatttaaga	660
atcctcatca	ctgttctgaa	gattccttca	gctgctggaa	agcgtaaagc	attttctacc	720
tgtggctctc	atctcacagt	ggtgaccctg	ttttatggaa	gcattagcta	tctctatttt	780
cagccccctg	ccaactatac	tgtcaaggat	caaataagca	caattatcta	caccgtactg	840
actcctatgc	taaatccatt	tatctatagt	ctgaggaaca	aagacatgaa	gcaggggtttg	900
gcaaagtga	tgcacaggat	gaaatgtcag				930

<210> 956

<211> 945

<212> DNA

<213> Unknown (H38g806 nucleotide)

<220>

<223> Synthetic construct

<400> 956

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gacatccctg	aactgcattt	cttggttttt	attgtattca	ctgctgtcta	tgtcttcac	120
atcatagga	atatgctgat	tattgtagca	gtgggttagct	cccagaggct	ccacaaacct	180
atgtatat	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
ccaaaaatgc	tggagggttc	cctgcaagaa	gcaactatct	ctgtggctgg	ttgtctgtc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggcccgaa	420
cggtagatgg	ggctgggtgg	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaaac	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tggatcccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgtc	gagagtctct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgtctct	cccacctagc	tgtagtgaac	acattctatg	gaacgctcat	gatcttttat	780
gttgaccctc	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tctgtgatc	tatacatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

<210> 957

<211> 565

<212> DNA

<213> Unknown (H38g807 nucleotide)

<220>

<223> Synthetic construct

<400> 957

cactggaaaa	ttttaagaag	aaacagcaag	atgatacatg	aaattatata	gaccttatgc	60
caaateccttt	actcagagga	caaaacttgt	tacatacaga	tacaaagctt	gttttgtaact	120
gacttgga	tcccaaactt	tttctgtgaa	cttaattagg	tggtccacct	tgccgtgtct	180
gacacctttc	tcaaagacat	agtgagggtat	tgtacaacta	tgctgctgag	tggtgggtccc	240
attgctggta	tttttttact	ctttctctaa	gatcatttca	tccatatgtg	caatcccac	300
agctcagggg	aagcataaag	catttcccac	ctgctgtgtc	cacctctcaa	atatgtcctt	360
attttattgt	aggagcacag	gattgtacct	tagttttgct	gctaccaca	actcatgtc	420
taatgcaact	gcctcagtga	ggcacactgt	ggttaaacc	ttactaaacg	ttttcatctt	480
aaagtcaagt	aataaagaca	taaaatgagc	tctgaaagta	ttcttcagag	gaaagcaatg	540
gaagcatcat	ttttcaaaaa	gtgca				565

<210> 958

<211> 939

<212> DNA

<213> Unknown (H38g808 nucleotide)

<220>

<223> Synthetic construct

<400> 958

atggaaaaaa	gaaatctaac	agttgtcagg	gaattcgtcc	ttctgggact	tcctagctca	60
gcagagcagc	agcacctcct	gtctgtgctc	tttctctgta	tgtatttagc	caccaccttg	120
gggaacatgc	tcatcattgc	gacgattggc	tttgactctc	acctccattc	ccctatgtac	180
ttcttcctta	gtaacttggc	ctttgttgac	atctgcttta	cgctcgactac	agtcccccaa	240
atggtagtga	atatcttgac	tggcaccaag	actatctctt	ttgcaggctg	cctcaccag	300
ctcttcttct	tcgtttcttt	tgtgaatatg	gacagcctcc	ttctgtgtgt	gatggcgat	360
gatagatatg	tggcgatttg	ccacccctta	cattacaccg	ccagaatgaa	cctgtgcctt	420
tgtgtccagc	tagtggctgg	actgtggctt	gttacttacc	tccacgccct	cctgcatact	480
gtcctaataag	cacagctgtc	cttctgtgcc	tccaatatca	tccatcattt	cctctgtgat	540
ctcaatcctc	tcctgcagct	ctcttgctct	gacgtctcct	tcaatgtaat	gatcattttt	600
gcagtaggcg	atctattggc	tctcacgccc	cttgtctgta	tcctcgtatc	ttatggactt	660
atcttctcca	ctgttctgaa	gatcacctct	actcagggca	agcagagagc	tgtttccacc	720
tgcagctgcc	acctgtcagt	ggtgggtgtg	ttttacggca	cagccatcgc	cgtctatttc	780
agcccttcat	ccccccatat	gcctgagagc	gacactctgt	caaccatcat	gtattcaatg	840
gtggctccga	tgctgaatcc	tttcatctat	accctaagga	acagggatat	gaagagggga	900
cttcagaaaa	tgcttctcaa	gtgcacagtc	tttcagcag			939

<210> 959

<211> 936

<212> DNA

<213> Unknown (H38g809 nucleotide)

<220>

<223> Synthetic construct

<400> 959

atggatggag	gcaaccagag	tgaaggttca	gagttccttc	tcctggggat	gtcagagagt	60
cctgagcagc	agcagatcct	gttttggtatg	ttcctgtcca	tgtacctggg	cacgggtggg	120
ggaaatgtgc	tcatcatcct	ggccatcagc	tctgattccc	gcctgcacac	ccccgtgtac	180
ttcttctctg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaa	240
atgctgggtga	acctccagtc	ccataacaaa	gccatctcct	atgcaggggtg	tctgacgcag	300
ctctacttcc	tggtctcctt	ggtggccctg	gacaacctca	tcctggctgt	gatggcatat	360
gaccgctatg	tggccatctg	ctgccccctc	cactacacca	cagccatgag	ccctaagctc	420
tgtatcttat	tcctttcctt	gtgttgggtc	ctatcgtctc	tctatggcct	catacacacc	480
ctcctcatga	ccagatgtgc	cttctgtggg	tcacgaaaaa	tccactacat	cttctgtgag	540
atgtatgtat	tgctgaggat	ggcatgttcc	aacattcaga	ttaatcacac	agtgtgtgatt	600
gccacaggct	gcttcatctt	cctcattccc	tttggattcg	tgatcatttc	ctatgtgctg	660
attatcagag	ccatcctcag	aataccctca	gtctctaaga	aatacaaagc	cttctccacc	720
tgtgcctccc	atttgggtgc	agtctccctc	ttctatggga	cactttgtat	ggtataccta	780

aagccccctcc	atacctactc	tgtgaaggac	tcagtagcca	cagtgatgta	tgctgtgggtg	840
acacccatga	tgaatccctt	catctacagc	ctgaggaaca	aggacatgca	tggggctctg	900
ggaagactcc	tagataaaca	ctttaagagg	ctgaca			936

<210> 960

<211> 951

<212> DNA

<213> Unknown (H38g810 nucleotide)

<220>

<223> Synthetic construct

<400> 960

atgggaatgt	ccaacctgac	aagactctct	gaatttattc	tcttgggact	ctcctctcgg	60
tctgaagacc	agaggccact	ctttgccctc	tttcttatca	tatacctggt	cactttgatg	120
ggaaatctgc	tcatcatctt	ggctatccac	tctgatcctc	gacttcaaaa	ccctatgtat	180
tttttcctaa	gcattctgtc	ctttgctgat	atttgctaca	caacagtcac	agtcccaaag	240
atgctcgtga	acttcttatc	agagaaaaag	accatttcct	atgctgaatg	tctggcacag	300
atgtatttct	tcctggtttt	tggaaacata	gatagttatc	tcctggcggc	tatggccatc	360
aaccgctgtg	tagccatttg	taaccatttc	cattatgtca	ctgttatgaa	ccgcagatgc	420
tgtgtgttgc	tactagcatt	ccccatcact	ttctcctatt	tccactctct	cctacatgtc	480
ctcctgggtga	atcggtcac	cttttgtaca	tcaaagtgtt	tccatcattt	tttttgtgat	540
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attctcatcg	ctgttctcaa	gattccctca	gcagctggaa	aacacaaagc	cttctccacc	720
tgcagctccc	atctcactgt	ggtgattctg	ttttatggga	gtattagcta	tgtctatttg	780
cagcctttgt	ccagctatac	tgtcaaggac	cgaatagcaa	caatcaacta	cactgtgttg	840
acatcagtgt	tgaaccatt	tatctacagt	ttaagaaaca	aagacatgaa	acggggctta	900
cagaaattga	taaacaagat	taagtctcaa	atgagtaggt	tctctacaaa	g	951

<210> 961

<211> 926

<212> DNA

<213> Unknown (H38g811 nucleotide)

<220>

<223> Synthetic construct

<400> 961

atgctgaata	caacctcagt	cactgaattt	ctccttttgg	gagtgcacaga	cattcaagaa	60
ctgcagcctt	ttctcttcgt	tgttttcctt	accatctact	tcatcagtgt	ggctgggaat	120
ggagccattc	tgatgattgt	catctctgat	cctagactcc	attcccctat	gtattttctt	180
ctgggaaacc	tgtcctgcct	ggacatctgc	tactccagcg	taacactgcc	aaaaatgctg	240
cagaacttcc	tctctgcaca	caaagcaatt	tctttcttgg	gatgcataag	ccaactccat	300
ttcttccact	tcctgggcag	cacagaggcc	atgttggttg	ccgtgatggc	atttgaccgc	360
tttgtggcta	tttgcaagcc	acttcgctac	actgtcatta	tgaaccctca	gctctgtacc	420
cagatggcca	tcacaatctg	gatgattggt	tttttccatg	ccctgctgca	ctccctaattg	480
acctctcgct	tgaacttctg	tggttctaac	cgtatctatc	acttcttctg	tgatgtgaag	540
ccattgctaa	agctgagctt	aatcagtggt	tgctcagtac	tgctcacagg	acaatcgcca	600
tgggcccctt	ctttctcaca	ttactctcct	atttctacat	tatcaccat	ctcttcttca	660
agactcattc	tttttagcatg	ctccgcaaag	cactgtccac	ttgtgcctcc	cacttcatgg	720
tagttattct	tttgtatgca	cctgttctct	tcacctatat	tcatcatgcc	tcagggaacct	780
ccatggacca	ggaccggatc	actgccatca	tgtatactgt	ggctactcca	gtactaaacc	840
cactgatcta	cactttgagg	aacaaggaag	tgaaaggggc	ctttaataga	gcaatgaaaa	900
ggtggctttg	gcctaaagaa	atcttg				926

<210> 962

<211> 983

<212> DNA

<213> Unknown (H38g812 nucleotide)

<220>

<223> Synthetic construct

<400> 962

tcagtggacc	aagtaaata	ctctctggta	acagaatttg	tattacttgg	acttgacaaa	60
tccttggaaa	tgcagttttt	cctttttctc	ttcttctctt	tattctatgt	gggaattatc	120
ctgggaaacc	tcttcattgt	gttcacagtg	atctttgatc	ctcacttaca	ctcccccattg	180
tatattctgc	tggccaacct	atcgctcatt	gacttgagcc	tttcatctac	cacagttcct	240
aggttgatct	acgatctttt	tactgattgt	aaagttattt	ccttccataa	ttgtatgata	300
caaaagttct	ttatccatgt	tacgggagga	gttgaaatgg	tgctgctgat	agtcattgaa	360
tatgataggt	acactgcat	ctgcaagcct	ctccactatc	caactattat	gaatcccaaa	420
atgtgcatgt	ttttggtagc	agcagcttgg	gtcattgggg	tgattcatgc	tatgtctcag	480
tttgtttttg	tcataaatta	accttctgtg	gccctaataa	tgtggggagc	ttttattgtg	540
atcttctctg	ggttattaaa	cttgcatgca	tggacactta	cgggctagaa	tttggtgtca	600
ctgccaacag	tggattcata	tcgatgggca	ccttcttttt	cttaattgta	tcatacattt	660
ttattctggg	cactgtccaa	cgacattcct	caaattgattt	atccaaagca	ttcttccatt	720
cgtaggctca	catcacctga	gtggttttgt	tttttgctcc	atgcatgttt	ctctacgtgt	780
ggcctttccc	tactaagctc	ttggataaat	ttttggccat	catgaacttt	gttgctaccc	840
ctgtcttaaa	tcctgccatc	tatactttta	ggaacaaaga	tatgaagttt	gcaatgagaa	900
ggctgaatca	acataatttt	aattctatgg	agacgacata	acacatttgg	ttgatgagag	960
cacaggataa	atgccatgga	cca				983

<210> 963

<211> 817

<212> DNA

<213> Unknown (H38g813 nucleotide)

<220>

<223> Synthetic construct

<400> 963

atgtggatca	acaatcaaag	ctcgctagat	gattttatcc	tattgggatt	ttctgaccgt	60
ccctggctag	agacaccctt	ctgtaatctt	tctgggtggc	tacatctttt	ccctatttgg	120
aaatatctcc	attatcctag	tttcccatct	ggatccccag	cttgacagtc	ccatgtactt	180
ttttgtctct	aatctatcct	ttctggacct	ctgctatacc	accagcactg	tcccacagat	240
gctgggtcaac	ctccggggac	cagaaaagac	cattagctat	gggggttggt	ttgcccactt	300
ctatatattt	ttggccctgg	gttctactga	atgcatactt	ctagccatca	tggcctttga	360
ccgttacgct	gccatattga	agccccctca	ctaccagctc	atcatgaacc	atagacgctg	420
tatcccatag	gctgctggca	cttggatcag	tggctttgct	aactcccttg	tccagtccac	480
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tccagccctt	ttgaaactag	cctgtattga	tattcgtgtg	aatgaaatgg	agctcaatgt	600
actaggcgct	ttgcttctcc	tgatgccact	caccctcatc	ctgggcactt	atgtgttcat	660
tgctcaggca	gtaatgagaa	tctgctctgc	tgaaagtcgc	tggaaggctt	tcaatacctg	720
tgctcaccat	ttgctgggtg	tctccctctt	ctacttcaca	gccatcagta	tgtatgtcca	780
gcctccctct	agctattctc	atgaccgggg	gaagatc			817

<210> 964

<211> 945

<212> DNA

<213> Unknown (H38g814 nucleotide)

<220>

<223> Synthetic construct

<400> 964

atgaatgtct	ctgagccaaa	ttccagcttt	gctttttgtaa	atgaatttat	actccaaggt	60
ttctcttgtg	agtggacaat	tcagatcttc	ctcttctcac	tctttactac	aacatatgca	120
ctgactataa	cagggaaatg	agccattgct	tttgtctgtg	ggtgtgaccg	gcgacttcac	180
actcccatgt	acatgttcct	gggaaaattt	tccttttttag	agatatggta	tgtctcttct	240
acagttccca	agatgttggt	caacttcctt	tcagagaaaa	aaaacatctc	ctttgctgga	300
tgttttctcc	agttttatatt	cttcttctct	ttgggtacat	cagaatgctt	gcttttgact	360

gtgatggcct	ttgatcagta	ccttgctatc	tgccgtccct	tgctctatcc	taatatcatg	420
actggggcatc	tctatgccaa	actgggtcata	ctgtgctggg	tttgtggatt	tctgtgggttc	480
ctgatcccca	ttgttctcat	ctctcagatg	cccttctgtg	gcccacacat	tattgaccat	540
gttgtgtgtg	acccagggcc	acgatttgca	ttggattgtg	tttctgcccc	aagaatccaa	600
ctgttttgc	acactctaag	ctcattagtt	atttttggtg	acttcctctt	tattattgga	660
tcctatactc	ttgtcctgaa	agctatgttg	ggtatgcctt	caagcactgg	gagacataag	720
gccttctcta	cctgtgggtc	tcatttggct	gtgggtatcac	tgtgctatag	ctctcttatg	780
gtcatgtatg	tgagcccagg	actcggacat	tctacaggga	tgcagaaaat	tgaaactttg	840
ttctatgcta	tggtgacccc	actcttcaat	ccccttatct	atagcctcca	gaataaggag	900
ataaaggcag	ccctgaggaa	agttctgggg	agttccaaca	taatc		945

<210> 965

<211> 915

<212> DNA

<213> Unknown (H38g815 nucleotide)

<220>

<223> Synthetic construct

<400> 965

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctg	cttggtcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtgat	cctcatagcc	atgggctatg	acagatatat	agcaatatgc	360
aaaccactaa	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgcccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtctt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgtctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 966

<211> 953

<212> DNA

<213> Unknown (H38g816 nucleotide)

<220>

<223> Synthetic construct

<400> 966

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cccaactttc	agagttggca	gcacttgcgt	tccttgcccc	tcagcctcat	ttcctcctgg	120
ccatggggac	caacacccac	cccccccatc	accatccacc	tgagggcctc	tctgcacctg	180
ccctgtact	acctgcccag	cctcctctcc	ctgctggaca	tcgtgctctg	cctcaccgtc	240
atccccaaag	tcctggccat	cttctgggtt	gatcttaggt	cgatcggctt	ccctgcctgc	300
ttccttcaga	tgttcatcat	gaacagtttc	ctccccatgg	agtcctgcac	attcatggtc	360
aaggactatg	atcattatgt	ggccatctgc	cacccactgc	agtacctgtc	catcatcact	420
catcaatttg	tggccaaagc	tagtgtcttc	attgtgggtg	agaatgcttt	gctgctttca	480
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taccaatttg	tggctgggtg	gaccttctctg	ggctcggatt	tcatectcat	cttctctctc	660
tacaccttca	ttctaagagc	tgtgcttaga	tcaagggtg	aggggggtgg	agtgagggcc	720
ctgagcacat	gtggctccca	ctttatcttc	atcctcttct	tcagcacctg	ctggttgtgg	780
tgttgacaaa	tgtggccaga	aagaaggctc	ccatggacat	cctgatcctg	tttaatgtcc	840
ttcctccctt	tagtctctct	gcattaaacc	ctatcatatg	tggatttcaa	actaaagagt	900

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg

953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

aaacacaatc	acacggcagt	gaccaagggtg	actgaattta	ttctcatggg	gattacagac	60
aaccctgggc	tgcaggctcc	actgttttga	ctcttctcca	tcatatatct	ggtcacagt	120
ataggcaatc	tgggcatggt	tatctttgac	ctacttttga	ctccaagcta	cacaccccca	180
tgtacttttt	ccttaaacad	ttggcaatca	ctgatctttg	gttactccac	tgtcattggg	240
ccccaaagat	gtttagttaa	acctcatatg	tgcacaaaga	acacaatttc	ttttacaatt	300
ggtatgcaa	tcacagagca	cgctttgaga	ggaacatcat	ctctcaccgc	ggcattctat	360
cagcaacgaa	caatgagccc	tacaaaccca	tcactaaaca	acttctgaac	ccgatcatca	420
tgccagagaa	aatacgggag	gagcaaataa	ccgttcccga	gctcgataaa	acgtgtgcgc	480
cactatttct	caaaaggaag	tgagtcaaaa	cagtctccac	caaccagagc	acaaccaaca	540
attgtcacgg	tgaagggacc	gctaaaatgt	gaatactccg	ttctgaaaaa	aagaaaataa	600
caataataaa	ggcgatgacc	gcaggaaccg	aacatgctca	tctccctctc	aattgttctc	660
atatactaca	tgtttattct	agtggccaat	ctcagaatga	actcaaggaa	agggagggtac	720
aaagccttct	ccacctgtag	ctctcatctg	acagtgggtga	tcatgttcta	tgggacattg	780
ttattttatt	acctgcaacc	caagtccagt	catacttttg	ctattgataa	aatggcctca	840
gtgttttata	ccctgttgat	tcctatgctg	aatccgttga	tctacagcct	aaggaacaaa	900
gaagtaaaag	atgctctaaa	gagaacttta	accaatcgat	tcaaaattcc	catt	954

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

tccaacctgt	gctgggctga	catcggtttc	acctcggcca	tggttcccaa	gatgattgtg	60
gacatgcagt	ctcatagcag	agtcateccct	tatgcgggct	gcctgacacg	gatgtctttc	120
ttggtccttt	ttgcatgtat	agaagacatg	ctcctgactg	tgatggccta	tgactgcttt	180
gtagccatct	gtcgccctct	gcactaccca	gtcatcatga	atcctcacct	ctgtgtcttc	240
ttcgtttttg	tgctcttttt	ccttagcctg	ttggattccc	agctgcacag	ttagattgtg	300
ttacaattca	ctttcttcag	taatgtggaa	attgctaatt	ttgtctatga	gccatctcaa	360
cttctcaacc	ttgactgttc	tgacaccgtc	atcaatagca	tatttatata	tttcgatagt	420
actgttttgt	tttcttccca	tttcagggat	cctttgtctt	agtataaaat	tgtcccctcc	480
attctaagga	tgatcatctc	agatgggaag	tataaagcct	tcgccacctg	tggtctctac	540
ctagcagttg	tttgctgatt	tgatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	600
tcaccacccc	ccaggaatgg	tgtggcgggc	tcagtgatgt	acgctgtggt	cacccccatg	660

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

atggaaaaaa	gcaataatag	cactttgttt	attctctttg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgattttctat	cacgtgcacc	cagctcattc	accaacccat	gtattttctc	180

ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgacccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttggagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttgttg	tactggggga	tttatacatt	ctgccagtca	gtttctcttc	480
accatctttg	taccattttg	tggcccaaat	gagatagtc	actacttctg	tgatgtgtat	540
cctttgctga	aattggcctg	ttctaataata	ccatgatag	gtctcttagt	cattgctaata	600
tcaggcttaa	ttgctttggt	gacatttgtt	gtcttgttgt	tgtcttatgt	ttttatattg	660
tataccatca	gagcatactc	tgcagagaga	cgcagcaaag	ctcttgccac	ttgtagtctt	720
catgtaattg	ttgtggtcct	gttttttgc	cctgcattgt	tcatttacat	tagaccggtc	780
acaacattct	cagaagataa	agtgtttgcc	cttttttata	ccatcattgc	tcccatgttc	840
aacctctca	tatacacgct	gagaaacaca	gagatgaaga	acgccatgag	gaaagtgtgg	900
tgttgtcaaa	tactcctgaa	aagaaatcaa	ctt			933

<210> 970

<211> 666

<212> DNA

<213> Unknown (H38g820 nucleotide)

<220>

<223> Synthetic construct

<400> 970

cggaacttct	ctttcttaga	aatctcattt	acaaccgtat	gcacccccag	atttctgggg	60
gcaattatca	ccaggaataa	gactatttcc	tataacaact	gtgcagccca	actctttttc	120
tttatcttca	tgggggtgac	tgaattttac	attttaactg	ccatgtccta	tgaccgctat	180
gttgccatct	gcaagcccoct	tcattacaca	tccatcatga	acaggaaact	ctgcactcta	240
cttgtgctgt	gtgcctgggt	aagtgggttt	ccgaccattt	tcccaccctt	tatgcttctc	300
ctccagctgg	actactgtgc	ttccaacgct	attgatcact	ttgcatgtga	ctattttccc	360
ctcttacaac	tatcttggtc	agatacatgg	ctcctagaag	taattgggtt	ttactttgct	420
ttggttactt	tgctgttcac	tttggcatta	gtgattttat	cttacatgta	cattatcagg	480
accattttga	gaatcccgtc	tgccagtcaa	agaaaaaagg	ctttctccac	ttgttcttct	540
cacatgattg	tcatttccat	ttcttatgga	agctgtatat	tcatgtatgc	taatccatct	600
gcaaaagaaa	aggcatcatt	gacaaaagga	atagctattc	tcaatacatc	tgttgccccc	660
atgctg						666

<210> 971

<211> 799

<212> DNA

<213> Unknown (H38g821 nucleotide)

<220>

<223> Synthetic construct

<400> 971

ataattttgt	gttttttcat	cataggtaac	tctcaggata	attcccaaata	gactttgatg	60
gataacattt	cagaagtgtg	agaattcggt	ctcgtggggt	taacagatgt	cctagagctt	120
caggctccct	tatttatcat	ctttactgtc	atttatctca	ccactctggt	tgggaacttt	180
gggatgatca	tggtgattct	gttggtactc	cgggtccaca	ttcccatgta	ctttttccct	240
ggcaaaactc	ctctgggtga	cagtgtttgt	cctgctagtc	actggctcct	acatctgtgg	300
actctttcaa	tcctccatcc	atgttgcttt	tactttccat	ctctccttct	gtcattctaa	360
tgtggttaat	cacttttttt	gtgatattcc	accactctta	gctctttctt	gctctgatat	420
ttacgcacat	gagattgtgc	tcttcataat	ggcagcattt	aatatctttt	tcactctctt	480
gattatcttg	aactcttatg	tttttatatt	tattgctatc	ctgaggatgc	attcagctga	540
gggacaaaag	aagggtcttt	ccacctgtgc	ctatcacctc	actactgttt	ccatcttcta	600
tgggacaatc	acctttatgt	acttacagcc	aagttctggt	cattccatgg	acacagacaa	660
aatctcatct	gtgttctaca	ccatgggtcat	ccccatgctt	aacctcttag	tctatagcct	720
gaggaacaaa	gaagtccaga	gtgcattcaa	ggtggttatt	ggaaaagcaa	agtcttcatt	780
gggcttagcc	tactattta					799

<210> 972

<211> 946
 <212> DNA
 <213> Unknown (H38g822 nucleotide)

<220>
 <223> Synthetic construct

<400> 972

tggtaacctg	tcttcaacca	gtctgcccc	ctgagtttgt	gttccgtgtg	ttcaccacag	60
tccctgaatt	tcaggttctt	ctcttccctc	tcttccctct	cttctacttg	atgacccctc	120
gtggcaacac	agccatcatc	tgggttgtgt	gcacatacag	cggtctccga	accccaatgt	180
atttcttctt	gtccaacctg	tcctttgtag	agatctgcta	caccaccgtt	gtggtgccct	240
tgatgctttc	caacattttt	ggggcccaga	agccatttcc	attggctgga	tgtggggccc	300
aaatgttctt	ctttctcaca	cttgggtggt	ctgactgttt	cctcttggcg	atcgtggcct	360
atgaccgcta	tgtggccatc	tgccaccctt	tgcactaccc	ctcatcatga	cctgcaatct	420
gtgctgagag	atgctgggag	gcgctgtggg	cctggccctc	tccctctccc	tgcagctcac	480
cgccttaatc	ttcaccttgc	ccttctgcgg	ctaccgccag	gaaattaacc	acttccctctg	540
cgatgtacct	cccgtcctgc	gcctggcctg	cgctgccatc	cggtgttacc	aggtgtgctt	600
ctatgtcgtg	agcatcctcg	tgtgaccgtg	ccccctcttg	ctcatctgag	tctctacgtt	660
gttcatcacc	tgtgccatcc	tgagcatccg	tctgtctgag	ggccgccacc	aggccttctc	720
cacctgctcc	tcccacctca	ccgtggctct	gctgcagtat	ggctgctgtg	ccttggcata	780
cttgcacccc	cagtccagct	cctctgcaga	tgaggatcgc	cagtttgccc	ttgtttacac	840
ctttatcaca	ccattactca	accctttgat	ttacaccctt	aggaacaagg	atgtcaaagg	900
tgccttgtaa	aaaagtgtct	agtaccaaag	ggacacctga	gtcctt		946

<210> 973
 <211> 936
 <212> DNA
 <213> Unknown (H38g823 nucleotide)

<220>
 <223> Synthetic construct

<400> 973

atgtagaaca	gtagagaggg	gtcacagttc	atcttccctag	gactaagcaa	tgtcccagaa	60
ctgcaggtcc	ccttctttat	catgtttgtt	ctcatctatc	tcataaatgt	agttggaaac	120
ttggggatga	tcattttgat	tctctgggtac	tctcagctcc	acaatccaat	gtacttcttc	180
ttcagtaatc	tgtctctggt	agactttttt	tactcttcag	ttgtcactcc	aaaggtcatg	240
actgggctcc	ttagagaaga	caaaatcatt	tcctatactg	tgtgggctac	tcagacattc	300
ttttctgatt	cctttgccag	tgtggtaaat	ttattattgg	ccttaatggc	ctctggccac	360
tatgcagcag	tgtgcaaacc	cctgcattac	accaccacca	tgatgacaag	tgtgtgtaca	420
tgtctggcca	taggttgata	cggtgggtgt	ttcctgaatg	cctccattca	cactggggaa	480
acattcagtc	tctttctgta	tgtccagtga	agtccatcac	tttttctgtg	aggttccagc	540
agtcattggc	ctgtcttgct	ctgatagaca	tgtgaatgta	gtggttcttg	tttatgtaac	600
cagctcaata	tcctctttgc	ccttctagtt	atcttgatat	cctacttatt	gatgtttatc	660
accatcctaa	agatgcactc	aactgcagga	taccagaagg	ctttggccat	ttgtgectct	720
cacctcactg	cagttgccat	cttctatggg	actattatct	tcatgcatat	acagcccagc	780
tccagtcatt	ccattgacac	agacaaaatt	gcagctgtgt	tttatactat	tgtcttcccc	840
atgggtgaacc	atgtggtcta	aagattgaag	aacaaggtga	agagtacatt	caagaaaatt	900
gttgagaagg	taaaattgtc	cctaggattg	tgagtt			936

<210> 974
 <211> 954
 <212> DNA
 <213> Unknown (H38g824 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(954)

<223> n = A,T,C r G

<400> 974

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aaggccctgc	agggccccc	gttctgggtg	gtgcttctgg	tctacctggt	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaactctc	agtgggtggg	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcattgt	cctgggcac	tcggagtgt	gcctgtcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgtatt	ccaccctctt	gagcccacgg	420
gcctgcatgg	ccatgggtgg	tacctcctgg	ctcacaggca	tcatacagg	ccaccacca	480
tgccctccct	atcttctctc	taccttttct	cagccaccgc	atcatccgc	acttttctct	540
tgacatcctg	ccagtactga	ggctggcaag	tgctgggaag	cacaggagcg	agatctccgt	600
gatgacagcc	accatagtct	tcattatgat	ccccctctct	ctgattgtca	cctcttacat	660
ccgcatacct	gggtgccaat	tagcaatggg	cctcacccag	agccgccgca	agtcttctcc	720
acctgtctct	cccataggct	cgtgggtctct	ctcttctttg	ggacagccag	catcacnnac	780
aaccggccgc	aggcaggctc	ctctgaaacc	acagaccgcg	tcatacgtct	cttcnacaca	840
gtcatcacac	ccatgtctaa	ccccatcata	aacaccacag	ggaacaagga	cgtgaggagg	900
gccttgcggt	acttggtgaa	gaggcgccgc	ccctgcgcgg	gaaggggctc	gggt	954

<210> 975

<211> 933

<212> DNA

<213> Unknown (H38g825 nucleotide)

<220>

<223> Synthetic construct

<400> 975

atggagacaa	agaattatag	cagcagcacc	tcaggcttca	tctcctggg	cctctcttcc	60
aaccctaagc	tgcagaaacc	tctctttgcc	atcttctca	tcatagtacct	actcactgcg	120
gtgggggaatg	tgctcatcat	cctggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagattatct	cttatgtggg	ctgcctgac	300
cagatgtact	tcttcatggc	atttggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccatgg	420
cattgcctac	tcatagtatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacaccacgc	ctgtgctaaa	gctctcctgc	tctgacacat	cctccagcca	gatgggtggg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttctgt	gtaccatctt	ctcctacctg	660
caaatcatcg	tcactgtgct	cagaatcccc	tctgcagcca	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgtagtggc	ctgttctatg	ggagtgtcat	ctatgtctat	780
tttaggcctc	tgtccatgta	ctcagtgatg	aagggccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaaaagg	900
ggtttgaaga	aattaagaca	cagaattttac	tca			933

<210> 976

<211> 390

<212> DNA

<213> Unknown (H38g826 nucleotide)

<220>

<223> Synthetic construct

<400> 976

atgaaaaata	aaaccgtggt	aactgagttt	atccttctgg	gtctaacaga	tgtccctgaa	60
ctccagggtg	cagttttcac	ctttcttttc	cttgcggtatt	tactcagcat	ccttggaat	120
ctgactatcc	tcatectcac	cttgctggag	tcccaccttc	agactcccat	gtatttcttt	180
ctccggaact	tctccttctt	ggaaatttcc	ttcacaaaca	tcttcattcc	aagggtcctg	240
attagcatca	caacagggaa	caagagtatc	agctttgctg	gctgcttcac	tcagtatttc	300
tttgccatgt	tccttggggc	tacagagttt	taccttctgc	tgccattcct	atgaccgcta	360

tgtgccatct gcaaactgat gactatgcac

390

<210> 977

<211> 933

<212> DNA

<213> Unknown (H38g827 nucleotide)

<220>

<223> Synthetic construct

<400> 977

atggagataa	agaactacag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aaccctcagc	tgcagaaacc	tctctttgcc	atcttctca	tcattgtacct	gctcgctgcg	120
gtggggaatg	tgctcatcat	ccgggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatattctgt	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagggttatct	cctatgtggg	ctgcctggcc	300
cagatgtact	tctttatggc	atttgggaaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccacgg	420
cattgcctgc	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacacccagc	ctgtgctaaa	gctctcctgc	tctgacacat	cctccagcca	gatggtggtg	600
atgactgaga	ccttagctgt	cattgtgacc	cccttctctgt	gtatcatctt	ctcctacctg	660
cgaatcatgg	tcactgtgct	cagaatcccc	tctgcagccg	ggaagtggaa	ggccttctct	720
acctgtggct	cccacctcac	tgcagtagcc	cttttctatg	ggagtattat	ttatgtctat	780
tttaggcccc	tgtccatgta	ctcagtgggt	agggaccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaagagg	900
ggtttgaaga	aattacagga	cagaatttac	cgg			933

<210> 978

<211> 939

<212> DNA

<213> Unknown (H38g828 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(939)

<223> n = A,T,C or G

<400> 978

atgccaaata	agattgtggt	gactgagttc	ttcttcacaa	ggcctgacgg	attacaaaag	60
agctttcagg	tggctgtttt	tctgtccct	gatgcttgcc	ataccttggt	actgtctctg	120
ggaacctgaa	tcattcatcag	ccatgacctt	gctggacacc	cgcatgcaga	catctatgta	180
cttattttctc	cagaatctgt	cctgcttaga	aatttggtcc	agacagtcac	cgtgcccaag	240
atgctgctca	acattgccat	ggggaccaag	accgttagct	ttgctgggtg	cattaccag	300
gactttttcc	acatcttctg	ggggccacag	agttcttctc	cctgacagcc	atggcctatg	360
accagtatat	tgccatctgc	aagcccctcc	actaccccat	gctcataagt	agtagagtct	420
gcacacagct	catcctcacc	tgctggctac	taggtttctc	cttcatcatc	atgcctgtca	480
tcctgaccag	tcagcttcca	ttctgtgata	cccacatcaa	gcatttcttc	tgtgactaca	540
cgctctctaat	ggaggtgggtc	tgcagtgggc	caaaggtgct	ggagatgggtg	gattttaccc	600
tggccttagt	agcactgttt	ggcaccttgg	tactcatcac	cctgtcctat	gtccagatca	660
tccagacaat	tgtcagaatc	cccgtgtgcc	aggagaggaa	gaaggctttc	tctacctgtt	720
cctctcatgt	cattatgggt	accatgtgtt	atgacagctg	cttctttatg	tatgtcaagc	780
cctctccagg	aaagtgggtt	gatgtcaaca	angggagtgt	ctctaataca	tacaattatt	840
gccccactgt	taaatccctt	catctgtact	ctgaggaaac	aacaagttaa	gcaggtaatg	900
aaagacctag	tcagaaaaat	gactttgtcc	gaaaataaa			939

<210> 979

<211> 951

<212> DNA

<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

atgaactcag	agaacctcac	ccgggccg	gttgccctg	ctgaattcgt	actcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttcctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcatggatgc	ccggctccac	180
acacctatgt	acttcttctc	ggccaacctc	tccctgctgg	atgcctgcta	ttctctcgcc	240
atcgcccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgccctcc	agatgtttgt	ctttgcagggt	ctggctgata	ctgagtgttg	cttgctggca	360
gccatggcct	atgaccgcta	cgtggccatc	agaaacccac	ttctctatac	aacagctatg	420
tcgcagcgtc	tatgcctggc	cttgctggga	gcatcaggcc	tgggtggggc	agtgagtgcc	480
tttgttcaca	caacctcac	cttccgctg	agcttctgcc	gctcccggaa	gatcaatagc	540
ttcttctgcg	atatccctcc	actgctggcc	atctcgtgca	gtgacaccag	tctcaatgaa	600
ctccttctct	tcgccatctg	tggcttcata	cagacagcca	cgggtgttagc	tatcacggtg	660
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gcagcctcca	ccggtgggtc	ccacctcaca	gccgtggcca	tgatgtacgg	gacactcatt	780
ttcatgtacc	tgcgccccag	ctccagctat	gccctggaca	ctgacaagat	ggcctctgtg	840
ttctataccc	tggctcatccc	gtctctcaac	ccactcatct	acagcctccg	caataaggag	900
gtcaaggagg	ccctcaggca	gacctggagc	cgattccact	gtccagggca	g	951

<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

atgggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtgtt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tctcctgggt	gaacttgtcc	tgtctggaga	tctggtatac	ctctaaccac	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgtacact	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
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atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcacttc	tcctgcatgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atccccatct	gcacaggcca	gaaaaaggcc	720
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acataccttg	tgccttcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggtg	tttgcctt		948

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

gagtaaattgg	gaacaagtaa	taatgttaca	gaatttgtcc	tcccaggcct	ctctcaggat	60
cctgatgtgc	aaaaagcatt	atttgtaatg	tttttactca	catacaatgt	gactatgggtg	120
ggcaaccttc	tcattgtggg	gaccattatt	gccatcgccct	ccttggactc	cccagtgtcc	180

ttcttccctcg	catgcctgtc	atattattgat	gctgtatatatt	ccacttcctt	ttccccctaag	240
ttgatgatag	acttactctg	tgataaaaaa	gactgtttct	ttcctggctt	gcatgggcca	300
gctatttata	aactacccat	ttggtggtat	tgaggtcttt	cttttggtgg	gtatggcctg	360
tgatcactat	gtggacatct	gtaagctact	gcactatttg	accatcatga	actggcaggt	420
ttgcatcctc	ctgtttatgg	tggtgtgtgac	tgagggtttt	tgcattctat	gtttcaaatt	480
gttgttgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccattt	tgtgacatgt	540
acccattatt	ggaaatgggtg	tgcactgaca	cttactttat	aggcctcact	gtgattgcca	600
atgggtggagc	agtctgtatg	gtcatcttca	tccttctact	aatctcctat	ggagtcaccc	660
taaaactccct	taaaacttat	agtcaggaag	gcgggcataa	agccctgtct	acctgcagct	720
ccaacattac	tgttgtgtcc	ccttttttga	tcctgttatt	ttcatctatg	ttagacctga	780
ttcaaacttt	cctattgata	aattcatgac	tgtgttttat	acaattatca	cacccatgtt	840
gaatccatta	atatacacac	tgagaaattt	agaggtgaga	attgctgtga	aaaatctctg	900
gtgtaaaaac	taaactatag	taaga				925

<210> 982

<211> 958

<212> DNA

<213> Unknown (H38g832 nucleotide)

<220>

<223> Synthetic construct

<400> 982

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atccttttct	tttttggttc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccaggctact	180
gcctactggc	caacatttat	cttcttgatc	tgggtcttct	cctacagtcc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcattgatac	agatattttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgctgtcat	aacctatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tactttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttctact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagacac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatcctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgcaggttct	900
agcaggatgt	cataataaat	ggtgcataatc	cagagtgcac	gatgattcag	tctcacca	958

<210> 983

<211> 927

<212> DNA

<213> Unknown (H38g833 nucleotide)

<220>

<223> Synthetic construct

<400> 983

atggaaggaa	taaataaaaac	tgcaaagatg	cagtttttct	ttcgtccatt	ctcacctgac	60
cctgagggtcc	agatgctgat	ttttgtgggc	ttcctgatga	tgtatctgac	cagcctcggt	120
ggaaatgcta	caattgcagt	cattgttcag	atcaatcatt	ccctccacac	ccccatgtac	180
tttttccctgg	ctaattctggc	agttctagaa	atcttctata	catcttccat	caccccatgtg	240
gccttggaac	acctcctttc	aatgggcaaa	actcctgttt	ccatcacggg	atgtggcacc	300
cagatgtttt	tctttgtctt	cttgggtggg	gctgattgtg	tcctgtctgt	agtcattggt	360
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ttgtgtgtgg	agctgctggt	aggctccttg	gtgctggggg	tcctgtttgt	actgccactc	480
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gacatgctgc	cctggcctgc	cttggcctgt	gcagacacac	gcgttcacaa	gactgctctg	600
tatatcatca	gcttcatcgt	ccttagcatc	ccccctctac	tgatctccat	ctcctatgtc	660
ttcatcgtgg	tagccatttt	acggatccgg	tcagcagaag	ggcgccagca	agcctactct	720

acctgctctt ctcacatctt agtggctctc ctgcagtatg gctgcaccag ctttatatac	780
ttgtcccccga gttccagcta ctctcctgag atggggccggg tggatatctgt ggcctacaca	840
tttatcactc ccatttttaa ccccttgatc tatagtttga ggaacaagga actgaaagat	900
gccctaagga aagcattgag aaaattc	927

<210> 984

<211> 987

<212> DNA

<213> Unknown (H38g834 nucleotide)

<220>

<223> Synthetic construct

<400> 984

gattcagtg accaagtaaa tgactctctg gtaacagaat ttgtattact tggacttgca	60
caatccttgg aaatgcagtt tttccttttt ctcttcttct ctttattcta tgtgggaatt	120
atcctgggaa acctcttcat tgtgttcaca gtgatctttg atcctcactt acactcccc	180
atgtatatct tgcctggccaa cctatcgctc attgacttga gcctttcacc taccacagtt	240
cctaggttga tctacgatct ttttactgat tgtaaagtta tttccttcca taattgtatg	300
atacaaaagt tctttatcca tgttacggga ggagttgaaa tgggtgctgct gatagtcagt	360
gcatatgata ggtacactgc gatctgcaaa cctctccact atccaactat tatgaatccc	420
aaaatgtgca tgtttttggg agcagcagct tgggtcattg ggggtgattca tgctatgtct	480
cagtttgggt ttgtcataaa tttacccttc tgtggcccta ataatgtggg gagcttttat	540
tgtgattttc ctccgggttat taaacttgca tgcattggaca cttatgggct agaatttgtg	600
gtcactgcca acagtggatt catatcgatg ggcaccttct ttttcttaat tgtatcatac	660
atctttatct tggctcactgt ccaacgacat tcctcaaagt atttatccaa agcattcttc	720
acttcgtagg ctcacatcac cgtagtgggt ttgttttttg ctccatgcat gtttctctac	780
gtgtggcctt tccctactaa gtcattggat aaattttttg ccatcatgaa ctttgttgct	840
accctgtct taaatcctgc catctatact ttaaggaaca aagatatgaa gtttgcaatg	900
agaaggctga atcaacatat tttaaattct atggagatga cataacacat ttggttgatg	960
agagcacagg ataaatgcca tggacca	987

<210> 985

<211> 770

<212> DNA

<213> Unknown (H38g835 nucleotide)

<220>

<223> Synthetic construct

<400> 985

tccatgtact tcttcctgac aaactttgca ggtctggaga tcttctactt tttcaccatt	60
gcccctctga ctctggccaa tgtcctaccc atggggagaa acctcatttc cctgcccggc	120
tgtggaggcc agatgttctt cttcatcttc ctgggaaggg ctgactgcat cctgctggcc	180
gtcatggcct ttgactgggt tgtggccatc tgttgtctc tctgttacgg cctcatcatg	240
agctggagggt tgtgtgtcca gctgacctg ggggtctctgc tgttgggggt cttcttagcc	300
atgcagctga ccgtgcttat cttccaactc cctttatgca gcagcaaaga aatcagcacg	360
ttctactgtg atgtcctccc tgtcatgaga ctggcctgtg cagatacctg ggtccatgag	420
gccactatgt ctatggctcag caccaccttt ctaccgtcc ccttctctgct catcactctt	480
tcctatgtct ccatcatggc cgccatcttg aagatttgc ctgcagaggg gaggcacaag	540
gccttctcca ccttctctcc cacctgactg tgggtctctc ccaggactga tgtacacgcc	600
tcgccttctt gtgtccacg tctagctact atcctgagag gggccaggca gtgtctgtgg	660
tttacacctt cattaccct gtgctgaacc ctttgatcta cagcatgagg aacacagaac	720
ttaaggatgc tttgaagaga gcaatgacga gggctcccgt gctctaaaca	770

<210> 986

<211> 915

<212> DNA

<213> Unknown (H38g836 nucleotide)

<220>

<223> Synthetic construct

<400> 986

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttecta	60
tttatgtgt	tttttgatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgytat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgac	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
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ggtgggagt	agatgggtgat	cctcatagcc	atggggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttacct	480
ttctgtggc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggctcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
tgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtgttt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 987

<211> 958

<212> DNA

<213> Unknown (H38g837 nucleotide)

<220>

<223> Synthetic construct

<400> 987

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atctttttct	tttttgggtc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcattgtgtt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacatttat	cttcttgatc	tgggtcttct	cctacagtgc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcatgatac	agatattttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgtgtctcat	aaccatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagatac	ttacaaacta	gagggtttag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatectata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttctct	ttgtatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgcaggttct	900
agcaggatgt	cataataaat	ggtgcatatc	cagagtgcac	gatgattcag	tctcacca	958

<210> 988

<211> 982

<212> DNA

<213> Unknown (H38g838 nucleotide)

<220>

<223> Synthetic construct

<400> 988

ctttctattt	gcttctttct	ttgcatattt	tcagctgata	tttaattctat	gctagccatg	60
gaacaaaata	atggcactga	agtgcactgaa	ttcattctcc	tgggatttgc	tgggtcaaac	120
aagtcttggc	atatectctc	catagcattt	ctagcaatct	atgtgggtac	cccagtaggt	180
aatattggaa	tgatcctact	tatcaaaatt	gatgcttctc	ttcatatccc	catgtaaatt	240
ttcctccaac	acttggcatt	tgttgatctc	tgttacacct	ctgctatcac	tcccaagatg	300
ttgaaaaact	ttgtagaaac	aaaaaaatct	atctcatgta	taggatgtat	ggtgcaatta	360

ctagtttatg	gtacttttga	acaagtgact	gctacatcct	ggctgctatg	gcagtagacc	420
gttatgtggc	cttctgtaac	ccactccatt	atccaggggt	tatgtccag	agactctgca	480
ttaagctatt	agttagtcca	tatgtcatgg	gtttcctaaa	tgccctctata	aacataagtt	540
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ttgtgggatt	aaatttgatg	tgcaactgtga	tggtgggtcat	catttcctgc	atatatgtcc	720
tggttgccat	cctgagata	tcttctgctg	caggggaagaa	aaaagtctct	ctacatgtgc	780
ctcccacctg	acagcagtc	ccatttttcta	tgggggttctc	tcttacatgt	atctatgcc	840
tcgtattaat	gagtcctaaa	aacaagaaaa	agtggcctct	gtgttttatg	gcattattat	900
tcccatgtta	aacccttga	tttacagcca	gagaaaccaa	gatgtgattg	aagccataaa	960
actaacagaa	aaaaagtatt	tc				982

<210> 989

<211> 1006

<212> DNA

<213> Unknown (H38g839 nucleotide)

<220>

<223> Synthetic construct

<400> 989

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ttccacttcc	acttcttttc	aacagacctg	gtgggtggctt	cctttataat	tgtggccttg	120
atgttgcacc	aagaagcctt	gttggacact	tcaccttttg	gcccacagtc	tggcaagatc	180
ccttctctca	tattccaatg	tatttatttt	tatttttttg	gcattgacta	tgttggaat	240
tggtacttcc	accaacattt	ctcctccaac	actggctacc	gtcctttaca	tggggaagat	300
gcttatctcc	ctccctggct	atggaactca	gatgctcttt	gtcatccttt	tgagaggatc	360
tgagtgtgtc	ttgcttgctg	tcattggctta	tgataggat	ataaccatct	gtcatccatt	420
caattacaat	ctcatcatga	gtgggtagct	ctgtgggcag	atgactttgg	gctctttgag	480
gctgggattc	ctgttgtcac	tgtttttgac	tatgttgatc	tgacaccctc	cattctgtgg	540
cctaataaaa	cctaccactt	cttctgtgac	atgcccacag	caagtgcctg	gtctgtgcag	600
acaccacatg	catgagtcag	ctctctgact	tccgtgtggc	caccatcacc	atccccctcc	660
ttcctccttg	tctgctctcc	ctatggctgc	cttgagacca	ccatcttgag	gatgcattca	720
gctaagagaa	agcactaggc	cttctctacc	agttcctccc	acctcattgt	ggttctcctg	780
aagtattggg	gttgcatcct	catctgcctt	tgccccagct	ctagttactc	cccagaggag	840
ggctggggag	tatctcttgt	tcacatgttt	ttctcccggg	gtggaatccc	ttgatctata	900
gcgtatggaa	ccaagacgta	actgatgcag	tatagagact	tgtggcaaga	atgtccttgt	960
tctaacagcc	agaaatattc	cttcttaaaa	aatattttccc	taacta		1006

<210> 990

<211> 987

<212> DNA

<213> Unknown (H38g840 nucleotide)

<220>

<223> Synthetic construct

<400> 990

gattcagtgg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggacttgca	60
caatccttgg	aaatgcagtt	tttccttttt	ctcttcttct	cctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatatcc	tgctggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaaagt	tctttatcca	tgttacagga	ggagttgaaa	tgggtgctgct	gatagtcatg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaacccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttc	ctcgggttat	taaacttgca	tgcatggaca	cctatgggct	agaatttgtg	600
gtcactggca	acagtgagtt	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatac	660
atttttattc	tggtcactgt	ccaacgacat	tcttcaaatg	atttatccaa	agcattcttc	720
acttcgtagg	ctcacatcac	cgtagtgggt	ttgttttttg	ctccatgcat	gtttctctac	780

gtgtggcctt	tccctactaa	gtcattggat	aaattttttg	ccatcatgaa	ctttgttgtc	840
acccctgtct	taaatcctgc	catctatact	ttaaggaaca	aagatagaa	gtttgcaatg	900
agaaggctga	atcaacatct	tttaaatctt	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgcca	tggacca				987

<210> 991

<211> 736

<212> DNA

<213> Unknown (H38g841 nucleotide)

<220>

<223> Synthetic construct

<400> 991

atgcaatcag	aacaccttgc	agaattttca	gaattcctca	ttttgagcct	ctcaggagat	60
ccagaactgc	agccccttct	tgggctgttt	ctgtccatga	acctggtcac	agtgccttga	120
aacctgctca	ttatcctggc	catcagttct	gactcccacc	tccacaagcc	tatgtacttc	180
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atggtaaacc	tcagggcaca	gagcaaagac	atctttactc	agccaagtgg	tagtccaatt	300
ccattctaaa	tgtgtagtct	tatcagattt	cttctaattc	agcagaaatc	tgttgtttta	360
atcttcgaat	actcactggg	tctaattctc	ctatttgaat	ctgaagatgt	aaactaatta	420
ttcttttcta	tgagcctttc	aaaataattg	aagacagtta	tgcccttttc	ttgataatca	480
ccatactttc	ttcacactaa	ttgatacaca	attgttaata	agtcattgat	tttctactca	540
aacaaccttt	attctatcat	cttatgcttc	tggttatgca	acagttgact	ctcaatgctt	600
tatttatatt	ttaaacatga	tgattactat	taacctcttt	gtaagattta	aaaatatctt	660
tatgcacagt	agtatctcaa	taaattacaa	ctattatttt	aaaaaataaa	ataaagggtg	720
tatctatgag	atatat					736

<210> 992

<211> 915

<212> DNA

<213> Unknown (H38g842 nucleotide)

<220>

<223> Synthetic construct

<400> 992

atggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
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acagtgggat	ctgactccca	ccttcactct	cccattgact	tccgtctagc	caacctctca	180
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ggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcac	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttaccc	480
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gcctgtacag	atacctacag	gctagatatt	atggctcatt	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttctctt	aatcatctca	tacatatca	tcctaattgac	catccagcat	660
cgcccttttag	ataagtctgc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
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gataaattcc	ttgtctgtatt	ttattctgtg	atcaccctct	tcttgaacct	aattatatac	840
acactgagga	acaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 993

<211> 927

<212> DNA

<213> Unknown (H38g843 nucleotide)

<220>

<223> Synthetic construct

<400> 993

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gggaacctgg	gcatgatcac	tctaatttgt	ctgaactctc	agctgcacac	ccccatgtac	180
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ctctacttct	tccttgtttt	tgctattgct	gagtggtaca	tgctgacagt	gatggcctac	360
gaccgctatg	ttgccatctg	ccaccctttg	ctttacaaca	tcattatgtc	tcatacacacc	420
tgctgtctgc	tggtggctgt	ggctctacgc	atcggactca	ttggctccac	aatagaaact	480
ggcctcatgt	taaaactgcc	ctattgtgag	cacctcatca	gtcactactt	ctgtgacatc	540
ctccctctca	tgaagctgtc	ctgctctagc	acctatgatg	ttgagatgac	agtcttcttt	600
tcggctggat	tcaacatcat	agtcacgagc	ttaacagttc	ttgtttctta	caccttcatt	660
ctctccagca	tcctcggcat	cagcaccaca	gaggggagat	ccaaagcctt	cagcacctgc	720
agctcccacc	ttgcagccgt	gggaatgttc	tatggatcaa	ctgcattcat	gtacttaaaa	780
ccctccacaa	tcagttcctt	gacccaggag	aatgtggcct	ctgtgttcta	caccacggta	840
atccccatgt	tgaatcccct	aatctacagc	ctgaggaaca	aggaagtaaa	ggctgccgtg	900
cagaaaacgc	tgaggggtaa	actgtttt				927

<210> 994

<211> 930

<212> DNA

<213> Unknown (H38g844 nucleotide)

<220>

<223> Synthetic construct

<400> 994

atggcagcca	aaaactcttc	tgtgacagag	tttatcctcg	aaggcttaac	ccaccagccg	60
ggactgcgga	tccccctctt	cttcctgttt	ctgggtttct	acacggtcac	cgtgggtggg	120
aacctgggct	tgataaccct	gattgggctg	aactctcacc	tgacactcc	catgtacttc	180
ttccttttta	acctctcttt	aatagatttc	tgtttctcca	ctaccatcac	tcccaaaatg	240
ctgatgagtt	ttgtctcaag	gaagaacatc	atttccttca	caggggtgat	gactcagctc	300
ttcttcttct	gcttctttgt	cgtctctgag	tccttcaccc	tgtcagcgat	ggcgtatgac	360
cgctacgtgg	ccatctgtaa	cccactgttg	tacacagtca	ccatgtcttg	ccaggtgtgt	420
ttgtctcttt	tggtgggtgc	ctatgggatg	gggtttgtcg	gggccatggc	ccacacagga	480
agcataatga	acctgacctt	ctgtgctgac	aaccttgtca	atcatttcat	gtgtgacatc	540
cttctctctc	ttgagctctc	ctgcaacagc	tcttacatga	atgagctggg	ggctctttatt	600
gtgggtggctg	ttgacgttgg	aatgcccatt	gtcactgtct	ttatttctta	tgccctcatc	660
ctctccagca	ttctacacaa	cagttctaca	gaaggcaggt	ccaaagcctt	tagtacttgc	720
agttcccaca	taattgtagt	ttctcttttc	tttgggtctg	gtgctttcat	gtatctcaaa	780
cccccttcca	tcctgcccct	cgagcaaggg	aaagtgtcct	ccctgttcta	taccataata	840
gtccccgtgt	taaaccatt	aatctatagc	ttgaggaaca	aggatgtcaa	agttgccctg	900
aggagaactt	tgggcagaaa	aatcttttct				930

<210> 995

<211> 473

<212> DNA

<213> Unknown (H38g845 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(473)

<223> n = A,T,C or G

<400> 995

atgggagaag	caaggaacag	gacagtagtc	caggaattta	tcctggaggg	atttctctgt	60
gtccagcatc	tggggaatgt	ccttttctcg	gtgcacctgc	tggcatacct	ggcctccatc	120
atggcaaaca	tgctcataat	caccatcacc	tgggctgacc	atcacctcca	gacacctatg	180

tattttcttcc	tcagcagttt	ttccttctgt	gaatgctggt	ttatcaccac	agttattcct	240
aaacttctgg	tcatcctttc	tttcaggcag	ggcaaataat	ccccctttct	actaccttgt	300
ctcatgcagt	ccccctttca	tttttatntt	cttgggtcæ	cagtttttct	tcccttaatg	360
gctgtgatgt	cccccttggat	tgatacctgg	ccatttgcaa	gcctctgcat	tactccacca	420
tcatgagcct	gaggactagc	ttccacaagg	tcactgcctg	gctttgtcct	ggg	473

<210> 996

<211> 998

<212> DNA

<213> Unknown (H38g846 nucleotide)

<220>

<223> Synthetic construct

<400> 996

acagacccac	agaatctaac	aacagatgtc	tcaatattcc	tcgtcctaga	actctcagag	60
gatccagaac	tacagccggg	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtcattggtg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatgggtt	cacctccacc	atgggtcccca	240
agatgattgt	ggacatccaa	tctcacagca	gtcatctcct	atgcgggctg	cctgactcag	300
atgtctcttt	ttgccatttt	tggaggcatg	gaagaaagac	atgtcctga	gtgtgatggc	360
cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatta	ttcagccatc	atgaacccat	420
gtttctgtgg	ctttctagtt	ctgttgctct	gttgctcag	tcttttagac	tcccagctgc	480
acaatttgat	tgcccttgcaa	attacctgct	tcaaggatgt	ggaaattcct	aatttcttct	540
gtgacccttc	tcaactcccc	caccatgcgt	gttggtgacac	cttcaccaat	aacatagtca	600
tgtatttccc	tgctgccata	tttggttttc	ttcccacctc	ggggatcctt	ttctcttact	660
ataaaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggaactat	aaagccctct	720
ctgcctgtgg	gtctcacctg	tcagttgttt	gcttatttta	tggaacaggc	gttgagggtt	780
acctcagttc	agatgtgtca	tcttccccca	gaaagggtgc	agtggcctca	gtgatgtaca	840
cggtggtcac	ccccatgctg	aacccttcca	tctacagcct	gagaaacagg	gatattaaaa	900
gtgtcctgcg	gcgcctgcac	ggcagaacag	tctaattctca	atatcttatt	atctgttcca	960
ttccttttgt	agtgtgggtt	taaaaaggca	gcaaggtc			998

<210> 997

<211> 666

<212> DNA

<213> Unknown (H38g847 nucleotide)

<220>

<223> Synthetic construct

<400> 997

agtcaactgt	cccttatgga	cctcatgtct	atctgcacca	ctctacccaa	gatgatcttc	60
agctacttgt	ctgggaagaa	atctatctct	ctggcagggt	gtggaaactca	gatattcttc	120
tatgtgtccc	tgcttgagc	tgaatgtttc	ttgttggtctg	tcattggctta	tgaccgctat	180
gtggctatat	gtcaccctct	tcagtacacc	atcctcatga	atccggaact	ctgtgtcttc	240
atgactgttg	cttcctggac	cttgggggtct	cttgatggga	tcatagtgtct	tgcagctgtc	300
ctgtcatttt	cttactgcag	ctctctggaa	attcatcatt	ttttctgtga	tggtgtgtcc	360
cttttacctc	tatcctgcac	agaaacatct	gcatttgaaa	gactacttgt	catttggtgt	420
gtggtaatgc	taatctttcc	agtttcagtt	atcatacttt	cctattccca	tgctcttcca	480
gccgtcatcc	acatgggctc	tggggaaaagt	cgctcgcaagg	ccttcactac	ctgtctctcc	540
caccgctctg	tggtcggact	ctactacggt	gctgtctatgt	tcattgtacat	gagaccagct	600
tctaaacata	cgccagacca	ggacaagatg	gtgtcggcct	tctacactaa	tctcaccctc	660
atgctg						666

<210> 998

<211> 342

<212> DNA

<213> Unknown (H38g848 nucleotide)

<220>

<223> Synthetic construct

<400> 998

cttgccctgca tagttggata gaagtttgca tttattattt ctccaaacca tcacttcatg	60
ataatgggtca cattcatattt agttaacatt taaaaacatt cttcaggaaa cttatccagt	120
gctcttatca ttttgttcat tttcatccct gttgtttctc tatttttcac tccatgcgta	180
gttctctatg tttggcctac tttgccacca tcacttgata aaaatatgtt cattgttgac	240
tttgttgtea accctgtctt gaagcctgcc acctacatat tacagaacaa agacataaag	300
gtagcacttt gaaatttgca tgaaaagaga acttattcca gc	342

<210> 999

<211> 915

<212> DNA

<213> Unknown (H38g849 nucleotide)

<220>

<223> Synthetic construct

<400> 999

atggtgactg aattcatttt tctgggtctc tctgattctc agggactcca gaccttccta	60
tttatgttgt tttttgtatt ctatggagga atcgtgtttg gaaaccttct tattgtcata	120
acagtgggtat ctgactccca ccttcactct cccatgtact tccgtctagc caacctctca	180
ctcattgate tgtctctgtc ttcagtcaca gcccccaaga tgattactga ctttttcagc	240
cagcgcaaag tcattctctt caagggctgc cttgttcaga tatttctcct tcacttcttt	300
gggtgggagt agatgggtgat cctcatagcc atgggctttg acagatatat agcaatatgc	360
aaacccttac actacactac aattatgtgt ggcaacgcat gtgtcggcat tatggctgtc	420
gcatggggaa ttggctttct ccattcgggt agccagttgg cctttgccgt gcacttacct	480
ttctgtggtc ccaatgaggt cgatagtttt tattgtgacc ttcctagggt aatcaaactt	540
gcctgtacag atacctacag gctagatatt atggtcattg ctaacagtgg tgtgctcact	600
gtgtgttctt ttgtttctct aatcatctca tacactatca tcctaataac catccagcat	660
cgccctttag ataagtcgtc caaagctctg tccactttga ctgctcacat tacagtagtt	720
cttttgttct ttggaccatg tgtctttatt tatgcctggc cattccccat caagtcatta	780
gataaattcc ttgctgtatt ttattctgtg atcacccctc tcttgaacct aattatatac	840
acactgagga acaaagacat gaagacggca ataagacagc tgagaaaatg ggatgcacat	900
tctagtgtaa agttt	915

<210> 1000

<211> 669

<212> DNA

<213> Unknown (H38g850 nucleotide)

<220>

<223> Synthetic construct

<400> 1000

tccaacctgt ccttgccctga catcggtttc ccctccccca cggcccccaa gatggttgtg	60
gacatccaat ctcacagcag tcattctcct atgcaggctg cctgactcag atgtctctct	120
ttgccatttt tggaggcatg gaagagacac atgctcctga atgtgatggc ctatgtccgg	180
tttgtagcca tctgtcaccc tctatatcat tcagccatca tgaacctgtg tttctgtggc	240
ttcttacttt tgttgtcttt tttttttctc agtcttttag acgcccagct gcacaacttg	300
attgccttac aaatgacctg cttcaaggat gtggaaattc ctaatttcct ctgtgacct	360
tctccactcc cccatcttgc atgttgtgac acctcacca ataacataat catgtatttc	420
cctgctgcca tatttggttt tcttcccac tcgggggaccc ttttctctta ctataaaatt	480
gtttcctcca ttctgagggt ttcacatca ggtgggaagt ataaggcctt ctccacctgt	540
gggtctcacc tgcgggttgt ttgctgattt tatggaacag gcgtggagg gtacctcggt	600
tcagatgtgt catcttcccc gagaaagagt gcagtggcct cagtgatgta cacggtgggtc	660
acccccatg	669

<210> 1001

<211> 986

<212> DNA

<213> Unknown (H38g851 nucleotide)

<220>

<223> Synthetic construct

<400> 1001

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctggga	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatattc	tgctggccaa	cctatcgctc	attgacttga	gcctttcacc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaaag	tctttatcca	tgttacggga	ggagtggaaa	tggtgctgct	gatagtcag	360
gaatatgata	ggtacactgc	gatctgcaag	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggt	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttggtt	ttgtcataaa	ttaaccttct	gtggccctaa	taatgtgggg	agcttttatt	540
gtgattttcc	tgggtttatt	aaacttgcac	gcacgtggac	ttacgggcta	gaatttgtgg	600
tcactgcca	cagtggtatc	atatcgatgg	gcaccttctt	tttcttaatt	gtatcataca	660
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cttcgtaggc	tcacatcacc	gtagtgggtt	tggtttttgc	tccatgcacg	tttctctacg	780
tgtggccttt	ccctactaag	tcattggata	aatTTTTTgc	catcatgaac	tttgttgtca	840
ccctgtctct	aaatcctgcc	atctatactt	taaggaaaca	agatatgaag	tttgcaatga	900
gaaggctgaa	tcaacatatt	ttaaattcta	tggagacgac	ataacacatt	tggttgatga	960
gagcacagga	taaatgccat	ggacca				986

<210> 1002

<211> 659

<212> DNA

<213> Unknown (H38g852 nucleotide)

<220>

<223> Synthetic construct

<400> 1002

agtgtgctgt	ctatttctga	gacctattat	accgtggcca	tcaaccccca	aatgctgtcc	60
ggtctcctca	gtcctcaaca	aacctatctc	atcccaggct	gtgccgctca	gctctttttc	120
tatctcactt	ttgggtgcaa	taaagtcttc	ctgctcacag	ccatggggta	tgaccactat	180
gtggccatct	gcaaccctct	acagtattca	gtcatcatgg	gcaaaaaggc	ttgtatacaa	240
ctggctcagt	gatcctggaa	cattggcctg	agcacagcta	tcattcaggt	gtcttctgta	300
ttcagccttc	ccttctgtga	tgctaattct	atctcccact	tcttttgtga	tatccggccc	360
ataatgaagc	ttgcctgtgc	agacactact	atcaaggagt	ttattacttt	gctcatcagt	420
ctctgtgtcc	ttgttctgcc	catggtattg	atcttcatct	cctatgtcct	aattgtcacc	480
accatcctca	agattgcac	agctgagggc	ggagaaaggc	ctttgctact	tgtgcctcac	540
acctcacagt	ggtcattgtc	cactatggcc	gtacttcttt	catctaccta	aaacccaaat	600
cccaaaattc	cctgcaggac	agacttatct	ctgtgacata	cactgttatt	actcctctg	659

<210> 1003

<211> 939

<212> DNA

<213> Unknown (H38g853 nucleotide)

<220>

<223> Synthetic construct

<400> 1003

atgtctacgt	ctaatacacac	ccagttccat	ccttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ttggattgga	gtcccttttt	tctttgtgta	tcttgttgca	120
ctcctgggaa	acactgctct	cttgtttgtg	atccagactg	agcagagtct	ccatgagcct	180
atgtactact	tcctggccat	gttggattcc	attgacctgg	gcttgtctac	agccaccatc	240
cccaaaatgt	tgggcatctt	ctggttcaat	accaaagaaa	tatcttttgg	aggctgcctt	300
tctcacatgt	tcttcatcca	tttcttcaat	gctatggaga	gcattgtgtt	gggtggccatg	360
gcctttgacc	gctacattgc	catttgcaaa	cctcttcggt	acaccatgat	cctcaccagc	420

aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcctgtacat	ggttgttcca	480
ctgggtgttc	tccttctgag	gctgcccttc	tgtgggcatc	gtatcatccc	tcatacttat	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattagggtt	600
ggccttggca	acatatctct	cttgttactg	gatgttatcc	ttattattct	ctcctatgtc	660
aggatcctgt	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtgggt	ctcatattgg	tgttatctta	gcctttttta	caccagcatt	tttttcattc	780
ttgacacatc	gttttggcca	taatatccca	cagtatatac	atattatatt	agccaacctg	840
tatgtggttg	tcccaccagc	cctcaatcct	gtaatctatg	gagtcaggac	aaagcagatt	900
cgagagagag	tgctgaggat	ttttctcaag	accaatcac			939

<210> 1004

<211> 877

<212> DNA

<213> Unknown (H38g854 nucleotide)

<220>

<223> Synthetic construct

<400> 1004

tacatgataa	ccatcttatg	ggaaatatct	aagccagtaa	ataatatattt	tctaacactt	60
tctgtaagat	atcaaatgct	aatcactact	gtgtcataat	tgtaaataaa	attataatat	120
aaatttactg	agtttttctg	agtacctaata	gagttaaaaa	atatgggagc	atatgtagta	180
ctgtgcttgt	atcaatatgg	ataaggtatc	tgggaagtctt	ttctgaacat	ctttcggtgc	240
tgctgagatt	attccactga	tggggatggg	ccatggctgc	tatgtgacca	tctgactgc	300
atgaaaatca	tgactcaata	taggtgtggc	catcttgctg	gaatggcatg	cactggaaga	360
tttatccagg	cacagtttag	atcctctccc	cagtctgact	tcctttctat	aattccaatg	420
tcacaatatg	aatagcccat	tcatatgtga	cttaaacact	ttgttgaagc	tcctctgcat	480
aggtagtatg	atacacttgg	tctctttggt	gctgccaatg	atgggttcaa	ctgcctgtta	540
aacatcatct	tcttgatggg	ttcttaagtg	gccatcctat	atactttgaa	atcccacagc	600
ttggaggaaa	gatacaaagc	tctctctacc	tgtgtctctc	acaccaccgt	ggccatctaa	660
ttcttttgtg	tctgtatact	tgtttatctg	tgcccagtga	cccttcccca	gtcagtaaag	720
cagtggctgt	gctttacacc	atgataacgc	ctacattaaa	ccctttagtc	taaccctcag	780
aaatgcagag	gtgaaaagtg	ttgagaaact	tctgggtcaa	aagatgactt	gaagagagaa	840
ataatccaaa	cataagatga	ttttactctt	tcaatgg			877

<210> 1005

<211> 927

<212> DNA

<213> Unknown (H38g855 nucleotide)

<220>

<223> Synthetic construct

<400> 1005

atggagaaga	aaaagaatgt	gactgaattc	attttaatag	gtcttacaca	gaaccccata	60
atggagaaag	tcacgtttgt	agtatttttg	gttctttaca	tgataaacact	ttcagggaac	120
ctgctcattg	tggttaccat	taccaccagc	caggctctga	gctcccccac	gtacttcttc	180
ctgacccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtggattcct	ttcaagagaa	gaaaatcatc	tcctttaatg	ggtgtatggc	tcaagcctat	300
gcagaacaca	tttttgggtg	tactgagatc	atcctgctga	cagtgtatggc	ctgtgactgc	360
tatgtggcca	tctgcaaacc	tctgaactac	acaaccatta	tgagccacag	cctgtgcatt	420
ctcctgggtg	cagtggcctg	ggtggggagga	tttcttcatg	caactattca	gattctcttt	480
acagtatggc	tgcccttctg	tggccccaat	gtcataggcc	acttcatgtg	tgacttgtac	540
ccattgttaa	aacttgtttg	catagacact	catacccttg	gtctctttgt	tgctgtgaac	600
agtgggttta	tctgcttatt	aaacttctct	atcttggtgg	tatcctatgt	gatcatcttg	660
agatctttta	agaacaatat	cttggagggg	aggtgtaaag	ccctctccac	ctgtatttct	720
cacatcatag	tagttgtctt	attctttgtg	ccctgtatat	ttgtgtatct	gcgctcagtg	780
accactctgc	ccattgataa	agctgttgct	gtattttata	ctatgggtgg	cccaatgtta	840
aatcccgtgg	tctacacact	cagaaatgct	gaggtaaaaa	gtgcaataag	gaagcttttg	900
agaaaaaaag	tgacttcaga	taatgat				927

<210> 1006
 <211> 738
 <212> DNA
 <213> Unknown (H38g856 nucleotide)

<220>

<223> Synthetic construct

<400> 1006
 tgtattcaac aacattgata tccactttgt ctctgcatgt tctcctttta ttttaatttg 60
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120
 ttggtataaa gtaaggatc tgattaacca aatttacact aaagccaatt ggccttttca 180
 tggattataa cactatgcac aaccactcca tactcaaaca tgcatttctt tctccaatgt 240
 tatatgatgc agcacctagc tctttacagg acattttttt ctgggtgggt cacagatttt 300
 ccttctgttg gtgatggcct aggccactat agggccatct gcaagtcctt gcagtatattg 360
 gttgtcatga agcaatggct gtgtgttggt ctgctgggtg tgcctgggc tggaggattt 420
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgtc 480
 attggtcatt ttatttgtga catggacccc ttaatgaagc ttgtctgtga ctacacactc 540
 aacagatttg cctattttgc aggtcatgat taaatactag gttttatgta tttcacttat 600
 gctcagactg gactgtttcc ttttgggtgat tgcacctcat tattcttttg tcattttttc 660
 cctagaggac ttggttctat aaatcttgct atacatagtt attatccctg tggcatctct 720
 agagatacgg agcctacc 738

<210> 1007
 <211> 786
 <212> DNA
 <213> Unknown (H38g857 nucleotide)

<220>

<223> Synthetic construct

<400> 1007
 ctaattgtag tcaccgtaac tgtcagtgag accctgggct caccaatgta cttctttctt 60
 gctggcttat ctttataga tatcatttat tcttcatcca tttccacag attgatttca 120
 gacttgttct ttgggaataa ttccatatcc tcccatctt gcttggccca gctctttaca 180
 gagcaccttt ttggtgggtc agaggctctt cttctgttgg tgatggccta tgaccttgca 240
 ttacttgggt atcatgagac aatgggtgtg tgttttgcgt ctggtagcgt cctgggttgg 300
 aggatttctg cactcagtat ttcaacttag tgttatttat gggctcccat tctgtgacct 360
 caatgtcatt gatcattttt tctgtgatat gcaccttta ttgaaactgg tctgtactga 420
 taccatggt attggcctct tagtgggtggc caatggagga ctaggttgca ctattgtgtt 480
 tctgctctta ctcatctct atgggtgcat ctgcactctc taaagaacct tagtcagaaa 540
 gggaggtgaa aagccctctc aacctgcagt tccacataa ctgtgggtgt tttcttctt 600
 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660
 agtgtgtttt atacagtcac aactccaatg ctgaacctt taatctacac tctgagaaat 720
 tctgagatga caagtgtat gaagaagctc tggagaagag acttcataac aagtagtaca 780
 taagtg 786

<210> 1008
 <211> 930
 <212> DNA
 <213> Unknown (H38g858 nucleotide)

<220>

<223> Synthetic construct

<400> 1008
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 ctgctcattg tgggtgactat tattgccagc ccttcccttg gctcctcaat gtacttcttc 180
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 gtagacttac tctgtgataa aaagactatt tctttccag cttgcatggg ccagttattt 300

atagaccagc	ctggatggcg	gagctgaggt	cgtgcttctt	gtggtgaagg	cctgtgatca	360
ccatgtggac	atctggaagc	cactgcgcta	tctcgactat	catgaatcga	cagggtgaa	420
tgcggctgct	cgtggctgtc	gtcgactgcg	agggtgtctg	cattcgctgt	ctcatattgt	480
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atgtaccag	ttattggaac	tggtatgcac	tgacacctac	tttattggcc	ttactgtttt	600
tgtcaatggt	ggaacaatct	gtatagtcgt	cttcaccctt	ctactaatct	cctatggagt	660
catcctaacc	tcccttaaaa	cttacagtca	agaaggagg	cataaagtc	tgtttacctg	720
cagctccac	attatcgtct	ttgccctctt	ttttgttccc	tgtattttca	tgtatgttag	780
acctgtttca	aacatccttt	tgataaattc	ctgacagtgt	tttatacagt	tatcacaccc	840
atgttgaatc	ctttaatata	cacattgaga	aattcagaga	tgagaaattc	tgtagaaaca	900
ctcttgtgta	aaaagttaac	tgtattagag				930

<210> 1009

<211> 915

<212> DNA

<213> Unknown (H38g859 nucleotide)

<220>

<223> Synthetic construct

<400> 1009

atgcagagga	gcaatcacac	agtgactgag	tttatactgc	tgggcttcac	cacagaccca	60
gggatgcagc	tgggcctctt	cgtggtgttc	ctgggcgtgt	actctctcac	tgtggttaga	120
aatagcaccc	tcacgtgttt	gatctgtaat	gactcccacc	tccacacacc	catgtatttt	180
gtcgttggaa	atctgtcgtt	tctggatctc	tggtattctt	ctgtctacac	cccaaagatc	240
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cgctacgtgg	ccatctccaa	gcccctgctt	tatgcccgag	ccatgtccat	aaagctgtgt	420
gcattgtctg	tagcagtcct	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
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ctgctggcct	ccaatgtcat	ctgccccgca	gtgctcatcc	tggcctccta	cctctttatc	660
atcaccagtg	tcttgaggat	ctcctcctcc	aagggctacc	tcaaagcctt	ctccacatgc	720
tcctcccacc	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	tgaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	tccca					915

<210> 1010

<211> 948

<212> DNA

<213> Unknown (H38g860 nucleotide)

<220>

<223> Synthetic construct

<400> 1010

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cccagatgc	aagtttccct	ctttattttt	ttcctggcca	tttatacagt	cactttgttg	120
ggcaactttc	ttattgtcac	agttaccagt	gtggatctcg	cacttcaaac	acccatgtac	180
ttctttcttc	aaaatctgtc	acttcttgaa	gtatgtttca	ccttgggttat	ggtgccaaaa	240
atgcttgtag	atctagtgtc	cccaaggaaa	attatctctt	ttgtgggctg	tggtagccag	300
atgtacttct	tcttcttctt	tggcagttct	gaatgtttcc	ttctctccat	gatggcttat	360
gatcgctttg	tggccatctg	taacctctc	cattattcag	tcataatgaa	caggctcccta	420
tgcttgtgga	tggccatagg	ctcttggatg	tccggtgttc	ctgtgtctat	gctacagaca	480
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ggtccccac	tgtaaaaact	agtcacagt	gatacaacca	tgtatgaaat	gcaagcactt	600
gcctccacac	tctgttttat	catgtttccc	ttttgtctca	ttttgggtttc	ctacaccgcg	660
attatcataa	caattctgtg	gatgtcctct	gccactggcc	gccagaaggc	attttctact	720
tgttcctcac	acctcattgt	ggtgtccctc	ttctacggaa	cagccagttc	gacctacctg	780
cggcccaaat	caaaccagtc	ccctgagagc	aagaagctag	tgtcattgtc	ctacactgtc	840

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900
gtcaagagga caatcactca aaaagtctta cagaagttag atgtgttt 948

<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

atggcgaata gaaacaatgt gacagagttt attctattgg ggcttacaga gaatccaaaa	60
atgcagaaaa tcatatttgt tgtgttttct gtcactctaca tcaacgccat gataggaaat	120
gtgtctcattg tggtcacccat cactgccagc ccatcactga gatcccccat gtactttttc	180
ctggcctatc tctcctttat tgatgcctgc tattcctctg tcaatacccc taagctgac	240
acagattcac tctatgaaaa caagactatc ttattcaatg gatgtatgac tcaagtcttt	300
ggagaacatt ttttcagagg tgttgaggtc atcctactta ctgtaatggc ctatgaccac	360
tatgtggcca tctgcaagcc cttgcaactat accaccatca tgaagcagca tgtttgtagc	420
ctgctagtgg gagtgtcatg ggtaggaggc tttcttcatg caaccataca gatcctcttc	480
atctgtcaat tacctttctg tggctcctaat gtcataagac actttatgtg tgatctctac	540
actttgatca atcttgccctg cactaatacc cacactctag gactcttcat tgctgccaac	600
agtgggttca tatgcctgtt aaactgtctc ttgctcctgg tctcctgcgt ggtcatactg	660
tactccttaa agaccacag cttagaggca aggcataag ccctctctac ctgtgtctcc	720
cacatcacag ttgtcatctt atcctttata ccctgcatat ttgtgtacat gagacctcca	780
gctactttac ccattgataa agcagttgct gtattctaca ctatgataac ttctatgtta	840
aaccctctaa tctacacctt gaggaatgct caaatgaaaa atgccattag gaaattgtgt	900
agtaggaaag ctatttcaag tgtcaaa	927

<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

tggaaaaatc atttcacctc tgtgaattgt ggttttgcca tctgcagagc tgaatgttaa	60
ccatagccca agatactaag tattatagga ttgaaatgaa atataaatga aactttgtaa	120
atgttaaatt ataacacaaa tcatatgggc agtgtcgatg tcctaattgt tcctaactcc	180
tcatcacact ctctacttct ttcatgtggt ctgccatcct gatatccgct ctgcagaggg	240
gaggcacaag gcttttccca cctgctcctt ccacctgggt taattctcct ccagcacaat	300
gaacaagcct cacctatttg tgccccagct ccatcttctc ttatgagagg ggcaaggtag	360
tgtctacggt ttacacatgc atcactcctg tgccaaaccc cttgatctgc agcatgagga	420
agaagggaact caagcatgct cttaaaaaaa aagaagaaat tgcaagggtc ttgctgtcca	480
gaacacat	488

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

atgttttagct ctgagccac catagatgga aatcagtcct tgtgtgcca attcacattt	60
gtggcttttt cttctataga agaattacag cttgtactct tcattgtgtt cttaatcact	120
acttatgcac tataggagga aatatcatca tcatctccct gatctggatc acccctgccc	180
tgcacactcc aatgtatttc ttcttggtga acctctcatt tctggagatg tgctatacca	240

ccagtgtggt	gcctcatgct	ggtgcacctg	ctggtggaga	ccaaaacccat	aagtgtgggt	300
ggctgtgcaa	cccagatgta	catatttgcc	atcttgggac	tgacagaatg	ctgcttgcta	360
gcagctatgg	cttacgatcg	ctttgtagct	atttgttacc	cactgcatta	cactctcttc	420
atgggccctc	gtgtttgttt	gaaattggct	gcagcatctt	ggttcactgg	agtgggtggt	480
gagtcagccc	agatcacccct	gatcttcact	ttgcctttct	gtggaacagg	aaagattcaa	540
cacttttttg	tgacataatg	cctgtactga	aactggcttg	tattgatacc	tcccaaattg	600
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gctcccatat	gcacatccct	gtgaccatct	tgagaatccc	ttcagcagct	ggaagacaca	720
aagctttctc	cacttgttct	tctcatatct	tggttgtttc	tctgttctat	ggcactgcct	780
tgttcactta	tctgcaacct	aagactgcac	acactccaga	aacagacaaa	gcaactgcac	840
tcatgtacac	aatggtcaca	cctgctttga	atcctgttat	ctataccttg	aggaacaagg	900
aagtaaagga	agcctttcaa	aggataaccc	aaaggaactc	tcttagacaa	acg	953

<210> 1014

<211> 873

<212> DNA

<213> Unknown (H38g864 nucleotide)

<220>

<223> Synthetic construct

<400> 1014

tccatgtacc	tggtcacgat	gctgaggaac	ctgttcatca	tcctggctgg	cagctctgac	60
ccccacttcc	acaccccat	gtacttcttc	ctctccaacc	tgctctgggc	tgacattggt	120
ttcacctcgg	ccacagttcc	caagatgatt	gtggacatgc	agtcgcatag	cagagtcac	180
tcttatgcgg	gctgcctgac	acagatgtct	ttctttgtcc	tttttgcatg	tatagaagac	240
atgctcctga	ctctgatggc	ctatgaccga	tttgtggcca	tctgcccac	tgtcaccccc	300
tgactaccg	agtcacatg	aatcctcacc	tctgtgtctt	cttagttttg	gtgtcctttt	360
tccttagcct	gttggtattc	cagctgcaca	gctggattgt	gttacacaac	tcaccttctt	420
caagaatgtg	gaaatctata	atttttttct	tgtgacccat	ctcaacttct	caaccttgcc	480
tgttctgaca	gcacatcaa	taacatatta	tgtatttttag	atatccctat	atttggtttt	540
cttcccattt	cagggatcct	tttgtcttac	tataaaattg	tctcctccat	tccaagaatt	600
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tgcttatttt	atgaaacagg	cattggcgtg	tacctgactt	cagctgtgtc	atcatctccc	720
aggaatggag	tggtggcatc	agtgatgtac	gctgtggtca	tccccatgct	gaaccctttc	780
atctacagcc	tgagaaacag	ggacattcat	agtgcctctg	ggaggctgcg	cagcagaaca	840
gtcaaatctc	atgatctggt	ccatcctttc	tct			873

<210> 1015

<211> 981

<212> DNA

<213> Unknown (H38g865 nucleotide)

<220>

<223> Synthetic construct

<400> 1015

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tcactgggct	gttccctgtc	atgtgcctgg	tcacagtgtc	ggggaagctg	ctcatcatgt	120
tggccttcag	ccctgactcc	cacctccaca	cccacatgta	cttcttctct	tccaacctgt	180
ccttgctcga	catcggtttc	acctccacca	ttgtcccca	gatgattgcg	gacatccagt	240
ctcacagcag	agtgatctcc	tatgcaggcc	gacctgacta	gatgtctctc	tttgccattt	300
ttggaggcat	ggaagacaga	catgctcctg	agtgtgatgg	cctatgaccg	gtttgtagcc	360
atctgtcacc	ctctatatca	ttcagccatc	atgaatccgt	gtttctgtgg	cttctacttt	420
ttgttgtctt	tttttttttc	tcagtctttt	agacacccag	ctgcacaact	tgattgcttt	480
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catatttggt	ttccttccca	tctcggggac	ccttttctct	ttaaaactgt	ttcctccatt	660
ctgagggttt	catcatcagg	cggaagatg	aaaaccttct	ccacctgtgg	gtctcacctg	720
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tcttccctga	gaaaggctgc	agtggcctca	gtgatgtaca	agatgggtcac	ccccatgctg	840

aacccttca	tctacagcct	gagaaacagg	gatatgaaaa	gtgtcctgcg	gcgggccgcac	900
ggcagcacgg	tctaattctca	atatcttctt	atctgttcca	ttccttttgt	aggggtgggtt	960
aaaaaaggca	gcaaggcca	a				981

<210> 1016

<211> 762

<212> DNA

<213> Unknown (H38g866 nucleotide)

<220>

<223> Synthetic construct

<400> 1016

atgggtgaca	agggaaacagg	caaccattca	gatgtaactg	atttcattct	tgaaggcttc	60
agggtccgcc	cagagttcta	cattctcctc	ttcttctgt	tctgtctgat	ctatagcatg	120
gttcttttgg	ggaacattag	tgtgatgaca	atcattgtaa	ctgattccca	gctgaacaca	180
ccaatgtatt	tttttctagg	caacctctcc	ttcattgacg	tctcctactc	cactgttatt	240
gctcctaaag	ccatggccca	cttctgtct	gaaaaaaaga	cagtctcttt	tgcaggttgt	300
gttgcccagt	tattctttt	tgccctgttc	attgtaacag	aggggtttgt	cctggcagcc	360
atggcctatg	accgcttcag	tgccatctgc	aatcctcttc	ttcatagtgt	tcacatgtca	420
agacgcctct	gcactcagtt	ggttgctgg	tcttatttct	gtggctgggc	cagttccatc	480
ctccaagtca	gtgtaacatt	ctcagtgtcc	ttctgtgctt	ccagagtcac	tgctcacttc	540
tactgtgatt	cttatcaa	tgaaaagatt	tcctgttcta	atctctttgt	caataagatg	600
gtatctctga	gtttgagtgt	catcattatt	ttgcctacaa	ttgttggtat	tatagtatct	660
tacctgtata	ttgtatctc	agtcttgaag	atcccccca	gtgaaggagg	aaagaaagac	720
ttttccactt	gcagctccca	tcggggtgtt	gtaagtttgc	tc		762

<210> 1017

<211> 1008

<212> DNA

<213> Unknown (H38g867 nucleotide)

<220>

<223> Synthetic construct

<400> 1017

tatacagacc	cacagaatct	aacagatgct	tcaaaatacc	tcctcctaga	actctcagag	60
gatccaaaac	tgcagctggc	cctcgagtgg	gcgtgaaccg	tgtacatgta	cctagtcatt	120
gggtgctggag	aatctgtctca	ttatcctggc	cgtcagctct	gacttccacc	tccacacccc	180
catgtacttc	ttcctctcca	acctgtcctt	ggctgacatc	ggtttcacct	ccaacacggg	240
ccccaaagatg	attgtggaca	tccaatctca	cagcagagtc	atctcctatg	caggctgcct	300
gactcagatg	tctctctttg	ctgttttttg	aggcatggaa	gaaagacatg	ctcctgagtg	360
tgaggggccta	tgaccggttt	gtagccatct	gtcacccctc	atattattca	gccatcatga	420
acccatgttt	ctgtggcttc	ctagttttgt	gttttttttt	ttctcagctc	tttagactcc	480
cagctgcaca	atttgattgc	cttacaaatg	acctgcatca	aggatgtgga	aattccta	540
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atagtcattg	atttccttgc	tgccatattt	ggttttcttc	ctatctcacg	gatcattttc	660
tcttactata	aaattgtttc	ctccatgctg	agtgtttcat	catcagggtg	gaagtataaa	720
gccttctcca	cctgtgggtc	tcccctgtca	gttgtttgct	tattttatgg	aaaagtcggt	780
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atcaaaagg	tcctgtgggtg	gttgcatggc	agaacagttt	aatctcatta	ttttattatc	960
tgttccattc	ctttttagt	gtgggttaaa	aaaggcagca	aggtcaaa		1008

<210> 1018

<211> 949

<212> DNA

<213> Unknown (H38g868 nucleotide)

<220>

<223> Synthetic construct

<400> 1018

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ctcgctttgc	tgtccctgtc	cctgtccatg	tatctgytca	cggtgctgag	gaacctgttc	120
agcatcctgg	ctgtcagctc	tgactgcccc	ctccacaccc	ccatgtactt	cttcctctcc	180
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acgcagtcgc	atagcagagt	catctctcat	g-gggctgcc	tgacacagat	gtctttcctg	300
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atgtttggtt	ttcttcccat	ttcagggatc	tttttgtctt	actataaaat	tgtccctctc	660
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tgaacctttt	catctgcagc	ctgagaaaca	gggacataca	aagtgccttg	cggaggctgg	900
gcagcagagc	attcgaatct	catgatctgt	tccatccttt	ttcttgtgt		949

<210> 1019

<211> 939

<212> DNA

<213> Unknown (H38g869 nucleotide)

<220>

<223> Synthetic construct

<400> 1019

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agggtacgcc	cagagctcca	cattctcctc	ttcctgctat	ttttgtttgt	ttatgccatg	120
atccttctag	ggaatgttgg	gatgatgacc	attattatga	ctgatcctcg	gctgaacaca	180
ccaatgtatt	ttttcctagg	caatctctcc	ttcattgac	ttttctatcc	atctgttatt	240
gaaccaagg	ctatgatcaa	cttctgggtc	gaaaacaagt	ctatctcctt	tgcaggctgt	300
gtggcccagc	tctttctctt	tgccctcctc	attgtgactg	agggatttct	cctggcggcc	360
atggcttatg	accgctttat	tgccatctgc	aaccctctgc	tctactctgt	tcaaagtgtc	420
acacgtctgt	gtactcagtt	ggtggctggt	tcctattttt	gtggctgcat	tagctcagtt	480
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atgtatctca	ctcctgacag	atttcctgag	ctgagtaaag	tggcatcctt	atgttactcc	840
ctagtcactc	ccatgttgaa	tcctttgatt	tactctctga	ggaacaaaga	tgtccaagag	900
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<210> 1020

<211> 828

<212> DNA

<213> Unknown (H38g870 nucleotide)

<220>

<223> Synthetic construct

<400> 1020

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ctctactctg	tgttttggtc	accctaactg	ggatgaccac	accacacctc	catgtaccca	120
ctgccacacc	tccatgtacc	tttatatctt	tagcttttcc	ttcatagggt	tcttctatcc	180
ctctgtcatt	tctcccaaaa	tgacaataag	ctttgtgaca	gaaaagaaca	tcatcaccta	240
tgtgacatca	aacactcagc	cctttcctct	ggcttctttg	tcattagtga	ttactccata	300
tttatcccac	tggccttgga	tcactatgag	gccatgacc	tgccgggtctc	tttcataagt	360
ttcatttctg	tagatgggtc	ataagttata	gaatttgctg	atgctgtggt	ccatcaaggg	420

acatggacca	attcctgttt	tgtgatcaca	gttgcacgag	ccttaacttg	tgtaacatag	480
gcccgcctca	ggctgcctga	atcagtacct	atgtcagaag	caggtggatt	tgtattcatg	540
agaaccagca	gtgtaccatg	ctgtgttatc	atttccatac	tttgttttca	ttcttttcaa	600
catttttcat	taacccagtg	gtccaaaatc	tcagccagat	tccataaaatc	tgtttatttc	660
tttttttga	ttagggacat	tcagtacat	cagatctcca	gaagctatgg	gttagtgtaa	720
attacagtgt	ccttcaccaa	gatggggcca	gtgatgacg	gtctgttcaa	caccttgagg	780
aacaagacta	tctaacttgc	tgcaatgaaa	cctttgtcat	tttcttct		828

<210> 1021

<211> 1001

<212> DNA

<213> Unknown (H38g871 nucleotide)

<220>

<223> Synthetic construct

<400> 1021

gatacagacc	cacagagtct	aacagatgtc	tctatatattcc	ttctcctcga	actctcagag	60
gatccagaac	tgcagccggg	cgctcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggagaacc	tgctcatcat	cctggccgctc	agccctgact	cccacctcca	caccccatgt	180
acttcttctc	ctccaacctg	tccttgcttg	acatcggttt	cacctccaca	cgggtcccca	240
gatgattgtg	gacatccagt	ctcacagcag	agtcattctc	tatgcagggt	gcctgactca	300
gatgtctctc	tttgccattt	ttggaggcag	ggaagagaga	catgctcctg	agtgtgatgg	360
cctacgacca	gtttgtagcc	atctgtcacc	ctccatatcg	ttcagccatc	ttgaaccctg	420
gtttctgtgg	cttcctagat	ttgttgtcct	tgtttttttt	tttttttttt	ttttttccct	480
cagtctttta	gactctcagc	tgcaacaact	gattgcctta	caaatgacct	gcttcaagga	540
tgtggaaatt	cctaatttct	tctgggaacc	ttctgtgaca	ccttcaccag	gaacatcaac	600
atgtatttcc	ctgctgccgt	atttggtttt	cttcccatct	cggggaccct	tttctcttac	660
tgtaaaattg	tttctcccat	tctgagggtt	tcattcatcag	gtgggaagta	taaaccctca	720
ccacctgtgg	gtctcaccct	tcagttgttt	gctgatttta	tggaacaggc	gttgagggtg	780
acctcggttc	agatgtgtca	tcttccccga	gaaagcgtgc	agtggcctca	gtgatgtaca	840
cgggtggcac	ccccatgctg	aacccttcca	tctacagcct	gagaaacagg	gatatgaaaa	900
gtgtcctgcg	gcgggcgcac	agcagcgcag	tctaattctca	atatcttctt	atctgttcca	960
ttccttttgt	aggatgggtt	aaaaaaggca	gcaagggtcaa	a		1001

<210> 1022

<211> 1025

<212> DNA

<213> Unknown (H38g872 nucleotide)

<220>

<223> Synthetic construct

<400> 1022

gatacagacc	cacagagtct	aacagatgtc	tctatatattcc	ttctcctcga	actctcagag	60
gatccagaac	tgcagccggg	cgctcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccgctc	agccctgact	cccacctccc	caccccatgt	180
tacttcttcc	tctccaacct	gtccttgccct	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgagcg	tggaacatcca	gtctcacagc	agagtcattct	cctatgcagg	ctgcctgact	300
caaatgtctc	tctttgccat	ttttggaggc	atggaaaaaa	gacatgctcc	tgagggtgatg	360
gcctatgacc	tgtttgtacc	catctgtcac	cttctatata	gttcaaccat	cttgaaccctg	420
tttgtccgtg	gcttcctaaa	tttgttgtct	ttgttgttgg	tttttttttt	ttttctctca	480
gtcttttaga	ctcccagctg	cacaacttga	ttgccttaca	aatgacctac	ttcaaggatg	540
tggaatattc	taatttcttc	tggaacactt	ctcaactccc	ccatcttgca	tgttgtgaca	600
ccttcaccag	gaacaacaac	atgtatttcc	ctgctgccgt	atttggtttt	cttcccatct	660
cggggaccct	tttctcttac	tgtaaaattg	tttctccat	tctgagggtt	tcattcatcag	720
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agtggcctca	gtgacgtacg	tacacgggtg	tcaccccat	gctgaactcc	ttcatctaca	900
gcctgagaaa	cggggatatt	aaaagtgtcc	tacggcggcc	gcatggcagc	acagtctaata	960
ctcaatacgt	tcttatctgt	tccattcctt	ttgtagggtg	ggtaaaaaa	gacagcaagg	1020

tcaaa

1025

<210> 1023

<211> 1044

<212> DNA

<213> Unknown (H38g873 nucleotide)

<220>

<223> Synthetic construct

<400> 1023

atggatctgg	ggaactcagg	gaatgattca	gttgtgacca	agtttgtcct	gctgggcctc	60
acagagactg	cagctctaca	gcccacctc	tttgtcatct	tccttcttgc	ttacgtcact	120
accattggag	gcaccctcag	catcctggcg	gccatcctta	tggaaccaa	actccacagc	180
cccatgtact	tcttcctggg	gaacttggtc	ctgccagatg	tgggggtgtg	cagtgtcact	240
gtccctgcca	tgctgagcca	tttcataatc	aacgacagaa	gcattcccta	taaggcctgc	300
ctctccgagc	tcttcttctt	ccacctcctg	gctggggcag	actgcttctt	gctgaccatc	360
atggcctatg	accgctatct	ggccatctgc	cagtcctctc	cctacagcag	ccgcatgagc	420
tggggaatcc	agcaagccct	ggtgggcatg	tcattgtgtc	tttcttcac	caatgcactg	480
acccaaactg	ttgccctgtc	tcctcttaac	ttctgtggcc	ccaatgtgat	caatcacttc	540
tactgtgacc	tcccacagcc	cttcacagtc	tcctgagcca	gtgttcactc	caatgggcag	600
ttgctgtttg	tgcagcagc	ttctatgggt	gtggccccct	tggtcctcat	cactgtgtcc	660
tatgcccattg	tggcagctgc	agtcctgcga	atccgctctg	cagagggcaa	aaagaaagcc	720
ttctccacgt	gtagtctcca	cctcactgtg	gtgggcatct	tctatgggac	gggcgtcttc	780
agctacacaa	ggctgggttc	agtggagtct	tcggacaagg	acaagggcat	tggcactctc	840
aacactgtca	tcagccccat	gctgaaccca	ctcatctact	ggacatctct	gctggacgtc	900
gggtgcatca	gtcactgttc	ctccgatgct	ggcgtgtctc	caggcccacc	agtgcagagt	960
tccctatgct	gcctgcagtt	cacagctctt	ctttccccac	ctcctggctg	gggtggactg	1020
tcacctctta	atagccatgg	ccta				1044

<210> 1024

<211> 688

<212> DNA

<213> Unknown (H38g874 nucleotide)

<220>

<223> Synthetic construct

<400> 1024

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ttcattctca	ggaaaaagcc	agcaagggtc	ccagctcccc	ctcttctagg	gatctgtttg	120
aaaaccgtag	tgggggccct	catcttgatc	actctagttt	tccttaattc	tcagcttcac	180
cctcccattg	actacgtcat	cagaaattta	tcatttatgg	atcactgcaa	ttgctctatt	240
agtaccctta	aaatactggg	gaagtttgtg	ttagagaaga	ccatcatctc	ctatgaggac	300
ggcatgtcac	agctttgtag	tgcttcgtgt	ttatatgttc	atggccaagc	gtaacatgcg	360
gaccagcaac	tgctgtcatc	acatttcac	aagtcagctc	cctgctggta	gttgtagtat	420
ttatatggag	ttgactggta	caacaataga	tattttgcct	tgtattaaaa	tagtactagt	480
gtgagttatt	catcagtcac	acttctctca	tgcactagca	tctatgatat	tgataggaca	540
atcttctttt	ttacttgatg	caatattgta	gtcactagat	taacagttgt	ttcctactcc	600
ttttctctcc	agcactctcc	acatcagctt	tacaaagggc	aagctctggg	tttttcccg	660
aggtctgacg	cattcatgct	gttgcctt				688

<210> 1025

<211> 993

<212> DNA

<213> Unknown (H38g875 nucleotide)

<220>

<223> Synthetic construct

<400> 1025

cacacagagc	cacggaatct	cacaagtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccgct	cctcgctttg	ctgtccctgt	ccctgtccat	gcactctggc	120
atgggtgctga	ggaacctgct	caacatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccacgtact	tcttctcttc	caacctgtgc	tgggctgaca	tcggtttcac	ctcggccacg	240
gttcccaata	tgattgtgga	catgcagtcg	catagcagag	tcactctctca	tgcggactgc	300
ctgacacaga	tttctctctt	gctccttttt	gcactgtatag	aaggcatgct	cctgactgtg	360
atgacctatg	actgctttgt	agccatctgt	tgcctctctgc	actaccagct	catcgtgaat	420
cctcacctct	gtgtctctct	cgttttgggt	tcctttttcc	ttagcctggt	ggattcccag	480
ctgcacagtt	ggattgtggt	acaattcacc	atcatcaaga	atgtggaaat	ctctaattct	540
gtctgtgacc	cctctcaact	tctcaaaact	gcttggtctg	acagcgtcat	caatagcata	600
ttcatgcatt	tccataatac	tatgtttggt	tttcttccca	tttcagggat	ccttgtgtct	660
tactataaaa	tcgtcccttc	cattcttagg	atttcacgtg	cagatgggaa	gtataaagcc	720
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tacgtgtggg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgtggaggct	gctcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
ttttcttgtg	tgggtaaggg	caaccacatt	aaa			993

<210> 1026

<211> 965

<212> DNA

<213> Unknown (H38g876 nucleotide)

<220>

<223> Synthetic construct

<400> 1026

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gatccagaac	tgcagccgct	ctcgctttgc	tgtccctgtc	cctgtccatg	tatctgggtca	120
cggtgctgag	gaacctgctc	agcatcctgg	ctgtccgctc	tgactcccc	ctccacaccc	180
ccatatactt	cttctctctc	aacctgtgct	gggctgacat	cggtttcacc	tcggccacag	240
ttcccaagat	gattgtggac	atgcagtcgc	atagcagagt	catctctcat	gcaggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgcttttga	gccatctgtc	accctctgca	ctaccagtc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttgggtg	cctttttcct	tagcctgttg	gattcccagc	480
tgcacagttg	gattgtgtta	caattcacca	tcatacaaga	tgtggaaatc	tctaattttg	540
tctgtgaccc	ctctcaactt	ctcaaatattg	cctgttctga	cagcatcatc	aatagcatat	600
tcataatatt	ccatagtact	atgtttgggt	ttcttcccat	ttcagggatc	cttttgtctt	660
actataaaat	catccctctc	attctaagga	tttcatcatc	agatgggaag	tataaagcct	720
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acgtgtgtgt	cacccccatg	ttgaaccttt	tcacttacag	cctgagaaac	agggacatac	900
aaagtgcctt	gtgggggctg	cacagcagaa	cagtcgaatc	tcatgatctg	ttccatcctt	960
tttct						965

<210> 1027

<211> 945

<212> DNA

<213> Unknown (H38g877 nucleotide)

<220>

<223> Synthetic construct

<400> 1027

atgcagccag	aactctggggc	caatggaaca	gtcattgctg	agttcatcct	gctgggcttg	60
ctggaggcgc	cagggctgca	gccagttgtc	tttgtgctct	tcctctttgc	ctacctggtc	120
acggtcaggg	gcaacctcag	catcctggca	gctgtcttgg	tggagcccaa	actccacacc	180
cccatgtact	tcttctctgg	gaacctatca	gtgctggatg	ttgggtgcat	cagcgtcact	240
gttccatcaa	tgttgagtcg	tctcctgtcc	cgcaagcgtg	cagttccctg	tggggcctgc	300
cttaccacgc	tcttcttctt	ccatctgttc	gttggagtgg	actgcttcct	gctgaccgcc	360
atggcctatg	accaattcct	ggccatctgc	cggccctca	cctacagcac	ccgcatgagt	420

cagacagtc	agaggatgtt	ggtggctg	tcctgggctt	gtgctttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgtgat	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgctcca	gcacccaact	caatgagctg	600
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ttctccacat	gtggctccca	cctcactgtg	gttgccatat	tctatggttc	aggtatcttt	780
aactatatgc	gactgggttc	aaccaagctt	tcagacaagg	ataaagctgt	tggaattttc	840
aacactgtca	tcaatcccat	gctgaaccca	atcatctaca	gcttcagaaa	ccctgatgtg	900
cagagtgtcca	tctggaggat	gctcacaggg	aggcggtcac	tggt		945

<210> 1028

<211> 969

<212> DNA

<213> Unknown (H38g878 nucleotide)

<220>

<223> Synthetic construct

<400> 1028

atgacagatt	acaatgaacc	aatggaacca	atggaagata	agaaccagac	agtagtgact	60
gaatttctct	tattgggcct	cacagatcat	ccctatcaga	agattgttct	cttcttcatg	120
tttctctttg	tttatcttat	cacctggga	ggtaacttgg	ggatgatcac	tctcatatgg	180
attgatccca	gactccacac	tcctatgtac	ttttttctta	ggcacttgct	ctttgtagat	240
atttgttcct	cttcttctgt	tgtgcctaag	atgctgtgta	atatctttgc	agagaaaaaa	300
gacatcactt	ttctgggttg	tgtgcacag	atgtggttct	ttggtctctt	tgaggcagct	360
gagtgttttc	tcctggctgc	catggcatat	gaccggtatg	tggccatctg	caagcccttg	420
ttgtatacgc	tcattatgtc	tcagcaggtc	tgtatgcagc	tgggtgtagg	gccttatgcc	480
atggctctta	taagcaccat	gactcataca	attttccactt	tttgcttacc	cttttgtggt	540
tcaaataatta	tcaatcactt	tttctgtgat	atttttccac	tgctttccct	agcatgtgca	600
gacacctggg	tgaataaatt	tgtgctgttt	gtcttggctg	gagctatagg	agtactagat	660
ggtctgatca	tcattggtctc	ctatatattgc	atcctgatga	ccatcttgaa	gatccagact	720
gctgatggga	agcaaaaagc	tttcttcacc	tgtttttctc	accttgcggc	tgtctccatc	780
ctgtatggga	ctcttttctt	gatttatgtt	cggccaagtt	caagttcctc	cctgggtatc	840
tataaagtga	tttctctatt	ttatactgtg	gtaatcccca	tggttaaccc	ccttattttac	900
agcttgagga	ataaggaggt	gaaagatgca	ttcagaagaa	aaattgagag	gaaaaaattt	960
attataggt						969

<210> 1029

<211> 687

<212> DNA

<213> Unknown (H38g879 nucleotide)

<220>

<223> Synthetic construct

<400> 1029

ttcttttctt	tagacctcat	tagaagccaa	gcaaatacaa	tgtcaaagaa	acactggaca	60
gccatagctg	agtttatcc	cctgggaccg	acagatcaag	ccgagttgca	gcttgtcctt	120
ttttctgtgc	acgttccctg	tcattttacct	tattatggta	atgggcaatt	tgagcatgat	180
tttgatcatt	agaagtgact	gaaaacttca	cattccaatg	tacttcttcc	tcagtcacct	240
ctcctttgca	gttctctgtt	atactctcaa	tgtcactcct	cagatattgg	ttaatttccct	300
atccaagaga	aaaaccattt	tcttcattgg	ttgtgtaagt	gttttataat	tctacttttt	360
cattgtcctg	ataatcagag	attatcatat	gcttacagtg	atggctaagt	actgctacat	420
ggccatttgc	aagcccttgt	tatatggtag	taaaatgtcc	agattttgtct	gcctctctct	480
ggcttctgtt	tcttaaatat	atggctttgc	aaactatctg	gcacagacca	tccggatgct	540
tcttctgtcc	ttctgaggat	ccaatgagat	caaccacttt	gactgtgcgg	acccccctct	600
gttagtcttc	ccttgccgag	gtacctgtgt	caaataaata	atcatgttga	tggagccaca	660
ctgtcttttg	aaacctggat	atattttt				687

<210> 1030

<211> 859

<212> DNA

<213> Unknown (H38g880 nucleotide)

<220>

<223> Synthetic construct

<400> 1030

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accttggcca	cggttcccaa	gatgattgtg	gacatggggg	cgcatagcag	agtcattctc	180
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gtcatcgtga	atcctcacct	ctgtgtcttc	ttcgttttgg	tgcccttttt	ccttagcctg	360
ttggattccc	agctgcacag	ttggattgtg	ttacaattca	ccttcttcaa	gaatgtggaa	420
atctctaatt	ttgtctgtga	gccatctcaa	cttctcaagc	ttgcctctta	tgacagcgtc	480
atcaatagca	tattcatata	ttttgataat	actatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttactataa	aattgtcccc	tccattctaa	ggatttcac	atcagatggg	600
aagtacaaag	ccttctcagc	ctgtggctgt	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gctgtgtacc	tgacttcagc	tgtggcacca	cccctcagga	atggatgggt	720
ggcgtcagtg	atgtacgctg	tggtcacccc	catgctgaac	cctttcatct	acagcctgag	780
aaacagggac	attcaaagtg	ccctgtggag	ggtgtgcaac	aaaacagtcg	aatctcatga	840
tctgttccat	cctttttct					859

<210> 1031

<211> 975

<212> DNA

<213> Unknown (H38g881 nucleotide)

<220>

<223> Synthetic construct

<400> 1031

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cctcagttgc	gggtcttctc	tttctactc	tttctgacaa	ctttctatgt	catcaatgta	120
actggaaact	tgggaatgat	tgccctcatc	cgaattgatt	cccgccttca	cacacccatg	180
tactttttcc	tcagccacct	gtcctttgtg	gacacctgct	tctcctcagt	tgtgagcccc	240
aagatgctca	ctgacttctt	tgtgaagagg	aaagccattt	ctttccttgg	ctgtgctttg	300
cagcagtgg	tctttgggtt	ctttgtggca	gcagactggt	tcctcttggg	gtccatggcc	360
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ctctgcatcc	agctagtgg	gggtccctat	gtcattggac	tcataaatac	catgactcac	480
acaacaaatg	cattttgtct	ccctttttgt	ggccctaatt	tcataaatcc	tttcttctgt	540
gatatgtccc	ccttactttc	ccttgatagt	gctgatacca	ggctcaataa	gttggcagtt	600
ttcatcgtgg	ctggagctgt	gggagctctc	agtggtctga	ctatcctgat	ttcctacatt	660
tacatcctca	tggccatcct	gaggatccgc	tctgctgatg	ggagggtgcaa	aaccttttct	720
acttgcctct	ctcacctgac	agctgttttc	atctcgatg	gtaccctttt	ctttatttat	780
gtacatccca	gtgcaacctt	ctccctggat	ctcaataaag	tagtgtctgt	gttttacaca	840
gcagtgattc	ctatgttgaa	cccacttata	tacagcttga	gaaacaagga	agtcacagat	900
gccatccaca	ggactgtcac	tcagaggaag	ttttgcaagg	cctaaattct	tatccagaag	960
gaattagggg	ggaaa					975

<210> 1032

<211> 941

<212> DNA

<213> Unknown (H38g882 nucleotide)

<220>

<223> Synthetic construct

<400> 1032

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cctatgctat	gtgccatttt	cttcgtgttt	tttctagcag	tttatatagt	tactataccg	120

ggaaatatta	gcataatcct	cttaatccaa	agcagcccac	agcttcacac	gctaattgtac	180
ctttttctca	gccatttggc	ttctgtggac	attgggtatt	ccatatcagt	tacgccaatc	240
attctcatca	atttcttaag	agagaaaacg	actattcctg	tcacaggctg	tatagcacag	300
cctggctctg	atgtcatgtt	tggaaccaca	gagtgttcc	tgctggtcac	tatgtggcta	360
tctgtctccc	cctgctttac	tccatccaaa	tgccccagt	cgtctgttcc	ctcctactgg	420
gagcctccta	cctgggtgga	tgccctgaacg	cttcgtcttt	tacaggctgt	ttgatgaacc	480
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tccttatcag	cacgctgttt	accataatcg	tgctctacat	ctacatcctt	cactccatcc	660
tgaagggtgtg	ctctactgag	ggaaggaaga	aggctttctc	cacctgctgt	tcccacctca	720
ctgcagtcac	tttgttctat	gggaccattt	tgtttgttta	tgtgatgcc	aagtcaagct	780
attcagcgga	tcagggtcaag	gtggcatttg	tgatctacac	ggtggtgatt	cccatgctga	840
acccctcat	ctacagtctc	aggaataagg	agggtgaaaga	ggccatgaga	aaattgatgg	900
caagaacaca	ttggttttcc	tgaattaaat	cagtataatc	c		941

<210> 1033

<211> 606

<212> DNA

<213> Unknown (H38g883 nucleotide)

<220>

<223> Synthetic construct

<400> 1033

atctttgcca	tcttgaccac	cattgactgc	tgtgtatttg	tctgggaatt	cctggagtgc	60
acagtctttg	tgaataagag	ggcatgtgcc	cagctggcgt	gtgggtgcctt	ttgcattggc	120
ctgatcatga	cagtgggtcta	aataaccaca	gtgtcacaga	ggtacaaaag	gagcacatat	180
gctattttaga	ctgcttcttg	tttgacaccc	ttcttgtcat	gaaactctcc	tgcatggaca	240
atactatcta	tgaaataaac	agtattttat	tcaccacaca	tgtgtgcagg	tgccatggg	300
tttgggtttgc	atttctctata	ttgacatccc	tgttacctcc	atcgtgctta	gaatttctcta	360
atctgaggtc	tttgccacct	gtgtccccca	acccccacct	catcatgggtc	attgtctata	420
tgtctgtgct	tgtactgctt	acctcaagca	caagccaatg	aattcaatag	aaaacagggtc	480
ttctataaga	gacctacatt	atcatcatc	attctgcctc	tggaactgtg	tgtttacact	540
ctgaggtaca	tggagggccaa	ggataccatg	tacagagctg	tggaacagaaa	tatttcttaa	600
cagatt						606

<210> 1034

<211> 945

<212> DNA

<213> Unknown (H38g884 nucleotide)

<220>

<223> Synthetic construct

<400> 1034

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtccc	tcctctttgc	ctatctgggtc	120
acaactgggg	gcaacctcag	catcctggca	gccgtcttgg	tggaagccaa	actccacgcc	180
cccattgtact	tcttctctggg	gaacctgtca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgcaa	tggtgggtcg	tctcttgtcc	cacaagtcca	caatttctcta	tgacgcctgc	300
ctctcccagc	tcttcttctt	ccaccttctg	gctgggatgg	actgcttctt	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagccccctca	cctacagcac	ccgcatgagt	420
cagacagtc	agaggatggt	ggtgggtgcg	tccttggctt	gtgccttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgtcctac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgtctcca	gcacccaact	caatgagctg	600
ctgtcttttg	ctgtgggttt	catcatggca	ggcacacctt	tggttctcat	catcactgcc	660
tacagccacg	tggcagctgc	agttctacga	atccgttcag	tggaagggccg	aaagaaggcc	720
ttctccacgt	gtggctccca	cctcacctgt	gtttgtcttt	tctttggaag	aggtatcttc	780
aactacatga	gactgggttc	agaggaggct	tcagacaagg	ataaaggggt	tggaattttc	840
aacactgtta	tcaaccctat	gctgaacctt	cttatctaca	gcctcagaaa	ccctgatgtt	900
cagggtgctc	tgtggcaaat	atttttgggg	aggagatcac	tgacc		945

<210> 1035
 <211> 927
 <212> DNA
 <213> Unknown (H38g885 nucleotide)

<220>
 <223> Synthetic construct

<400> 1035
 atgaagagaa agaacttcac agaagtgtca gaattcattt tcttgaggatt ttctagcttt 60
 ggaaagcatc agataaccct ctttgtggtt tctctaactg tctacatttt aactctgggt 120
 gctaacatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180
 ttcttcctaa gcatgctggc tagttcagag acggtgtaca cactgggcat tgtgccacga 240
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat 360
 gaccgctatg tggccatctg cagaccctg agatacactg tcatcatgag caagggacta 420
 tgtgccacgc tgggtgtgtg gtcccttggc attggtctga ctatggcagt tctccatgtg 480
 acagccatgt tcaatttggc gttctgtggc acagtggtag accacttctt ttgtgacatt 540
 taccagtc tgaactttc ttgcattgat accactatca atgagataat aaattatggt 600
 gtaagtccat ttgtgatttt tgtgccata ggcctgatat ttatctccta tgccttgtc 660
 atctcttcca tccttcaaat tgccctcagc gagggccgga agaagacctt tgccacctgt 720
 gtctcccacc tcaactgtgtt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780
 ccgaagtcat aaagtccaat agaaaaagac cttgttctct cagtgcgta caccatcatc 840
 actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcacct 900
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036
 <211> 958
 <212> DNA
 <213> Unknown (H38g886 nucleotide)

<220>
 <223> Synthetic construct

<400> 1036
 atgttgacaga gagggtggga aatggatgga ggcaaccaga gtgaagggtc agagttcctt 60
 ctctgtggga tctcagagag tcctgagcag cagcagatgc tgttttgat gttcctggtc 120
 aggtaccctg tcacggtgct gggaaatgtg ctcatcatcc tggccatcag ctctgattcc 180
 cgctgcaca ccccatgta cttcttctc gccaacctct ccttactga cctcttctt 240
 gtcaccaaca caatcccaa gatgctggtg aacctccagt cccagaacaa agccatctcc 300
 tacacagggt gtctgacaca gctctacttc ctggtctcct tgggtggcct ggacaacctc 360
 aacctggccg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccactatgtc 420
 acagccatga tccctgggct ctgtatcttg ctctctcct tgtgttgggt gttctctgcc 480
 ctctatggcc tcatccatat cctcctcatg accaggtgac cttctgtggg tctcaaaaga 540
 tccactacct cttctgtgag atgtacttcc tgctaaggct ggcattgtcc aacatccacg 600
 tcaaccacac agtactgggt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660
 tgatcacatc ctacgcccgc attgtcagag ccacctcca aataccctca gccactggga 720
 agtacaaagc cttctccacc tgtgcttccc atttggctgt ggtctccctc ttctatggga 780
 ctctgggtat ggtgtacctg cagccccctc aaacctactc catgaaggac tcagtagcca 840
 cagtgatgta tgcggtggtg acgcatgat taacctttc atctacagcc tgaggaaaca 900
 ggacatgcat ggggctctg gaagacttcg ccaaggaaaa gccttccaga agttgaca 958

<210> 1037
 <211> 828
 <212> DNA
 <213> Unknown (H38g887 nucleotide)

<220>
 <223> Synthetic construct

<400> 1037

atgcgaagaa	agaacctcac	agaggtaaca	gagtttggtt	tcctgggatt	ctccagattc	60
cacaaacatc	acatcactct	ctttgtgggt	tttctcatcc	tgtacacatt	aactgtggct	120
ggcaatgcc	tcatcatgac	catcatctgc	attgaccgtc	acctccacac	tcccatgtac	180
ttcttctctga	gcattgtggc	tagctcaaa	acagtgtaca	cactgttcat	cattccacag	240
atgctctcca	gcttcgtaac	ccagaccag	ccaatctccc	tagccggttg	taccacccaa	300
acgttcttct	ttgttacctt	ggccatcaac	aattgcttct	tgtcacagt	gatgggctat	360
gaccactata	tggccatctg	caatcccttg	agatacaggg	tcattacgag	caagaagggtg	420
tgtgtccagc	tgggtgtgtg	agccttttag	attggccttg	ccatggcagc	tgtccaggta	480
acatccatat	ttaccttacc	tttttgtcac	acgggtgggtg	gtcatttctt	ctgtgacatc	540
ctccctgtca	tgaacctctc	ctgtattaat	accactatca	atgagataat	caattttgtt	600
gtcagggttat	ttgtcatcct	gggtcccatg	gggtctgggtc	tcatctccta	tgtcctcatc	660
atctccactg	tcctcaagat	tgcttcagct	gagggttgg	agaagacctt	tgccacctgt	720
gccttcacc	tcactgtggt	cattgtccat	tatggctgtg	cttccattgc	ctacctcatg	780
cccaagtcag	aaaactctat	agaacaagac	ctccttctct	cagtgacc		828

<210> 1038

<211> 936

<212> DNA

<213> Unknown (H38g888 nucleotide)

<220>

<223> Synthetic construct

<400> 1038

atggatggag	ataaccagag	tgagaactca	cagttccttc	tcctggggat	ctcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggt	cacgggtgctg	120
ggaaatgtgc	tcatcatcct	ggccatcagc	tctgattccc	acctgcacac	ccccatgtac	180
ttcttctctg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaa	240
atgctgggtg	acttccagtc	ccagaacaaa	gccatctcct	atgcagggtg	tctgacacag	300
ctctacttcc	tgggtctcct	gggtgacctg	gacaacctca	tcctggccgt	gatggcgat	360
gatcgctatg	tggccatctg	ctgccccctc	cactatgtca	cagccatgag	ccctgggctc	420
tgtgtcttgc	tcctctcctt	gtgttggggg	ctgtctgttc	tctatggcct	cctcctcacc	480
ttcctcctga	ccaggggtgac	cttctgtggg	cctcgagaga	tccactacct	cttctgtgac	540
atgtacatcc	tgtgtgtggt	ggcatgttcc	aacaccacac	tcattcacac	agcattgatt	600
gccactgggt	gcttcatctt	cctcaccctc	ttaggggttca	tgaccacatc	ctatgtacgt	660
attgtcagaa	ccatccctca	aatgcctctg	gcctctaaga	aatacaaaa	tttctctacc	720
tgtgcctcgc	atttgggtgt	gggtctccctc	ttttatggga	cgcttgctat	gggtgacctg	780
cagccccctc	atacctactc	catgaaggac	tcagtagcca	cagtgatgta	tgtgtgtctg	840
acacctatga	tgaacctttt	catctacagc	ctgaggaaca	aagacatgca	tggggctccg	900
ggaagagtcc	tatggagacc	ctttcagagg	cctaaa			936

<210> 1039

<211> 898

<212> DNA

<213> Unknown (H38g889 nucleotide)

<220>

<223> Synthetic construct

<400> 1039

atggctgatg	gaaatataaa	aggatcacag	aattcatttt	tgtaggctta	aggtatcatc	60
ttcagctgca	agtcttctct	ttcttaccat	ttctaccttt	tttacctcat	tactatgaca	120
gaaaacttgg	gcattgatgg	tcgcatctgg	ctcgattcct	gctttcacac	acctatgtac	180
tttgtctctc	gctacctgtc	ctttgtggac	atctgcttct	catccgttgt	gggccacaag	240
ttgtcactg	acttatttgc	tgtaaagaaa	gccatctctt	tcctgggctg	tcccttgacg	300
cagtggttct	ttgggttctt	cgtagtcatt	gagtatcttc	tcttggcttc	catggcctat	360
gacaattatg	tggccatctg	taaccattg	ttgtactcag	tggccatgta	atagagactg	420
tgcatccagc	tgggtgttgt	acgttatgca	gctgatttct	tcaacacat	aactcacaca	480
acggctgctt	ttcattttct	cttttttcac	tccaacatta	tcaatcattt	cttctgtgac	540
atgtctctcc	ttctttctct	cgtgtgtgct	gacgcccgga	tcaataaatt	gttagttttc	600

attgtggctg	gagctgtact	agttgtcagt	agcctgacca	ttataatctc	ctatTTTTac	660
atccttactg	acattctgag	gatctgctct	gctaattggg	aagaacaaaa	ctTTTTccac	720
ctgctcttca	cacttaacag	ctgtttccat	cttttatggg	tctctcttct	ttagctacgt	780
ttcgaccagg	tgcaactttt	tacccggaac	tcaataaaaat	agtgttggtg	ttctgtacat	840
ccccatgttg	aaacctctca	tctacagctt	gataaataaa	gaagtatcct	agccacta	898

<210> 1040

<211> 934

<212> DNA

<213> Unknown (H38g890 nucleotide)

<220>

<223> Synthetic construct

<400> 1040

atggaaaaaa	taaacaacgt	aactgaattc	atTTTTctggg	gtcttttctca	gagcccagag	60
attgagaaaag	tttgttttgt	ggtgttttct	ttcttctaca	taatcattct	tctgggaaat	120
ctcctcatca	tgctgacagt	ttgcctgagc	aacctgttta	agtcacccat	gtatttcttt	180
ctcagcttct	tgtcttttgt	ggacatttgt	tactcttcag	tcacagctcc	caagatgatt	240
gttgacctgt	tagcaaaagga	caaaaaccatc	tcctatgtgg	ggtgcatgtt	gcaactgctt	300
ggagtacatt	tctttgggtg	cactgagatc	ttcatcctta	ctgtaatggc	ctatgatcgt	360
tatgtggcta	tctgtaaacc	cctacattat	atgaccatca	tgaaccggga	gacatgcaat	420
aaaatgttat	tagggacgtg	ggtagggtggg	ttcttacact	ccattatcca	agtggctctg	480
gtagtccaac	tacccttttg	tggacccaat	gagatagatc	actacttttg	tgatgttcac	540
cctgtgttga	aacttgcctg	cacagaaaca	tacattgttg	gtgttgttgt	gacagccaac	600
agtgggtacca	ttgctctggg	gagttttgtt	atcttgctaa	tctcctacag	catcatccta	660
gtttccctga	gaaagcagtc	agcagaaggc	aggcgcaaag	ccctctccac	ctgtggctcc	720
cacattgcca	tggctgttat	ctttttcgag	cccctgtact	tttatgtaca	tgcgccctga	780
tacgaccttt	tcagaggata	agatggtggc	tgtattttac	accattatca	ctcccatgtt	840
aaatcctctg	atttatacac	tgagaaatgc	agaagtaaag	aatgcaatga	agaaactgtg	900
gggcagaaat	gttttcttgg	aggctaaagg	gaaa			934

<210> 1041

<211> 951

<212> DNA

<213> Unknown (H38g891 nucleotide)

<220>

<223> Synthetic construct

<400> 1041

atggactata	gaaatcaaac	tttggttact	gaattttttt	ccgtgggatt	aacaaatctc	60
tttcagcaca	agattgctct	ctttctggta	tttctctttg	tttatcttgt	cactgttccg	120
ggaaacttgg	gaatgatcac	tcttatttgg	atggattctc	gactccagac	ccccagtac	180
ttttctctct	gccacttgte	ctttgtggat	gtctgtctct	cttctgccat	cgggtcccaag	240
atgttgactg	atatcttcgt	ggagaaaaaa	gtaatctctt	tggttgtgtt	gcccagttat	300
ggtttttttg	ccatttttga	gtaactgaat	gtttccttct	ggctgccatg	gcatatgacc	360
ggtataggct	atctataagc	ctttgttga	tacactcatt	atgtcccaac	aggctctgtg	420
gcagctgggtg	gtgggcctta	tgctgtgggc	cttataagca	ccatgacca	tatgactttc	480
acctttcgcc	tactctactg	tggtcctaac	atcatcaatc	acttctctctg	tgacctctc	540
cctgtcctct	ccctggcata	tgcagatacc	catattaata	aatgtttact	ttttatcttg	600
gtgggtgccc	tgggagtact	cagtgggtgtg	atcatcttgg	tctcctacat	ttacattgtc	660
attgccatcc	tgagaattcg	ctctgctgac	gcgagacgca	aagacttctc	cacttgctct	720
tcacacctga	tggctgtctc	catcctgtat	gggacactct	tctttatctg	tgatgttcca	780
agctctagtt	tctctatcaa	catcaataaa	gtggtttccc	tggtctacac	agcagtgate	840
cccatgttga	atcccccttat	ctacagcctg	agaaacaagg	aggtaaaaga	ttcattcagc	900
aagaagtgtg	aaagaaagaa	gtttcttata	ggtagggtgaa	ctagaatacc	a	951

<210> 1042

<211> 930

<212> DNA

<213> Unknown (H38g892 nucl otide)

<220>

<223> Synthetic construct

<400> 1042

atggtgaatt	ttacacatgt	ctcagaattt	gttctacttg	ggttccaagg	gggtcccggg	60
atgcaggcta	tgctatttct	gatttttctg	atcctgtatg	gcatagctgt	gggtgggaaac	120
cttggcatga	ttgtaattat	ctgggtagat	gcacacctcc	acacccaat	gtatgccttc	180
ctgcaaagcc	tttcattggt	ggacatctgc	tattcctcca	caattgcacc	cagggctctg	240
gcgaactcca	tgcaagagga	ccacacaatt	tcctttggcg	gatgtgctgc	tcagttcttt	300
ttcttgtctc	tctttgggat	cacagaggct	ttcctcctgg	ctgccatggc	ctatgaccgc	360
ttcatcgcca	tctgcaaccc	tcttctgtac	tctgtgagca	tgtctcacca	ggtctgtgtg	420
ctgttaatat	caggatccta	cttgtggggg	gtagtcaatg	ccattgtctc	aacaaccatg	480
accttcagg	tgcttttctg	tgggtccaat	gagatcaacg	actttttctg	tgtgttccc	540
ccactcttgt	ccctctcatg	ttcagatacc	tttataaacc	aactgggttct	tcttggttta	600
tgtggctcca	ttattgtcag	tacctttttg	attgtcctgg	tctcatacat	ttacatcatc	660
tcaacaattc	tgaggatccc	gaccatgcag	ggacgctaga	aagccttctc	cacgtgcgct	720
tcccaccta	caggagtgtg	cttgtttttt	ggtactgttt	tcttcatgta	tgcaaaccc	780
agtgccatct	tcttcatgga	gcaaagtaaa	atagtgtcca	tattctacac	tatgggtcatc	840
cccattgctga	atccccctgat	atacagcctg	aggaacaaag	aggtaacgca	ggctctgaga	900
cggagcatgc	agaagctgtc	tttgtgatca				930

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

atgagggaaa	ataaccagtc	ctctacactg	gaattcatcc	tcctgggagt	tactgggtcag	60
caggaacagg	aagatttctt	ctacatcctc	ttcctgttca	tttaccat	cacattgatt	120
ggaaacctgc	tcattgtcct	agccatttgc	tctgatgttc	gccttcacaa	ccccatgtat	180
tttctccttg	ccaacctctc	cttgggtgac	atcttcttct	catcggtaac	catccctaag	240
atgctggcca	accatctctt	gggcagcaaa	tccatctctt	ttgggggatg	cctaacgcag	300
atgtatttca	tgatagcctt	gggtaacaca	gacagctata	ttttggctgc	aatggcatat	360
gatcgagctg	tggccatcag	ccaccactt	cactacacaa	caattatgag	tccacggtct	420
tgtatctggc	ttattgctgg	gtcttgggtg	attggaaatg	ccaatgccct	ccccacact	480
ctgctcacag	ctagtctgtc	cttctgtggc	aaccaggaag	tggccaactt	ctactgtgac	540
attacccccct	tgctgaagtt	atcctgttct	gacatccact	ttcatgtgaa	gatgatgtac	600
ctaggggttg	gcattttctc	tgtgccatta	ctatgcatca	ttgtctccta	tattcgagtc	660
ttctccacag	tcttccagg	tccttccacc	aagggcgtgc	tcaaggcctt	ctccacctgt	720
ggttccacc	tcacggttgt	ctctttgtat	tatgggtacag	tcattgggcac	gtatttccgc	780
cctttgacca	attatagcct	aaaagacgca	gtgatcactg	taatgtacac	ggcagtgacc	840
ccaatgttaa	atcctttcat	ctacagtctg	agaaatcggg	acatgaaggc	tgccctgcgg	900
aaactcttca	acaagagaat	ctcctcg				927

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

atgaagaaag	aaaatcaatc	ctttaacctg	gattttattc	tcctgggagt	tactagtcag	60
caagaacaga	ataatgtctt	ctttgtgatt	ttttgtgca	tttaccat	cacactgact	120
ggaaatctgc	tcattcatctt	ggccatctgt	gctgacattc	gccttcacaa	ccccatgtat	180

tttctccttg	ccaacctctc	cttggttgac	atcatcttct	catccgtaac	catccctaag	240
gtgctggcca	accatctctt	gggcagcaag	ttcatctcct	ttgggggatg	cctaattgcag	300
atgtatttca	tgatagcctt	ggccaaggca	gacagctata	ccttggctgc	aatggcatac	360
gatcgagctg	tggccatcag	ctgcccactt	cattacácaa	caattatgag	tccacggctc	420
tgtatcctgc	ttattgctgg	gtcttgggtg	attggaaaca	ccagtgtctc	ccccacact	480
ctgctcacag	ctagtttgtc	cttctgtggc	aaccaggaag	tagccaattt	ctactgtgac	540
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ctaggggtcg	gcgttttctc	tttgccatta	ctatgcatca	ttgtctccta	tggtcaggtc	660
ttttccacag	tcttccaagt	tccatctacc	aagagtctat	tcaaagcctt	ctgcacctgt	720
ggctcccacc	tcacagttgt	ttttttatat	tatggtacaa	cgatgggcat	gtatttccgc	780
cctctgacca	gttacagccc	caaagatgca	gtgataactg	tgatgtatgt	ggcagtgacc	840
ccagcattaa	atcctttcat	ctatagtctg	agaaattggg	atatgaaggc	agccctacag	900
aaactcttca	gcaagagaat	ctcctca				927

<210> 1045

<211> 990

<212> DNA

<213> Unknown (H38g895 nucleotide)

<220>

<223> Synthetic construct

<400> 1045

gctcttcttt	tccattccta	caaacatccc	accagagga	gaatgactgt	caaaagtcac	60
tctatagtga	cagagttcag	tctcagggga	ttaacgaagc	agccagatct	ccagctcttt	120
cacttctctca	ttttccttga	tatccatatg	gtcacatgg	tggggaactt	gggcatgac	180
actctaattt	gtcttaactc	tcagcttcac	acccccatgt	actacttctt	cagcaatctg	240
tcactcttgg	atctctgcta	ttcctccatt	actaacccta	agatgctggg	gaactttgtg	300
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cacatcagca	ccactgaggg	caggtccaaa	gtcttcagca	cctgcagctt	ccaccttgca	780
gctatagggg	tggtccatgg	atagactgca	ttcaggtact	taaaaccgcg	cataaccagt	840
tccctggccc	aagagaatgt	ggcctctgtg	ttctacacta	cagtaatcta	cgtgccgaat	900
cccctaattg	acagcctgaa	aaacaaggat	gtaaaagctg	ccatgcagaa	aacactaagg	960
agtaagtttt	gttgccagatg	taattatctt				990

<210> 1046

<211> 948

<212> DNA

<213> Unknown (H38g896 nucleotide)

<220>

<223> Synthetic construct

<400> 1046

ctcctggaag	gagggaaatca	gactagcacc	tttgagttcc	tcctctgggg	actctcagac	60
cagccacagc	agcaacacat	cttcttctctg	ctgtttctgt	ggatgtacgt	ggtcactgtg	120
gctgggaacc	tgctcattgt	cctggccatt	ggcactgaca	cacacctcca	cacctctatg	180
tacttcttcc	ttgccagctt	gtcgtgtgca	gatatctttt	ccacctccac	cactgtggcc	240
aaggcccttg	tgaatatcca	gacccagagc	aggtccattt	cctacgcagg	gtgtttggca	300
cagctctact	tcttcttgac	ttttggggac	atggacatct	ttctcccggc	tacaatggcc	360
tatgaccgct	atgtggccat	ttgccacctg	ctccactata	tgatgatcat	gagcctccac	420
cgctgtgcct	tcctggtgac	agcctgctgg	accctcacaa	gtcttctcgc	catgactcgc	480
accttctctca	tattccggct	ttccttgtgc	tcttagatcc	ttcctggctt	cttctgtgat	540
ttgggaccgc	tgatgaaggt	gtcttgtctc	gacgcccagg	tcaatgagct	tgtgtctctc	600
ttcctagggg	gagcagtcac	tttaatccct	tttatgtcca	tcctgggtctc	ttatatccgc	660

attgtttcag	ccatcctcag	ggccccctct	gcccagggaa	ggcgcaaggc	cttctctacc	720
tgcgactctc	acctcggtgt	tggtgctttg	ttctttggga	cagtgatcag	ggcttatctg	780
tgcccccat	cctcttcctc	caactcagta	aaggaggata	cagcggctgc	tgcatgtac	840
acagtgggtga	ctccccgtct	gaaccccttt	atttacagca	tgcggaacaa	ggacatgaag	900
gcggcgggtg	ttagacttct	caagggcagg	gtctccttct	cacagggc		948

<210> 1047

<211> 1007

<212> DNA

<213> Unknown (H38g897 nucleotide)

<220>

<223> Synthetic construct

<400> 1047

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gatccagaac	tgcagcaggt	cgtcgctggg	ctgttcctgt	ccatgtgcct	ggcacagggtg	120
ctggggaacc	tactcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttggtcc	tctccaacct	gtcccttgcc	tgacatcggt	ttcacctcca	ccacgggtccc	240
caagatgatt	gtggacatcc	agtctcacag	cagagtcatc	tcctatgcag	gctgcctgac	300
tcagatgtct	ctctttgccca	tttttgagg	tatggaagag	agacatgctc	ctgagtgtga	360
tgccctatga	ccggtttgta	gccatctgtc	accctctata	ttgttcagcc	atctttaacc	420
cgtgtttctg	tggcttccta	gatttggtgt	cttttttttt	ttttttctca	gtctttcaga	480
ctcccagctg	cacaacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaaattcc	540
taattttctc	tgggaacctt	ctcaactctc	ccatcttgca	tggtgtgaca	ccttcaccag	600
gaacatcagt	atttcctctg	tgccatattt	ggttttcttc	ccatcttggg	gacccttttc	660
tcttactgta	aaattgtttc	ctccattctg	aggggttcat	catcagggtg	gaagtataaa	720
ccttctccac	ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcattg	780
gagggtacct	cgggttcagat	gtgtcatctt	ccccgagaaa	gggtgcagtg	gcctcagtga	840
tgatcatggt	ggtcaccccc	atgtggaacc	ccttcattcta	cagcctgaga	aacagggata	900
tgaaaagtgt	cctgcggcgg	ccgcatggca	gcacagtcta	atctcaacat	cttcttatct	960
gttcattccc	ttttgtaggg	tggtttaaaa	aaggcgccaa	ggtcaaa		1007

<210> 1048

<211> 926

<212> DNA

<213> Unknown (H38g898 nucleotide)

<220>

<223> Synthetic construct

<400> 1048

atgagacaga	ataataatat	tacagaattt	gtcctcctgg	gcttctctca	ggatctggat	60
gtgcaaaaag	cattattttg	catattttta	ctcacatact	tggtgacagt	ggtaggggaa	120
ctgctcattg	tggtgactat	tattaccagc	ccttccttgg	gctccccaat	gtacttcttc	180
cttgccctgcc	tgatcatttt	agatgctgca	tattccacta	caatttctcc	caaattgatt	240
gtagacttac	tctgtgataa	aaagactatt	tctttcccag	cttgcatggg	ccagttattt	300
atataccact	tgtttggtgg	ttctgagggtc	ttccttcttg	tggtgatggc	ctgtgatcac	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgaatc	420
cttctgttgg	tggtgggtcg	gactggagggt	tttctgcatt	ctgtgtttca	aattgttggt	480
gtatacagtc	tcgctttctg	tggtcccaat	gtcattgact	actttgtctg	tgacatgtac	540
ccattattgg	aactgggtatg	cactgacacc	tactttattg	gccttactgt	ttttgtcaat	600
ggtaggaacaa	tctgtatagt	cgtcttcacc	cttctactaa	tctcctatgg	agtcaccta	660
aactccctta	aaacttacag	tcaagaagg	aggcataaag	tcctgtttac	ctgcagctcc	720
cacattatcg	tctttgccct	cttttttggt	ccctgtatgt	tcattgtatg	tagacctgtt	780
tcaaacatcc	ttttgataaa	ttcctgacag	tggtttatac	agttatcaca	cccatgttga	840
atcctttaat	atacacattg	agaaattcag	agatgagaaa	ttctgtagaa	acactcttgt	900
gtaaaagtta	actgtattag	agtaag				926

<210> 1049

<211> 939

<212> DNA

<213> Unknown (H38g899 nucleotide)

<220>

<223> Synthetic construct

<400> 1049

atggaaagaa	tcaacagcac	actggtgact	gcgtttatcc	tgacaggaat	tccgtatcca	60
ctcaggctaa	ggacactctt	ttttgtgttc	ttttttctaa	tctacatcct	gactcagctg	120
ggaaacctgc	ttattttaat	cactgtctgg	gcagacccaa	ggctccatgc	ccgccccatg	180
tacatctttc	ttgggtgttc	ctcagtcatt	gatatgagca	tctcctccat	cattgtccct	240
cgcctcatga	tgaacttcac	tttaggtgtc	aaacccatcc	catttggtgg	ctgtgttgct	300
caactctatt	tctatcactt	cctgggcagc	acccagtgtc	tcctctacac	cctaattggc	360
tatgacaggt	acctggcaat	atgtcagccc	ctgcgctacc	ctgtgtcat	gactgctaag	420
ctgagcgcct	tgcttgtggc	tggagcctgg	atggcaggat	ccatccatgg	ggctctccag	480
gccatccctaa	ccttccgcct	gccctactgt	gggcccacac	aggtggatta	cttcttctgt	540
gacatccctg	cagtgttgag	actggcctgt	gctgacacaa	cagtcaacga	gctgggtgacg	600
ttttagagca	ttgggggtgt	ggttgccagt	tgcttctccc	tgatcctcct	ctcctacata	660
cagatcattc	aggccatcct	gagaatccac	acagctgatg	ggcggcgccg	ggctttttca	720
acttgtggag	cccatgtaac	cgtgggtcacc	gtgtactatg	tgccctgtgc	cttcatctac	780
ctgaggcctg	aaaccaacag	ccccctggat	ggggcagctg	ccctagtccc	cacggccatc	840
actcctttcc	tcaacccctt	tatctacact	ctgcggaacc	aagaggtgaa	gctggccctg	900
aaaagaatgc	tcagaagccc	aagaactccg	agtgaggtt			939

<210> 1050

<211> 954

<212> DNA

<213> Unknown (H38g900 nucleotide)

<220>

<223> Synthetic construct

<400> 1050

atgggaaaga	ccaaaaaacac	atcgctggac	actgtggtga	gagatttcat	tcttctgggt	60
ttgtctcacc	ccccgaatat	aagaagcctc	ctcttctctg	tcttctctgt	cattttacatc	120
ctcactcagc	tggggaacct	gtcattctct	ctcaccgtgt	gggctgaccc	gaagctccgt	180
gctcgcccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctctctca	240
gtcatcggtc	cttgaattat	tttaaaactc	actcctgcca	acaaggctat	cccgtttgggt	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttctctctac	360
accttgatgg	cctatgacag	gtacctggca	atatgtcagc	ccctgcgcta	cccagtgtct	420
atgaatggga	ggttatgcac	agtccttggt	gctggagctt	gggtcgccgg	ctccatgcgt	480
gggtctatcc	aggccaccct	gaccttccgc	ctgccctact	gtgggcccac	tcaggtagat	540
tactttatct	gtgacatccc	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagcttgtga	cctttgtgga	catcggggta	gtggccgcca	gttgcttcat	gttaattctg	660
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tacactgttg	tactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt	caagggactg	aatgaaaata	agta	954

<210> 1051

<211> 930

<212> DNA

<213> Unknown (H38g901 nucleotide)

<220>

<223> Synthetic construct

<400> 1051

atgggaaaga	ccaaaaaacac	atcgctggat	gccgtggtga	cagatttcat	tcttctgggt	60
ttgtctcacc	ccccaaatct	aagaagcctc	ctcttctctg	tcttcttcat	cattttacatc	120

ctcactcagc	tggggaacct	gctcattctg	ctcaccatgt	gggctgaccc	gaagctctgt	180
gctcgcccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctcctca	240
gtcaccgttc	ctcggttat	tttggatttt	actccttcca	tcaaggctat	cccgtttggg	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttcctctac	360
accttgatgg	cctatgacag	gtacctagca	atatgtcagc	ccctgcaacta	cccagtgtc	420
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cgggccttct	ccacctgtgg	ctcccaccta	atcgtgggtc	cagtctacta	tgtcccctgt	780
attttcatct	accttagggc	tggtccaaa	gacccctgg	atggggcagc	ggctgtgttt	840
tacactgttg	tactccatt	actgaacccc	ctcatctata	caactgaggaa	ccaggaagtg	900
aagctcgccc	tgaagaggat	aacagcagg				930

<210> 1052

<211> 900

<212> DNA

<213> Unknown (H38g902 nucleotide)

<220>

<223> Synthetic construct

<400> 1052

atgtttatat	tgacaggcct	cacagatgat	tttgagctgc	aagctcttct	atttttacta	60
ttttttgcaa	tctatctctt	taccttgata	ggcaatttag	ggctgggtgt	gttggtcatt	120
gaggattcct	ggctccacaa	ccccatgtat	tattttctta	gtgttttata	attcttggat	180
gcttgctatt	ctacagttgt	cactccaaaa	atgttggtca	atttcctggc	aaaaataaaa	240
tccatttcat	ttatcgggat	tgcaacacag	atgcttcttt	ttgttacttt	tggaactaca	300
gaatgttttc	tcttggtgtc	aatggcttat	gatcactatg	tagccatcta	caacctctc	360
ctgtattcag	tgagcatgtc	accagagtc	tatgtgccac	tcatactgc	ttctacgtt	420
gctggcattt	tacatgctac	tatacatata	gtggctacat	ttagcctgtc	cttctgtgga	480
tccaatgaaa	ttaggcattg	cttttgtgat	atgcctctct	tccttgctat	ttcttgttct	540
gacactcaca	caaaccagct	tctactcttc	tactttgtgg	gttctattga	gatagtcact	600
atcctgattg	tctctatttc	ctgtgatttc	attctgttgt	ccattctgaa	gatgcattct	660
gctaagggaa	ggcaaaaggc	cttctctaca	tgtggctctc	acctaaactg	agtgaacaatt	720
tatcatggaa	caattctcgt	cagttatatg	agaccaagtt	ccagctatgc	ttcagaccat	780
gacatcatag	tgtcaatatt	ttacacaatt	gtgattccca	agttgaatcc	catcatctat	840
agtttgagga	acaaagaagt	aaaaaaggca	gtgaagaaaa	tgttgaaatt	ggtttacaaa	900

<210> 1053

<211> 974

<212> DNA

<213> Unknown (H38g903 nucleotide)

<220>

<223> Synthetic construct

<400> 1053

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tctcctctggg	actctcagag	60
gatccagaac	tgcagccagt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acgggtgctga	ggaacttgct	gagcatcctg	gctgtccgct	ctgagtcctc	gtccacaca	180
accatgtact	tcttctcttc	catcctgtgc	tgggctgaca	tcggtttcac	ctcagccaca	240
gttcccaaga	tgattgtgga	catgcagtg	tatagcaaag	tcattctctca	tcggggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatg	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	aggcatctgt	cgccctctgc	actaccagct	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaaact	gctgttctg	acagcgtcat	caatagcatc	600
ttcatatatt	ttggtagtac	tatgtttggt	ttcttctcca	tttcagggat	ccttttgtct	660
tactataaaa	tcgtcccttc	cattctaagg	atttcatcgt	cagatgggaa	gtataaagcc	720

ttctccacct	atggctctca	cctagcagtt	ttttgctgat	ttgatggaac	aggcattggc	780
gtgtacctga	cttcagctgt	ggcaccaccc	ctcaaggaa	gggtggtgg	tgtcagtga	840
gtaagctgtg	gtcaccccc	atgccgaacc	ttttcatcta	cagcctggag	aaacagggac	900
atacaaagt	ccctgcggag	gctgccaac	aaaacagtcg	aatctcatga	tctgttccat	960
cctttttctg	gtgt					974

<210> 1054

<211> 1006

<212> DNA

<213> Unknown (H38g904 nucleotide)

<220>

<223> Synthetic construct

<400> 1054

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gattcagaa	tgcaaccggt	cgctcgtggg	ctgttcctgt	ccatgtgcct	cgctcaggtg	120
ctggggaacc	tgctcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tactttctcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgattg	tggacatcca	gtctcacagc	aaagtcactc	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tggaggcatg	gaaaaaagac	atgctcctga	gtgtgatggc	360
ctatgaccgg	tttgtacc	tctgtcaccc	tctatatcgc	tcagccatct	tgaaccctgt	420
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agctgcacaa	cttgattggc	ttacaaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	tttccctgct	gccgtatttg	gttttctttc	catctcgggg	acccttttct	660
cttactgtaa	aatgggtttc	tccattctga	gggtttcatc	atcagggtggg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tgtttgctga	ttttatggaa	caggcggttg	780
agagtacctc	gggttcagatg	tgtcatcttc	cccagagaa	gggtgcagtg	cctcagtgat	840
gtacacgggtg	gtcaccccc	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcggcggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaa		1006

<210> 1055

<211> 929

<212> DNA

<213> Unknown (H38g905 nucleotide)

<220>

<223> Synthetic construct

<400> 1055

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gccaaaaagt	tttattttgtc	acattcttac	tcattctacat	tgtgacgata	atgggcaacc	120
tccttatcat	ggtgaccatc	atggccagcc	agtcctctggg	ttcccccatg	tacttttttc	180
tggtctcttt	atcattttata	cataccgtct	attatactgc	cattgctccc	aaaatgattg	240
ttgacctgct	ctctgagaaa	aagaccattt	cttttcaggg	ttgtatggct	caacttttta	300
tggatcattt	atttgctggg	gctgaagtca	ttcttctggg	ggtaatggcc	tatgatcaat	360
atgtggccat	ctgtaagcct	cttcattatt	tgatcatcat	gaatcgctga	gtctgtgttc	420
tcattgtgtt	ggtggcctgg	attggaggct	ttcttctactc	attgggttcaa	tttctcttta	480
tttatcagct	ccctttctgt	ggacccaatg	tcattgacaa	cttcctgtgt	gatttgatc	540
ccttattgaa	acttgcttgc	accaatacct	atgtcactgg	gctttctatg	atagctaattg	600
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acatcactgt	gataccttta	ttctttgtcc	cctgcattct	cctgttagca	aggcccaact	780
ccacctttcc	cattgataaa	tccatgactg	tggttttaac	ttgtataact	cccatgctga	840
aaccactaat	ctatgccttg	aggaatgcag	aaatgaaaag	tgccatgagg	aaacttttga	900
gtgaaaaagt	aagcttagct	ggaaaaggg				929

<210> 1056

<211> 925

<212> DNA

<213> Unknown (H38g906 nucleotide)

<220>

<223> Synthetic construct

<400> 1056

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ttgcagaaaa	tactctttat	tgtattttta	tttatttttc	tatttaccat	gctggccaat	120
ctgttcattg	tcatacccat	ctcctgtagc	cccacacttt	catcacccat	gtacttcttt	180
ctcacttact	tatcctttat	agatgcctcc	tacacctctg	tcacaacccc	caaatgac	240
accgacctgc	tctaccagag	gagaactatt	tccttggtg	gctgcctgac	tcagctcttt	300
gtggagcact	tgctgggagg	ctcagagatc	atcctcctta	ttgtcatggc	ctatgaccgc	360
tacgtggcca	tctgcaagcc	cctgcactac	acaaccatta	tgcaacaagg	gatctgccac	420
cttctgggtg	tgatagcctg	gattggaggc	atcctgcatg	ccactgtgca	gattcttttc	480
atgaccgact	tgcccttctg	tggtcccca	tgctattgac	cactttatgt	gtgatctctt	540
cccattgttg	aaacttgctt	gcagagacac	ctacagactt	gggatgctgg	tggcagccaa	600
cagtggagcc	atgtgcttgc	tcattctttc	cctgctctgc	atctcctaca	tagtcatcct	660
gagctccctg	aaatcctata	gctctgaagg	acagcacaaa	gccctctcca	cctgtggctc	720
ccactttact	gtcgttgtag	tcttttttgt	gccttgcata	ttcacctaca	tgcattcctgt	780
ggtcacctac	tctgtggaca	agttggtgac	tgtgttcttt	gcaatcctca	ctcccatgtt	840
aaatcctata	atttacctg	tgagaaacac	agaggtaaaa	aatgccgtga	ggagtttgtt	900
gagggaaaaga	gtaacagttt	atgca				925

<210> 1057

<211> 499

<212> DNA

<213> Unknown (H38g907 nucleotide)

<220>

<223> Synthetic construct

<400> 1057

atgtacacga	ctttactcat	ggcccagggt	gtgtctctgt	gcagacaatg	gatcccacac	60
tctttctgtg	atatgtctgc	tctgctgaag	ctggccctct	ctgacactcg	agttaatgaa	120
tgagtatat	ttatcatggg	agggtcatt	ctgtcatcc	catccatact	catccttggg	180
tcctatgcaa	gaattgtctc	ctccatcctc	aaggctccct	cttctaagt	tatctgcaag	240
gccttctcta	cttgtggctc	ccaccctgtc	tgtggtgtca	ctgttctatg	gaaccgttat	300
tggtctctac	ttatgtctcat	cagctaatag	ttctactcta	aaggacactg	tcatggctat	360
gatgtacact	gtggtgaccc	ccatgctgaa	ccccttcac	tacagcctga	ggaacagaga	420
catgaaggga	gccctgagca	gagtcattca	tcagaagaaa	actttcttct	ctctctgatg	480
ataacacttg	gagctatta					499

<210> 1058

<211> 996

<212> DNA

<213> Unknown (H38g908 nucleotide)

<220>

<223> Synthetic construct

<400> 1058

atgggaccaa	agaatctaac	tcgtgttttg	gaattcttcc	tcctccactt	cttagatgac	60
ttggaactgc	agcctttcct	cttcaggctg	tcctgaacc	atgcacctag	tcacagtgtc	120
tgcgaacttg	ctcacatcct	tctgactgtc	agctttgccc	tcacctccac	aaccccatga	180
acttcaacct	gtccttagct	gacattggtt	tcacctctgc	cacaatttca	aagataactg	240
tagacctcca	aactcacagc	agaatcattt	tatacatgag	ctgcctgaaa	tagatgtctt	300
ttaaaattat	ttttggatgt	ttgcacaatc	tactcatgac	tgtgatggcc	tatgacccat	360
ttgtggcgac	ctgtcatctc	ttgtactaca	cagtgatcag	gaatccccac	ctctgtggcc	420
tcctgtctct	ggtctctctc	tctctctctc	tttttttttt	ttgatcagtc	ttttggaaac	480
ccagctgtac	agtttgatgg	tgtcacaagt	tctctcatgc	aaatgtagac	attcctcatt	540

tcttctgtga	cccttctcag	tttctccacc	tttcctgttc	tgacactgcc	accaataaca	600
cattaatgca	ttttattggt	gccatctctg	tgggtccattc	tcagggatcc	tttactgtta	660
tactcaaat	atgttctcca	tactcataac	cctataaaat	gtgggaagta	taaagcaaac	720
cttctccacc	catcgctctc	acctgtcagt	tgtttgctta	ttttatggaa	caggccttgg	780
agtatacctt	agtttggtcg	gtcacacctc	cccaagaaca	ggtgtggtgg	cctcaatggt	840
atataccaca	gtcacctcca	tgttgaaccc	tgcattcaca	gcctgaggaa	cagagacatc	900
aagaatacct	ggtggtggct	cctcagcata	actgcctggg	atcaatacct	gtgctatcct	960
ttatggagtg	tgggttagaaa	aaacagcaaa	ctcaaaa			996

<210> 1059

<211> 923

<212> DNA

<213> Unknown (H38g909 nucleotide)

<220>

<223> Synthetic construct

<400> 1059

atggggactt	caaataatga	gactgaattc	attcttttgg	gcattacaaa	aaatccagaa	60
ctaaggaaaa	tattctctgc	tttgtttcta	gccatgtatg	tgaccacagt	gttgggaaat	120
ctattcattg	tgggtgactct	ggctgcaagt	tggagtctga	gatcacctat	gtacttttcc	180
cttacttctt	tgtctctcat	gggtgccacc	tactcttcca	tactgcccc	taagatgact	240
gtggactctt	tgagaacact	accatttccc	ttgaaggctg	catgaccag	ctctttgcag	300
agcatttctc	tgatggtgta	gcgatcatcc	ttctcactgt	gatggtctgt	gactgctatg	360
aggccatcag	taagcccctg	catgacacaa	ccatcatgag	tccacgggtg	tgctgctgtt	420
ggtggtagaa	gcttgggtgg	ggggattaac	acatgccaca	atacagcttt	ttttttttca	480
tatatcaaat	acccttctgt	ggtcccaata	ttattgacca	ttttatatgt	gatttgtttc	540
cattgttaaa	acttgcttac	atggacaccc	acatgctggg	tctcttagtc	atcctcaaca	600
gtggggtgat	gtgtatggcc	atcttcccta	tcctaattgc	atcctacatt	gtcacctgtt	660
actctctgaa	gtcttgacgc	tcggtaggtc	gacgcaacac	actttccacc	tgtggctccc	720
accacacagt	ggtcatcttg	ttcttcgtgg	agtgtatttt	cttgtagata	agacctgtgg	780
tcacttacct	catagacaag	gatatggcta	tttccctttac	tattgttgca	cccatgttaa	840
atcctctgat	ctataccctg	aggggcatca	aggtaaaaaa	tgccataaga	aaaatgtgga	900
tgaaacaggg	gaccctaggt	ggt				923

<210> 1060

<211> 950

<212> DNA

<213> Unknown (H38g910 nucleotide)

<220>

<223> Synthetic construct

<400> 1060

atggctccga	ccaacctcac	atctgcccc	gctgttcttc	ctcctcggcc	tggtggacgg	60
aacagacgcc	caccgcgtgc	tgttctctgt	ctgccttggg	tctatctgct	caacgccttg	120
agcaacctga	gcatggtggc	gctggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcactgagc	ctcgtggacg	tctgctttac	caccgtcacg	gtccccaggc	240
tgctggccgg	cctgctccac	ccggggccagg	ccatatcctt	ccaggcgtgt	ctgccgagat	300
gtacttcttc	gtgactctgg	catcaccgag	agctacctca	tggcggccat	gtcctagcga	360
gcccagacggc	gcgtgcccgc	acctctgtac	ggcgcgctgg	tgacgccatc	ggcgtgcgcc	420
tgctggtgcg	tgcgtcgtgg	gccgtgacgc	acctgcactc	gctgctgcac	acgctgctcc	480
tctccgcgct	ctcctacccc	tacccacccc	ccgtgcgccc	cttcttttgc	gacatgacgg	540
tgatgctgag	cttggcgacc	tcggacacgt	ccggccgagg	gacggccatc	ttctccgagg	600
gcctggccgt	ggtgttggcc	ccgtgctctc	tcgtgttctc	tttcttacgc	gcgcaccttg	660
gtcgcggtgc	tcggcttgcg	cggccgcgcc	gcgccttctc	cacctgcggg	gcccacctag	720
tggcggtggc	ggtggcgctt	ttctttggct	ctgtcctctc	cgtgtatttc	ccgcccgtcg	780
ctgcctactc	agccccgtac	gaccgcctgg	ccagcgtggg	ctacgctgtc	atcacgccga	840
ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	caagggcgcc	ctgaaaaggg	900
ggctcagcat	ggagggctgc	accccaagag	gcgtgagggc	aaatctggct		950

<210> 1061
 <211> 933
 <212> DNA
 <213> Unknown (H38g911 nucleotide)

<220>
 <223> Synthetic construct

<400> 1061
 atgaaagggg caaacctgag ccaagggatg gagtttgagc tcttgggcct caccactgac 60
 cccagctcc agaggctgct cttcgtgggtg ttcttgggca tgtacacagc cactctgctg 120
 gggaacctgg tcatgttccct cctgatccat gtgagtggca ccctgcacac acccatgtac 180
 tccctcctga agagcctctc cttcttggat ttctgctact cctccacggg tgtgccccag 240
 accctgggtga acttcttggc caagaggaaa gtgatctctt attttggctg catgactcag 300
 atgttcttct atgcggggtt tgccaccagt gagtgtctatc tcatcgctgc catggcctat 360
 gaccgctatg ccgctatttg taacccccctg ctctactcaa ccatcatgtc tcctgagggtc 420
 tgtgcctcgc tgattgtggg ctctacagt gcaggattcc tcaattctct tatccacact 480
 ggctgtatct ttagtctgaa attctgcggg gctcatgtcg tcaactcact cttctgtgat 540
 gggccaccca tctgtctctt gtcttgtgta gacacctcac tgtgtgagat cctgctcttc 600
 atttttgctg gtttcaacct tttgagctgc accctcacca tcttgatctc ctactttctta 660
 attctcaaca ccattcctgaa aatgagctcg gcccagggca gggttaaggc attttccacc 720
 tgtgcattcc acctcactgc catctgcctc ttcttgggca caacactttt tatgtacctg 780
 cgccccaggt ccagctactc cttgaccag gaccgcacag ttgctgtcat ctacacagtg 840
 gtgatccag tgctgaacct cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062
 <211> 948
 <212> DNA
 <213> Unknown (H38g912 nucleotide)

<220>
 <223> Synthetic construct

<400> 1062
 atgcaaaacc aaagctttgt aactgagttt gtcctcctgg gactttcaca gaatccaaat 60
 gttcagggaa tagtatttgt tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120
 atgctaattg tagtaacatc tctcagcagc cctgctcttc tgggtgtctcc tatgtacttc 180
 ttcttgggct tctgtctctt cctggatgag tgcttctcat ctgtcatcac cccaaagatg 240
 attgtagact ccctctatgt gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300
 tttgtgtaac acttctttgc tgggggtggag gtgattgtcc tcacagccat ggcctatgat 360
 cgttatgtgg ccatttgcaa gcccttgcac tactcttcta tcatgaacag gaggctctgt 420
 ggcattctga tgggggtagc ctggacaggg ggctcttgc attccatgat acaaattctt 480
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcaacttat gtgtgacttg 540
 taccggttac tggagcttgc ctgcaactgat actcacatct ttggcctcat ggtggtcatc 600
 aacagtgggt ttatctgcat cataaacttc tcttgtttgc ttgtctccta tgctgtcatc 660
 ttgtctcttc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720
 tctcacattg ctgttgtgat tttgttcttt gtcccatgca tatttgtata tacacgacct 780
 ccactctgct tttcccttga caaatggcg gcaatatttt atatcatctt aaatcccttg 840
 ctcaatcctt tgatttacac tttcaggaat aaggaagtaa aacaggccat gaggagaata 900
 tggaacagac tgatggtggt ttctgatgag aaagaaaata ttaaactt 948

<210> 1063
 <211> 930
 <212> DNA
 <213> Unknown (H38g913 nucleotide)

<220>
 <223> Synthetic construct

<400> 1063

atgcaactga	ataataatgt	gactgagttc	attctgcttg	gattgacaca	ggatcctttt	60
tggaagaaaa	tagtggttgt	tatttttttg	cgtctctact	tgggaacact	gttgggtaat	120
ttgctaataca	ttattagtgt	caaggccagc	caggcactta	agaacccaat	gttcttcttc	180
cttttctact	tatccttata	tgatacttgc	ctctctactt	ccatagcccc	tagaatgatt	240
gtggatgccc	ttttgaagaa	gaaactatac	tccttcagcg	agtgcacgat	ccaagtcttt	300
tcattcccatg	tctttggctg	cctggagatc	ttcatcctca	tcctcacggc	tgttgaccgc	360
tatgtggaca	tctgtaagcc	cctgcactac	atgaccatca	taagccagtg	ggctctgtgg	420
gttttgatgg	ctgtggcctg	gggtgggatcc	tgtgtgcatt	ctttagttca	gatttttctt	480
gccctgagtt	tgccattctg	tggccccaat	gtgatcaatc	actgtttctg	tgacttgcag	540
cccttgttga	aacaagcctg	ttcagaaacc	tatgtgggta	acctactcct	gggttccaat	600
agtggggcca	tttgtgcagt	gagttatgtc	atgctaatat	tctcctatgt	catcttcttg	660
cattctctga	gaaaccacag	tgtctgaagt	ataaagaaag	cactttccac	atgtgtctcc	720
cacatcattg	tggctatctt	gttctttgga	ccttgcatac	ttatgtacac	atgccctgca	780
accgtattcc	ccatggataa	gatgatagct	gtattttata	cagttggaac	atcttttctc	840
aaccctgtga	tttacacgct	gaagaataca	gaagtgaaaa	gtgccatgag	gaagctttgg	900
agcaagaaat	tgatcacaga	tgacaaaaga				930

<210> 1064

<211> 964

<212> DNA

<213> Unknown (H38g914 nucleotide)

<220>

<223> Synthetic construct

<400> 1064

atggagacaa	caaatacctc	tgccgtgact	gaattctttc	tggtggggct	ttcccaatat	60
ccagagctcc	agctttttct	gttcctgtct	tgccctcatc	tgtacatgat	aatcctcctg	120
ggaaatagct	tcctcattat	catcaccatc	ttggattctc	gcctccatac	ccccatgtat	180
ttctttcttg	gaaacctctc	attcttgggc	atctgttaca	catcatcatc	cattcctcca	240
atgcttatta	tatttgtatc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atggttggtg	cccttggctt	gggctccatt	gagtgatccc	tcctggctgt	gatggcctat	360
gaccgctatg	tggccatctg	caaccactg	aggtactcca	tcacatgaa	cagagtgtctg	420
tatgtgcaaa	tggctgcatg	gtcctggatc	ataggctgtc	tgacctccct	attgccaaca	480
gttctgacaa	tgatgttgcc	tttctgtggg	aataatatca	ttgatcatct	tacctgtgag	540
atcctggctc	ttcttaaagt	catatgctca	gatatctcca	taaatgtgtt	tataatgaca	600
gtgtcaagta	ttgttttatt	ggtgatccct	cttaattttt	atctcctatg	tgtttattct	660
ctcttccatc	ttgagaatta	attctgtctg	gggaagaaag	aaagcctttt	ttacctgttc	720
agcgcacttg	actgtggtca	tcttattcta	tggttcagtt	cttttcatgc	acatgaagcc	780
caaatcaaaag	ttcacaaacag	catctgatga	aatcattgga	ttgtcttatg	aagtgatcac	840
cccaatgaac	cccatcatct	acagcctgag	gaataaggag	ataaaagaag	ctgtgaagaa	900
aatcctcagc	agacacgtgc	atctatggaa	aatatgaaag	gccttgaggc	atgtgacgtt	960
ctca						964

<210> 1065

<211> 620

<212> DNA

<213> Unknown (H38g915 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(620)

<223> n = A,T,C or G

<400> 1065

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ctttttcctg	aagaacctct	ctgttttggg	tctgtgctac	atctcagtc	ctgtgcctaa	120
atccatccgt	aactccctga	ctcgacagaag	ctccatctct	tatcttggct	gtgtggctca	180
agcctatttt	ttctctgcct	ttgcatctgc	tgagctggcc	ttccttactg	tcatgtctta	240

tgaccgctat	gttgccattt	gccaccccct	ccaatacaga	gccgtgatga	catcaggagg	300
gtgctatcag	atggcagtca	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggcaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tgttccgtga	420
catccctcag	gtgttgcccc	tggtttcctg	ngaggltttc	ttttagagac	tttgacccng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anactttctn	aanggggctc	nagaatccct	tnaggaccag	antcnaagta	aaagcctttn	600
cccnctgct	ccccccacg					620

<210> 1066

<211> 611

<212> DNA

<213> Unknown (H38g916 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 1066

gatgcatgct	cgagcgggcg	ccagtgtgat	ggatatctgc	agaattcgcc	cttccaatgt	60
atttattttct	ctctgacctc	tccttcttgg	acctctgctt	taccacaagt	tgtgtccccc	120
agatgctggg	caacctctgg	ggcccaaaga	agaccatcag	cttccctggga	tgtctgtgtcc	180
agctcttcat	cttccctgtcc	ctggggacca	ctgagtgcag	cctccctgaca	gtgatggcct	240
ttgaccgata	cgtggctgtc	tgccagcccc	tccactatgc	caccatcatc	cacccccgcc	300
tgtgctggca	gctggcatct	gtggcctggg	ttatgagtct	ggttcaatcg	atagtccaga	360
catcatccac	cctccacttg	cccttctgtc	cccaccagca	gatagatgac	tttttatgtg	420
aggteccatc	tctgattcga	ctctcctgng	gagataacctc	ctacaatgaa	atccagttgn	480
ctgtgtccag	tgtcatcttt	ggtggntgtg	cctctcagcc	tcatecttgc	ctcttatgga	540
gccactgccc	aggcnggggc	tgaggattaa	ctttgcnna	gccatggaag	aaaggtcttt	600
nggacctngn	n					611

<210> 1067

<211> 619

<212> DNA

<213> Unknown (H38g917 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 1067

gatgcatgct	cgagcgggcg	ccagtgtgat	ggatatctgc	agaattcgcc	ctttctttat	60
ttcgaagagt	atacactagt	ggattgaaga	gaaacaaata	cataggaagg	gcgaattcca	120
gcacactggc	ggccgttact	agtggatccg	agctcgggtac	caagcttgat	gcatagcttg	180
agtattctaa	cgcgtcacct	aaatagcttg	gcgtaatcat	ggatcatagct	gtttcctgtg	240
tgaattgtt	atccgctcac	aattccacac	aacatacgag	cgggaagcat	aaagtgtaaa	300
gcctgggggtg	cctaattgagt	gagctaactc	acattaattg	cgttgcgctc	actgtccgct	360
ttccagtcgg	gaaacctgtc	gtgccagctg	cattaatgaa	tcggccaacg	cgcgngnaga	420
ggccggnttg	cgtattgggc	gctcttccgc	ttctcgctca	ctgactcgct	gcgctcggga	480
cgtccggctg	cggcgagcgg	tatcagctta	ctcaanggcc	gtantacggt	tattcncagg	540
aatnnggggt	taacgccngg	naaagaacat	tgtnggccan	angncaagcn	taatgcccag	600
gaaccgntan	aacgntccc					619

<210> 1068

<211> 621

<212> DNA

<213> Unknown (H38g918 nucleotid)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

gnnnnntntt cantccattg ggcctcttag atgcatgctc gagcgccgc cagtgtgatg	60
gatatctgca gaattcgccc ttattccgga gggatatacat gaagggattg gtaactagac	120
gtaaaactcga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa	180
gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag	240
actctgaaag aggtggaag gattgaatac aatcaaaagt atgggtgactg ctagtccaa	300
gatgggtggcg taggggcaag ctggctttgc ttacccccct ggcagaaaac caaaaacaaa	360
tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc	420
cagggcccg agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt	480
tctaaggag acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc	540
cataaaacaa agattgaaa atgttgaatt ttgcaaccag gagcaatac tgggaaaggc	600
gaattccagc cactgcngc c	621

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

gnnnnntnnt tcantgcct ngggccctct agatgcatgc tcgagcgcc gccagtgtga	60
tgatattctg cagaattcgc ccttgttgcg caaggtgtaa atgaaaggt ttgcgaggga	120
gtaaatgaag ggattacgca ggagtaaag aagggtattc gcaggagtaa atgaaggat	180
tacgcaggag taaatgaagg gattacgcag gagtaaagta agggattacg caggagtaa	240
tgaagggtatt acgcaggagt aaatgaagg attacgcagg agtaaagta gggattacgc	300
aggagtaaag gaagggatta cgcaggagta aatgaaggga ttacgcagga gtaaagtaag	360
ggattacgca ggagcaata cataggaagg gcgaattcca gcacactggc ggccgttact	420
agtggatccg agctcggtac caagcttgat gcatagcttg agtattctaa cgcgtcacct	480
aaatagcttg gcgtaatcat ggtcatagct gtttctctgt tgaaattgtt atccgctcac	540
aattccacac aacatacgag cccggaagca taaagtgtaa agnctggggt gcctaatag	600
tgacttactc catta	615

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

ggnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatata	60
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tgcagaattc gcccttccga tgtattttct tctacgttaa ggtatttttaa attgttacta	120
atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat	180
gatgctgtta cctcaciaaat atgtatgtgt ggatgtatat atatctattc aatatatgta	240
actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct	300
agtgtctcag ataagttggc tagttttttg tttcacataa aggaacaaac atttatagat	360
ttatatgtat attaaaaatg gtaaaaattg gctgggtgca gtggttcacg cctataatac	420
cagcactttg ggaagccgag gtgggcggat tacttgaggt aaggagccc3 gcctgaccaa	480
caaggtgaaa ccccatccct actaaaaata caagaattag cccgggggatg gtgggtggcca	540
cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng	600
aggttgcagg ngag	614

<210> 1071

<211> 857

<212> DNA

<213> Unknown (H38g921 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(857)

<223> n = A,T,C or G

<400> 1071

atggnnnnnn nntttnnnaa anttttnccc antttgggcc gnccccccct tctttaagggn	60
aatgggcccc ttgggccctt cccggaaggc cggggggcnc ccggccccaa aggtttgggt	120
tgggaaatgg ggggaattta aattcctttg ggccaaggna aaaattttcc ngccccctt	180
tttttcccc tttggttttt anccggggga angggggggg tgattaatta atcggaagn	240
tnggggggaa nttttttaaa aaaaacctg ggggaagggt ccaaccaac aaggttggtt	300
ttccanggga ccgttgggac caggcttttn gaatcaagaa tcccaaaggg cattcttttg	360
gattaaggaa nggtgcccgg accggtgaaa gggaaaaaac tgggtggacc cataccaaaa	420
tgagaaccac ggtgagatgc cgaggagcac gtggagaaag gctttgcttc cggccactgg	480
cagaggggat cctgaggatg gtgcttgatg atgtacacat agggagacaa ggggtgatgag	540
gcatgaactc aggataacca caacagcnat caciaaggcc acaaagctct actgcctgtg	600
tggtgggtgc aggccagggc aatccagggg tgcaatgtca caagaaagaa agtgggtgat	660
ggcacgggng ggccacagaa ggacaggcca ctgatgaag ggcttggtgg cactgcaatg	720
gtccagaaac cccagacc caggaaccan ggccaagctt gcgcctgaag agcaaggcta	780
ctcatgaatg gcttccgtag tngtaaagga tagcaagatg gcaaaggcaa gccgggtcatn	840
aagccatggc ttgccng	857

<210> 1072

<211> 593

<212> DNA

<213> Unknown (H38g922 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 1072

aacgcagagt accgcccact acgtaatctg tacatgaaag ggtttaaaag agactgggaa	60
gagaggaatt ggcaagatca agcagaggca actccttcta gtccttctag taccgcaagg	120
ggcagataaa tggaaatgggt aacacctaga ggaaagtata cttgccaaaa gcaaatncat	180
aggggggagt acattatcgg gttgaaaaaa gtattccatg cagataaaaa ccaaaagcaa	240
atacatcggg ggcgtacttc tgtcgtcttt gagcgtactg atggtaccca gcttttgntc	300
ctttagttag ggttaattgc gcgcttggcg taatcatggt catagctggt ttctgtgtga	360
aattgttatc ccgctcaciaa ttcacacaa atacgagccc gggagcataa agtgtaaagc	420
ctgggggtgcc taatgagtgg agcttactta cattaaattg cgttgcgctc actggccgct	480

tttccaagtc gggaaacctg tegtgnacgc ttcantaatg aatcggccaa cgccgcgggg 540
agaggcgggt tgcgtattgg gcgctcttcc gcttcttngt tnaactgactt cgg 593

<210> 1073

<211> 624

<212> DNA

<213> Unknown (H38g923 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 1073

gnrntttaac nccggngctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60
tctttttcag tctcaagtc tctcttctc caaagatttt gtcttttcta ctacctgagc 120
taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcatt caacttcaaa 180
cgtgtcatct cagaacaagc ttcattgtac ttccaatttt atccttcttg tttgctgatt 240
ccaagaattc cagtcccatc taggcccgcga atgcattgtt cctgccaccc ttttcataac 300
ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360
ataattatgt ttttttttgc atgtgctctt aatttccttt cttgctccta ttatcttcta 420
tcatactttt ctggaaacac taattctggg gaaatatact ctttgtggac tttgcaacta 480
tgctcagtca gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540
tttatagtca tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600
tctgcgcttg agcgtccggg gggg 624

<210> 1074

<211> 637

<212> DNA

<213> Unknown (H38g924 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(637)

<223> n = A,T,C or G

<400> 1074

ttatnnccat tggagctcca aagcagtggg aacaaccgca gagtacgccc cccatgtatt 60
ttctttttct tggggnagct gnatgcttcc tntgggtac catggnatat gaccggctat 120
gnngncatct gcagtcctct gnntcccag tcattatgaa ccaaaggaca cgggccaac 180
tggttggtgn ttcttggtgc ccaagcttcc ctgnagctac tngcaagac cacaatggct 240
cttnagnntt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc 300
tgtgctgaaa gctggtctgn tgcaagacac agcactgtt gagatctacg ccacgtcgg 360
aaccattctg gtggtcaatg aaccctgct tgctgatctt gngttcctat actcgnattg 420
gtgctgctat cctcaagaa cccatcaagc taaangggaa gcaataaagn cctttctcta 480
cgtgctcctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca 540
acctacttct tgggcctnaa ntcaataaaa ttcttctgga gaggcaagaa ggtggtattc 600
atttatncta cactggtngn gactccatgn tggaact 637

<210> 1075

<211> 621

<212> DNA

<213> Unknown (H38g925 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(621)
 <223> n = A,T,C or G

<400> 1075

gtnatncnt	ttaatncnt	tggagctcca	agcagtggta	acaacgcaga	gtacgcccg	60
tcctcagaca	gtatatgaat	gggttaaaaa	tgggccagag	cagatgcagg	aagatcaa	120
aggaggctac	tgcagtagag	tcaaacttag	ggctgatgg	ttcttgggat	gcataagta	180
aggtagatag	agaaagtctt	taggaggtag	aatggacagg	acttcacaa	gcattaaat	240
tagggagaaa	aaaaatgatt	cctgggtttc	tagcttgagc	tagtagggat	agtggtagaa	300
tttactgata	tggaaaactg	gaggaaaaag	agtttggaag	agaaagatgg	caagttaa	360
acctgtggga	aatataatca	cagacactaa	ataggcagct	gtgtgggtgg	caaaggagag	420
ccatgggcta	ggaacataca	gtgggattcc	ctggcatgtc	attggttact	gaagtcagag	480
tgtatgagac	agcctaagga	gagaatncac	acaggagaag	aaagaactaa	acattcagtg	540
gctggccaga	ggatgagaaa	cccaagagat	tggactgttt	aggagcaaca	gtgttgngaa	600
aaggagagaaa	nggttgaaat	t				621

<210> 1076
 <211> 631
 <212> DNA
 <213> Unknown (H38g926 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 1076

ggnntttannc	nctggagctc	caaagcagng	gtaacaacgc	agagtacgcc	cattgcgtag	60
cgtgtacata	aaggggttgg	agctgaagga	ggagataaag	aagaagacag	ccagaacctt	120
gtcctctgtc	ggagatcgca	gggatccttg	gccgtagata	ggtataagca	aaggggtgcat	180
agtagaaagt	cactacagtg	aggtgggtgc	tgcaggtcga	ataggccttc	ttcctccctt	240
ctgcagagtg	catgtggtag	acagcaagga	gaatccggcc	ataggaacat	gcaatacaaa	300
tgaaggga	cacaagaaaa	atggtggtgc	tcaaaaacac	cgtgcactca	tagaccagg	360
tatccgtgca	ggctagggtc	aacatagctg	gaacatcaca	gaaaaaatga	ttgatggctc	420
tggacttgca	atatgggata	cggagtgc	ataccgtgtg	agcacaagag	ttgatggagc	480
ctatcatcca	agatcctgtt	atcatcagtg	cacacactct	ttttctcata	cggatgagat	540
agtggagagg	aaagcaaata	gccacataac	gatcataggc	cattgatgtc	aggagcagcg	600
cttctgcacc	tgctaaagtc	aggaagaaga	t			631

<210> 1077
 <211> 620
 <212> DNA
 <213> Unknown (H38g927 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 1077

tggtantecn	ntttncncc	attggagctc	ccaagcagtg	gtaacaacgc	agagtacgcc	60
ctccttggtt	ctgagagtgt	agatgaaggg	ggtataggag	ataaagatca	gggcaatatg	120
taggacaagg	acacagacac	tgacaacaaa	gttgattatc	tcattgacag	tggtgtctgt	180
gcaggccagg	ttcagcaggc	gtctcacatc	acagaagaag	tgggagatga	caaagtcac	240
acaaaagggc	aggccaaaca	tagatgttac	ttggacaata	gccatgccca	ggccaatcct	300
cagtgaacca	gatcccgatc	agacacaagc	cctcttacct	atgaataccg	taaggggttg	360

cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcca	420
aaagtcacat	agaagagctg	agtgacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcagggtctc	agagatagac	540
agcaatgctt	aggaaaaagt	acatggggccg	tactttctgtc	gtcttgagcg	tactgatggg	600
accagctttt	tgttcccttt					620

<210> 1078

<211> 627

<212> DNA

<213> Unknown (H38g928 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(627)

<223> n = A,T,C or G

<400> 1078

tgtagctcca	aagcagtggg	aacaacgcag	agtacgccct	cttgggttacg	taaggggaata	60
gatgatggg	ttcagcatgg	gggtgactac	agtgtacatg	acagtggcca	cacggtccca	120
ctctgctcgc	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gtccaccaca	nccaggtggg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggg	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggncct	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgcngcgcc	ctnggtgaag	atgagcagct	tggatgtggg	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtggngc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgtccgtggg	acaccagcca	tgccattcca	accagggtcg	cgcacatngc	cggggacatt	540
ctcgtgggat	aagggaaggg	gtgccggatn	ggcacgtatc	agtcataaggc	cttggncgcc	600
agaagacagc	tttnaattta	ccccagg				627

<210> 1079

<211> 549

<212> DNA

<213> Unknown (H38g929 nucleotide)

<220>

<223> Synthetic construct

<400> 1079

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgaactg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggccgactc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttctctcg	180
gagcattgag	tgcttcttgt	ttacgggtgat	ggcctatgac	cgcttccactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaacct	aaggatctgt	gtggccctgg	ctgtgggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtggtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttggcc	tcatatctct	480
ggctgcttcc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

<210> 1080

<211> 616

<212> DNA

<213> Unknown (H38g930 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 1080

gnnnnnnnnnt	tcattccatt	gggccctcta	gatgcatgct	cgagcggccg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttgttgctt	agagtgtaaa	taaaagggtt	aacattggct	120
ragaggtgaa	gagtaaatac	ataggaaggg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcgggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgtt	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcggtttgcg	tattgggcgc	480
tcttcgctt	cctcgtcac	tgactcgctg	cgctcggtcg	ntcggctgcg	gcgagcggta	540
tcaagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcaggggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

ngnnnnntna	ntcnangccn	ngngccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttccaatg	tatttacttc	tcagccagct	ctcccttatg	120
gacctgatgt	acatctccac	caccgtcccc	aagatggcgt	acaacttcct	gtccggccag	180
aaaggcatct	ccttctctggg	atgtggtgtg	caaagcttct	tcttcttgac	catggcgtgt	240
tctgaaggct	tactcctgac	ctccatggcc	tacgaccgtt	atttggccat	ctgccactct	300
ctctattatc	ctatccgcat	gagtaaaatg	atgtgtgtga	agatgattgg	aggctcttgg	360
acactggggg	ccatcaactc	cttggcacac	acagtctttg	cccttcatat	tccctactgc	420
aggctctagg	ctattgacca	tttcttctgc	gatgtcccag	ccatgttgct	tcttgctgta	480
cagatacttg	ggtctatgaa	tatatggttt	ttgtaaggac	aaagcctctt	tcttcttttn	540
cctttcattg	gcatacttct	ttctgngggc	cgagtcctaa	ttgctggcta	tataatgcac	600
tcaaaggagg	ggagg					615

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

gnnnnnnnat	ttnatgcct	tnttgattcc	cnttnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttccccc	acttctctat	taagaagcat	gtgagatact	180
tgttacaaac	ataacatcct	ggtcccccac	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tggttgagaa	300
tctaggcaac	aatgaattaa	ggaaaagctc	ctaccatttg	gtactgggtac	caggtttgag	360
gatcacaggg	aagagggtaa	gcatatcaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccattgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480

```

ctctgaggaa caagggggcg tacttctgtc gtcttgagcg tactgatggg acccagcttt 540
tgccccctta gtgagggtta attgcgcgct tggcgtaatc atgggcatag ctgtttcctg 600
tgtgaaattg ttatccgctc acaattct 628

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<210> 1083
 <211> 613
 <212> DNA
 <213> Unknown (H38g933 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(613)
 <223> n = A,T,C or G

```

<400> 1083
annncntng gagctccaaa gcagtggtaa caacgcagag tacgccccct atgtacttac 60
ttttgttaag tccaacctcc atcctccttg gccttttgat tcaattgatc actccttctc 120
cctcaaaaaca ccttggtcac tcatcctttc tcagtctcct ttgtggattc ttctcatttt 180
atttgacctc ttgctgggtga accctttcat atacactctc cgtaacaaaag agggcgact 240
tctgtcgtct tgagcgnact gatggnaccc agcttttggt cccttttagtg agggntaatt 300
gcgcgcttgg cgnaatcatg gncatagctg ntttctgngn gaaantgnta ttctcgtnac 360
aattncacac aacatacnag ccgggagcat aaaggggnaa gncctggggg gcctaatagag 420
ggagcttact cacaataatt ggggtgngcc cactggcccc ttttcaggcg ggaaaacctn 480
gcggggccag ctggaataaaa tgaatcgggc cacgcgccgg ggaggagggc ggggttnngga 540
attgggcgct ttttccnttt ctnggttaat ggactnggtn ggcnnngtcc gttcgggttg 600
ggggancggn nnt 613

```

<210> 1084
 <211> 886
 <212> DNA
 <213> Unknown (H38g934 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(886)
 <223> n = A,T,C or G

```

<400> 1084
ggccccntcg ngatatnctt naccctctga tgcgtctcga gcggccggca ggggtgatgga 60
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ataaatgggt tactgaggaa taaataaatg ggttactgag gaacaaatac ataggggtga 180
aagaactgta aaatagaaaa aggacctntt gctgctcctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgngg ctgccnntna agagtcccac tntcancng cctcagcccc 300
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cccttcnct cctccctttt gentnaccat tgnccctnat cctttaatt cmntcnntcn 420
tctccctctt attccttcnn tnttcgnctt cantctctnc ctctttctcc cccnctttct 480
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nctcttccn ctccgtctnc cctttctct tcntnacgcc acccctcnnt cntnctctct 660
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ctcncttct ncttnactt tgcacgctc tctcctctct ctctacgcac nttttatctc 780
ttatctcnct catnccctc nttctnctc nctattnact cttttctcnc atactntatn 840
ctcctntcnn cttanactnc ctccctctcn tnancnntc actgcn 886

```

<210> 1085
 <211> 125
 <212> PRT

<213> Unknown (H38g1 protein)

<220>

<223> Synthetic construct

<400> 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1           5           10           15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
          20          25          30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
          35          40          45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
          50          55          60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
65          70          75          80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
          85          90          95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
          100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
          115          120          125

```

<210> 1086

<211> 322

<212> PRT

<213> Unknown (H38g2 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1086

```

His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20          25          30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
          35          40          45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
          50          55          60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

```

[illegible]

<210> 1087

<211> 312

<212> PRT

<213> Unknown (H38g3 protein)

<220>

<223> Synthetic construct

<400> 1087

Met	Asp	Gly	Asp	Asn	Gln	Ser	Glu	Asn	Ser	Gln	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Ile	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Arg	Ile	Leu	Phe	Trp	Met	Phe	Leu
		20						25				30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Val	Leu	Ile	Ile	Leu	Ala
		35					40				45				
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro	Lys
65					70					75				80	
Met	Leu	Val	Asn	Phe	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ser	Tyr	Ala	Gly
			85						90					95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Thr	Leu	Asp	Asn
			100					105					110		
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Thr	Cys	Cys
		115						120				125			
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Val	Leu	Leu
	130					135					140				
Leu	Ser	Leu	Cys	Trp	Gly	Leu	Ser	Val	Leu	Tyr	Gly	Leu	Leu	Leu	Thr
145					150					155					160
Phe	Leu	Leu	Thr	Arg	Val	Thr	Phe	Cys	Gly	Pro	Arg	Glu	Ile	His	Tyr
			165						170					175	
Leu	Phe	Cys	Asp	Met	Tyr	Ile	Leu	Leu	Trp	Leu	Ala	Cys	Ser	Asn	Thr
			180					185					190		
His	Ile	Ile	His	Thr	Ala	Leu	Ile	Ala	Thr	Gly	Cys	Phe	Ile	Phe	Leu
		195						200				205			
Thr	Pro	Leu	Gly	Phe	Met	Thr	Thr	Ser	Tyr	Val	Arg	Ile	Val	Arg	Thr
	210					215					220				
Ile	Leu	Gln	Met	Pro	Ser	Ala	Ser	Lys	Lys	Tyr	Lys	Thr	Phe	Ser	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Gly	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu	Ala
			245						250					255	
Met	Val	Tyr	Leu	Gln	Pro	Leu	His	Thr	Tyr	Ser	Met	Lys	Asp	Ser	Val
			260					265					270		

Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg Pro Lys
 305 310

<210> 1088

<211> 305

<212> PRT

<213> Unknown (H38g4 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(305)

<223> Xaa = Any Amino Acid

<400> 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro
 1 5 10 15
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile
 20 25 30
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe
 35 40 45
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp
 50 55 60
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser
 65 70 75 80
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe
 85 90 95
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met
 100 105 110
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu
 115 120 125
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu
 130 135 140
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu
 145 150 155 160
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro
 165 170 175
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val
 180 185 190
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val
 195 200 205
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser
 210 215 220
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val
 225 230 235 240
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser
 245 250 255
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val
 260 265 270
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val
 290 295 300
 Cys
 305

<210> 1089
 <211> 317
 <212> PRT
 <213> Unknown (H38g5 protein)

<220>
 <223> Synthetic construct

<400> 1089

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
          20           25           30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
          35           40           45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50           55           60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
65           70           75           80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
          85           90           95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
          100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
          115          120          125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
          130          135          140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
145          150          155          160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
          165          170          175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
          180          185          190
Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
          195          200          205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
          210          215          220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
225          230          235          240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
          245          250          255
Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
          260          265          270
Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
          290          295          300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
305          310          315

```

<210> 1090
 <211> 342
 <212> PRT
 <213> Unknown (H38g6 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(342)
 <223> Xaa = Any Amino Acid

<400> 1090

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu L u Gln Pro Val Ile Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met
 35          40          45
Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
 115          120          125
Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
 130          135          140
Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe
 145          150          155          160
Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
 165          170          175
Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser
 180          185          190
Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
 195          200          205
Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr
 210          215          220
Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser
 225          230          235          240
Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser
 245          250          255
Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser
 260          265          270
Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
 275          280          285
Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
 290          295          300
Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa
 305          310          315          320
Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys
 325          330          335
Lys Gly Ser Lys Val Lys
 340

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<210> 1091

<211> 313

<212> PRT

<213> Unknown (H38g7 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1091

Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly

1	5	10	15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu			
20		25	30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu			
35		40	45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser			
50		55	60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys			
65		70	75
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala			
85		90	95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys			
100		105	110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn			
115		120	125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met			
130		135	140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr			
145		150	155
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His			
165		170	175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile			
180		185	190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu			
195		200	205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser			
210		215	220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr			
225		230	235
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala			
245		250	255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys			
260		265	270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu			
275		280	285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe			
290		295	300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys			
305		310	

<210> 1092

<211> 328

<212> PRT

<213> Unknown (H38g8 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1092

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu	
1	5
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu	
20	25
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu	
35	40
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser	
50	55
	60

Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
 65 70 75 80
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
 85 90 95
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser L u Ala Leu Cys Gly Ser
 100 105 110
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
 130 135 140
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
 145 150 155 160
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
 165 170 175
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
 180 185 190
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
 195 200 205
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
 210 215 220
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
 245 250 255
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
 260 265 270
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
 290 295 300
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
 305 310 315 320
 Leu Ser Ser Lys Pro Lys Arg Arg
 325

<210> 1093

<211> 318

<212> PRT

<213> Unknown (H38g9 protein)

<220>

<223> Synthetic construct

<400> 1093

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
 20 25 30
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
 35 40 45
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

130	135	140
Ile Ile Met Ile Trp Ser	Ile Ser Leu Ala Asn Ser Val Val Leu Cys	
145	150	155
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His		160
	165	170
Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr		175
	180	185
Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu		190
	195	200
Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala		205
	210	215
Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr		220
225	230	235
Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile		240
	245	250
Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys		255
	260	265
Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu		270
	275	280
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu		285
	290	295
Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys		300
305	310	315

<210> 1094

<211> 324

<212> PRT

<213> Unknown (H38g10 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1094

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu	
1	5
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser	10
	15
	20
Leu Ser Leu Ser Thr Tyr Leu Ala Thr Val Leu Arg Asn Val Leu Asn	25
	30
	35
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe	40
	45
	50
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr	55
65	60
	65
Val Pro Lys Met Ile Val Asp Met Gln Ser Tyr Ser Arg Val Ile Ser	70
	75
	80
	85
His Glu Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys	90
	95
	100
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala	105
	110
	115
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys	120
	125
	130
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln	135
145	140
	145
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu	150
	155
	160
	165
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu Ala Cys	170
	175
	180
	185
	190

```

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile
210                215                220
Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
260                265                270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
275                280                285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290                295                300
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305                310                315                320
Phe Phe Leu Cys

```

<210> 1095

<211> 311

<212> PRT

<213> Unknown (H38g11 protein)

<220>

<223> Synthetic construct

<400> 1095

```

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
1          5          10          15
Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
20          25          30
Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
35          40          45
Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
50          55          60
Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
65          70          75          80
Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
85          90          95
Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
100         105         110
Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
115         120         125
Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
130         135         140
Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
145         150         155         160
Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
165         170         175
Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
180         185         190
Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
195         200         205
Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
210         215         220
Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
225         230         235         240
Ser His Leu Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
245         250         255
Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

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260 265 270
 Ser Ile Ph Tyr Ala Ile Val Thr Pro Ser Leu Asn Pr Phe Ile Tyr
 275 280 285
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr
 290 295 300
 Cys Gln Ala Ser Arg Ser Asp
 305 310

<210> 1096
 <211> 313
 <212> PRT
 <213> Unknown (H38g12 protein)

<220>
 <223> Synthetic construct

<400> 1096
 Met Glu Gln Val Asn Lys Thr Val Val Arg Glu Phe Val Val Leu Gly
 1 5 10 15
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20 25 30
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
 35 40 45
 Ile Val Leu Asp Arg Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Phe Gly Ser Ser His Ser
 100 105 110
 Phe Leu Leu Ala Ala Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
 130 135 140
 Met Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr
 145 150 155 160
 Ser Leu Val Phe His Leu Pro Phe His Ser Ser Asn Gln Leu His His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser
 180 185 190
 Gly Phe Ser Gln Leu Val Ile Phe Met Leu Gly Val Phe Ala Leu Val
 195 200 205
 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala
 210 215 220
 Ile Leu Lys Ile Pro Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Thr Val His Tyr Ser Cys Ala Ser
 245 250 255
 Phe Ile Tyr Leu Arg Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr
 260 265 270
 Leu Ile Ser Val Ser Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr
 290 295 300
 Ile Gly Gln Thr Phe Tyr Pro Leu Ser
 305 310

<210> 1097
 <211> 318
 <212> PRT

<213> Unknown (H38g13 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1097

```

Cys Val Asp Ser Ser Leu Lys Xaa Glu Ile Thr Gln Xaa Cys Leu Ser
 1           5           10           15
Leu Leu Leu Xaa Met Ala Glu Gly Trp Arg Leu Tyr Phe Ile Ile Leu
 20           25           30
Ile Ile Ser Tyr Lys Phe Cys Thr Leu Leu Gly Asn Val Ile Phe Arg
 35           40           45
Thr Leu Val Cys Ser Leu Gly Phe His Thr Ser Cys Met Tyr Phe Phe
 50           55           60
Pro Xaa Lys Ile Ser Leu Xaa Leu Ala Xaa Val Cys His Ser Ile Ile
 65           70           75           80
Ala Leu Pro Ser Thr Gln Lys Xaa Ala Ile Asn Val Gln Gly Ala Ala
 85           90           95
Val His Val Phe Ser Phe Pro Cys Leu Tyr Cys Pro Glu Ile Phe Leu
 100          105          110
His Ser Leu Thr Gln Cys His Pro Phe Ile Ala Ile Gly Tyr Pro Leu
 115          120          125
Gln Gly Met His Thr Ile Thr His Lys Leu Tyr Ile Leu Leu Thr Thr
 130          135          140
Gly Pro Trp Arg Gly Cys Xaa Leu His Val Asn Leu Leu Thr Ala Ile
 145          150          155          160
Leu Gly Ser Tyr Pro Asn Pro Val Pro Thr Lys Leu Trp Leu Ser Phe
 165          170          175
Pro Ser Ile Pro Glu Val Lys Leu Xaa Pro Met Gln Ala Tyr Thr Lys
 180          185          190
Pro Tyr Ala Gly Leu Ser Leu Cys Leu Ser Leu Ser Leu Ser Leu Ser
 195          200          205
Phe Ser Leu Phe Ser Ile Ile Ser Ile Ser Tyr Ile Cys Asn Glu Ile
 210          215          220
Asp Ile Pro Lys Ile Ile Ser Ala Asp Ser Val His Gly Ala Phe Ser
 225          230          235          240
Thr Cys Leu Ala His Leu Phe Ala Phe Ser Thr Cys Ile Ala Gln Pro
 245          250          255
Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser
 260          265          270
Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser
 275          280          285
Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala
 290          295          300
Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile
 305          310          315

```

<210> 1098

<211> 333

<212> PRT

<213> Unknown (H38g14 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
          20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
          210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
          290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

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<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
 305 310 315 320
 Phe Ser

<210> 1100

<211> 279

<212> PRT

<213> Unknown (H38g16 protein)

<220>

<223> Synthetic construct

<400> 1100

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 1 5 10 15
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
 35 40 45
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
 50 55 60
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
 65 70 75 80
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu

<400> 1101															
Phe	Ile	Leu	Trp	Gly	Phe	Phe	Asp	His	Pro	Xaa	Pro	Glu	Met	Phe	Leu
1				5					10					15	
Phe	Ile	Met	Gly	Leu	Val	Gly	Leu	Ser	Leu	His	Thr	Gly	Gly	Gln	His
			20					25					30		
Leu	Asn	Tyr	Cys	Gly	Thr	Gln	Gly	Ile	Phe	Xaa	Gly	Ser	Thr	Lys	Cys
		35					40					45			
Ile	Ile	Leu	Ala	Val	Thr	Ser	Leu	Asp	Pro	Tyr	Ile	Ala	Ile	Cys	Lys
	50					55					60				
His	Leu	Arg	Tyr	Pro	Ala	Ile	Met	His	Gln	Gln	Leu	Cys	Val	Leu	Leu
65					70					75					80
Val	Ala	Met	Ala	Trp	Leu	Ser	Ser	Leu	Ala	Asn	Ser	Leu	Gln	Ser	Ser
			85						90					95	
Leu	Ala	Val	Gln	Leu	Pro	Leu	Gly	Gly	Asn	Lys	Val	Asp	Asp	Phe	Leu
			100					105					110		
Cys	Glu	Val	Ser	Ala	Met	Ile	Lys	Ile	Ser	Arg	Phe	Asp	Thr	Thr	Phe
		115					120					125			
Asn	Val	Ser	Met	Leu	Ser	Ile	Val	Arg	Ile	Phe	Xaa	Ser	Leu	Val	Leu
	130					135					140				
Xaa	Ser	Ile	Ile	Phe	Ala	Tyr	Cys	Gly	Phe	Ile	Val	Ala	Thr	Val	Leu
145					150					155					160
Arg	Ile	Gln	Ser	Ser	Gly	Gly	Lys	Lys	Glu	Val	Phe	Asn	Thr	Cys	Gly
				165					170					175	

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val
 180 185 190
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe
 195 200 205
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser
 210 215 220
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr
 225 230 235 240
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe
 245 250 255
 Ile

<210> 1102

<211> 334

<212> PRT

<213> Unknown (H38g18 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu
 1 5 10 15
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro
 65 70 75 80
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100 105 110
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130 135 140
 Leu Leu Leu Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu
 145 150 155 160
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile
 165 170 175
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 180 185 190
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe
 195 200 205
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val
 210 215 220
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr
 245 250 255
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
 260 265 270
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

275 280 285
 Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
 290 295 300
 Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser
 305 310 315 320
 Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330

<210> 1103

<211> 333

<212> PRT

<213> Unknown (H38gl9 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1103

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
 305 310 315 320

Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
 325 330

<210> 1104

<211> 339

<212> PRT

<213> Unknown (H38g20 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 1104

Asp	Thr	Asp	Pro	Gln	Ser	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5				10					15		
Glu	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe
		20						25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Ile	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Phe	Pro	Asp	Ser	Arg	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70				75					80	
Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
			85					90					95		
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Asp	Met	Glu
		100						105				110			
Glu	Asn	Met	Phe	Leu	Ser	Val	Val	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile
	115					120						125			
Cys	His	Pro	Leu	Tyr	Arg	Ser	Ala	Ile	Leu	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Asp	Ser	Leu	Ser	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Ser	Leu
145					150				155					160	
Leu	Asp	Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe
			165					170					175		
Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Pro
		180					185						190		
His	Leu	Ala	Cys	Cys	Asp	Ile	Phe	Thr	Arg	Asn	Ile	Asn	Leu	Tyr	Phe
	195					200						205			
Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser
	210					215					220				
Tyr	Tyr	Lys	Ile	Val	Ser	Phe	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly
225					230				235					240	
Lys	Tyr	Lys	Ala	Phe	Ser	Ala	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Tyr
			245						250					255	
Xaa	Val	Tyr	Gly	Thr	Gly	Phe	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser
		260					265						270		
Ser	Ser	Pro	Arg	Lys	Gly	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val
		275					280					285			
Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Gly	Asp	Ile
	290					295					300				
Lys	Ser	Val	Leu	Arg	Gln	Pro	His	Gly	Ser	Thr	Val	Xaa	Ser	Gln	Tyr
305					310				315					320	
Leu	Leu	Ile	Cys	Ser	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser
			325						330					335	
Lys	Val	Lys													

<210> 1105
 <211> 314
 <212> PRT
 <213> Unknown (H38g21 protein)

<220>
 <223> Synthetic construct

<400> 1105
 Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly
 1 5 10 15
 Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu
 20 25 30
 Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile
 35 40 45
 Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ile Pro Pro
 65 70 75 80
 Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
 85 90 95
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met
 130 135 140
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr
 145 150 155 160
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His
 165 170 175
 Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile
 180 185 190
 Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val
 195 200 205
 Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser
 210 215 220
 Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu
 260 265 270
 Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val
 290 295 300
 Leu Ser Arg His Leu His Leu Leu Lys Met
 305 310

<210> 1106
 <211> 319
 <212> PRT
 <213> Unknown (H38g22 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1106

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1          5          10          15
Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
      20          25          30
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Val Val Thr Ile Thr
      35          40          45
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
      50          55          60
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ala Pro Lys Leu Ile
65          70          75          80
Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
      85          90          95
Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
      100          105          110
Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
      115          120          125
His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
      130          135          140
Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
145          150          155          160
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
      165          170          175
Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
      180          185          190
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195          200          205
Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
      210          215          220
Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
225          230          235          240
His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
      245          250          255
Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Val Phe
      260          265          270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275          280          285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
      290          295          300
Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
305          310          315

```

<210> 1107

<211> 311

<212> PRT

<213> Unknown (H38g23 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1107

```

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro
 1          5          10          15
His Thr Glu Gly Leu Glu Thr Ile Leu Leu Val Leu Phe Leu Ser Phe
      20          25          30
Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

```

35	40	45
Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Lys Leu		
50	55	60
Ser Val Phe Asp Leu Phe Phe Pro Ser Val Ser Ser Pro Lys Met Leu		
65	70	75
Cys Tyr Leu Ser Gly Asn Ser Arg Ala Ile Ser Tyr Ala Gly Cys Ala		
85	90	95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu		
100	105	110
Tyr Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu		
115	120	125
Arg Tyr Thr Ile Ile Met Ser His Arg Ala Cys Ile Ile Leu Ala Met		
130	135	140
Gly Thr Ser Phe Phe Gly Cys Ile Gln Ala Thr Phe Leu Thr Thr Leu		
145	150	155
Thr Phe Gln Leu Pro Tyr Cys Val Pro Asn Glu Val Asp Tyr Tyr Phe		
165	170	175
Cys Asp Ile Pro Val Met Leu Lys Leu Ala Cys Ala Asp Thr Ser Ala		
180	185	190
Leu Glu Met Val Gly Phe Ile Ser Val Gly Leu Met Pro Leu Ser Cys		
195	200	205
Phe Leu Leu Ile Leu Thr Ser Tyr Ser Gly Ile Val Phe Ser Ile Leu		
210	215	220
Xaa Ile Cys Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser		
225	230	235
Ala His Leu Thr Ala Ile Leu Leu Phe Tyr Met Pro Val Val Leu Ile		
245	250	255
Tyr Leu Arg Pro Thr His Ser Leu Trp Leu Asp Ala Thr Val Gln Ile		
260	265	270
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu		
275	280	285
Arg Asn Lys Glu Val Lys Leu Ser Leu Arg Lys Val Leu Tyr Gln Leu		
290	295	300
Gly Phe Leu Pro Glu Gln Leu		
305	310	

<210> 1108

<211> 302

<212> PRT

<213> Unknown (H38g24 protein)

<220>

<223> Synthetic construct

<400> 1108

Met Asp Ile Pro Gln Asn Ile Thr Glu Phe Phe Met Leu Gly Leu Ser
1 5 10 15
Gln Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile
20 25 30
Tyr Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr
35 40 45
Ser Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu
50 55 60
Ser Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile
65 70 75 80
Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met
85 90 95
Ala Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu
100 105 110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
115 120 125

```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
 130                      135                      140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
145                      150                      155                      160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
                      165                      170                      175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
                      180                      185                      190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
                      195                      200                      205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
210                      215                      220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
225                      230                      235                      240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
                      245                      250                      255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
                      260                      265                      270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275                      280                      285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
290                      295                      300

```

<210> 1109

<211> 266

<212> PRT

<213> Unknown (H38g25 protein)

<220>

<223> Synthetic construct

<400> 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
 1                      5                      10                      15
Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
                      20                      25                      30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
                      35                      40                      45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
50                      55                      60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
65                      70                      75                      80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
                      85                      90                      95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
100                      105                      110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
115                      120                      125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
130                      135                      140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
145                      150                      155                      160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
                      165                      170                      175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
180                      185                      190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
195                      200                      205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
210                      215                      220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```

225 230 235 240
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala
 245 250 255
 Val Lys Lys Ile Leu His Gln Thr Ala Cys
 260 265

<210> 1110
 <211> 318
 <212> PRT
 <213> Unknown (H38g26 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(318)
 <223> Xaa = Any Amino Acid

<400> 1110
 Met Gly Asn Ser Asn Gln Ser Phe Met Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Glu Leu Glu Ala Ile Tyr Phe Val Leu Val Leu
 20 25 30
 Cys Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Ile Ile Val
 35 40 45
 Ser Val Tyr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Leu
 65 70 75 80
 Phe Leu Ser Ser Phe Leu Thr Ser Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Gly Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys
 100 105 110
 Val Leu Leu Ser Met Met Ala Phe Asp Cys Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Xaa Tyr Pro Ile Ile Met Ser Lys Ala Ser Tyr Met Ser Met
 130 135 140
 Ala Ala Gly Ser Trp Ile Gly Gly Gly Ile Asn Ser Val Leu Gln Thr
 145 150 155 160
 Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His
 165 170 175
 Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asn Ile
 180 185 190
 Ser Ile Asn Ile Ile Ser Met Val Val Ala Ser Met Ile Phe Leu Val
 195 200 205
 Gly Pro Val Leu Phe Ile Phe Val Thr Tyr Val Phe Ile Leu Ser Thr
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Ala Ser Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Arg Thr Ile Leu
 245 250 255
 Phe Met Tyr Ala Lys Pro Lys Ala Lys Asp Ser Ser Gly Ala Asp Lys
 260 265 270
 Glu Gln Val Thr Asp Lys Ile Ile Ser Leu Phe Tyr Gly Val Val Thr
 275 280 285
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Ser Ile Leu Xaa Gln Lys Cys Phe Leu Glu
 305 310 315

<210> 1111

<211> 329
 <212> PRT
 <213> Unknown (H38g27 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1111
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu
 20 25 30
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile
 35 40 45
 Ile Phe Ile Ser Pro Ala Leu Gly Ser Pro Met Tyr Ser Phe Pro Ser
 50 55 60
 Tyr Leu Phe Ile Ile Asp Ile Phe Cys Ser Ser Ile Ala Pro Lys
 65 70 75 80
 Met Asn Phe Asp Leu Ile Ser Glu Lys Asn Thr Ile Ser Phe Asn Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Thr Glu His Phe Phe Thr Glu His Phe Phe
 100 105 110
 Glu Ala Ala Glu Ile Ile Leu Leu Ser Val Met Ala Tyr Asp His Tyr
 115 120 125
 Val Ala Ile Arg Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 130 135 140
 Met Cys Gly Phe Leu Met Val Val Ala Gly Ile Leu Gly Phe Val His
 145 150 155 160
 Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
 165 170 175
 Asn Val Ile Asn His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 180 185 190
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 195 200 205
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 210 215 220
 Ile Ile Leu Cys Phe Leu Arg Thr His Ser Ser Glu Gly Arg Arg Lys
 225 230 235 240
 Ala Leu Ser Ser Cys Ala Ser His Ile Phe Ile Val Ile Leu Phe Phe
 245 250 255
 Val Pro Phe Ser Tyr Leu Tyr Leu Arg Pro Ile His Ser Phe Pro Thr
 260 265 270
 Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu Asn
 275 280 285
 Pro Leu Ile Tyr Thr Leu Lys Asn Lys Glu Val Lys Asn Val Ile Lys
 290 295 300
 Lys Leu Trp Lys Gln Ile Met Thr Thr Asp Asp Lys Xaa Val Leu Xaa
 305 310 315 320
 His Lys His Leu Gly Lys Asn Ile Trp
 325

<210> 1112
 <211> 318
 <212> PRT
 <213> Unknown (H38g28 protein)

<220>

<223> Synthetic construct

<400> 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1           5           10           15
Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20           25           30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35           40           45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65           70           75           80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85           90           95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100          105          110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115          120          125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
 130          135          140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
 145          150          155          160
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
 165          170          175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180          185          190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
 195          200          205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
 210          215          220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
 225          230          235          240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245          250          255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
 260          265          270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
 275          280          285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290          295          300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
 305          310          315

```

<210> 1113

<211> 264

<212> PRT

<213> Unknown (H38g29 protein)

<220>

<223> Synthetic construct

<400> 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1           5           10           15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
 20           25           30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Il Phe Asp Leu Leu
 35           40           45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
 50           55           60

```

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met
65              70              75              80
Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile
85              90              95
Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val
100            105            110
Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu
115            120            125
Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe
130            135            140
Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe
145            150            155            160
Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu
165            170            175
Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser
180            185            190
Thr Cys Ala Phe His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys
195            200            205
Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala
210            215            220
Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile
225            230            235            240
Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp
245            250            255
Ser Gln Ile Ile Trp Gly Asn Asn
260

```

<210> 1114

<211> 312

<212> PRT

<213> Unknown (H38g30 protein)

<220>

<223> Synthetic construct

<400> 1114

```

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
1      5      10      15
Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
20     25     30
Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Tyr Ile Lys
35     40     45
His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
50     55     60
Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
65     70     75     80
Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
85     90     95
Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
100    105    110
Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
115    120    125
Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
130    135    140
Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
145    150    155    160
Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
165    170    175
Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
180    185    190
Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

195	200	205
Ser Leu Ile Ile Leu Phe	Ser Tyr Ile Leu Ile	Leu Asn Thr Val Ile
210	215	220
Gly Ile Ala Ser Gly Glu	Glu Arg Ala Lys Ala	Leu Asn Thr Cys Ile
225	230	235
Ser His Ile Ser Cys Val	Leu Ile Phe Tyr Val	Thr Val Met Gly Leu
245	250	255
Thr Phe Ile Tyr Arg Phe	Gly Lys Asn Val Pro	Glu Val Val His Ile
260	265	270
Ile Met Ser Tyr Ile Tyr	Phe Leu Phe Pro Pro	Leu Met Asn Pro Val
275	280	285
Ile Tyr Ser Ile Lys Thr	Lys Gln Ile Gln Tyr	Gly Ile Ile Arg Leu
290	295	300
Leu Ser Lys His Arg Phe	Ser Arg	
305	310	

<210> 1115

<211> 285

<212> PRT

<213> Unknown (H38g31 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(285)

<223> Xaa = Any Amino Acid

<400> 1115

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu	
1 5 10 15	
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe	
20 25 30	
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu	
35 40 45	
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu	
50 55 60	
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro	
65 70 75 80	
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly	
85 90 95	
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp	
100 105 110	
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys	
115 120 125	
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu	
130 135 140	
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His	
145 150 155 160	
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser	
165 170 175	
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp	
180 185 190	
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly	
195 200 205	
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe	
210 215 220	
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser	
225 230 235 240	
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly	
245 250 255	

Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro
 275 280 285

<210> 1116
 <211> 317
 <212> PRT
 <213> Unknown (H38g32 protein)

<220>
 <223> Synthetic construct

<400> 1116
 Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu
 20 25 30
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
 35 40 45
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Val Pro Ser
 65 70 75 80
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
 100 105 110
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met
 130 135 140
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr
 145 150 155 160
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His
 165 170 175
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val
 195 200 205
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
 210 215 220
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
 245 250 255
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys
 260 265 270
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr
 275 280 285
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His
 305 310 315

<210> 1117
 <211> 309
 <212> PRT
 <213> Unknown (H38g33 protein)

<220>

<223> Synthetic construct

<400> 1117

```

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
1      5      10      15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
20      25      30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
35      40      45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
50      55      60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
65      70      75      80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
85      90      95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
100     105     110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
115     120     125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
130     135     140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
145     150     155     160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
165     170     175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
180     185     190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
195     200     205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
210     215     220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
225     230     235     240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
245     250     255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
260     265     270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275     280     285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
290     295     300
Ser Leu Gly Glu Lys
305

```

<210> 1118

<211> 329

<212> PRT

<213> Unknown (H38g34 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
1      5      10      15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
20      25      30

```

```

Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr
   35           40           45
Leu Ile Lys His Asp His Ser Leu His Glu Pr Met Tyr Cys Phe Leu
   50           55           60
Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr
   65           70           75           80
Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala
           85           90           95
Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu
           100          105          110
Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His
           115          120          125
Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile
           130          135          140
Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile
           145          150          155          160
Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His
           165          170          175
Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile
           180          185          190
Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe
           195          200          205
Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr
           210          215          220
Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met
           225          230          235          240
Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile
           245          250          255
Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val
           260          265          270
His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn
           275          280          285
Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val
           290          295          300
Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe
           305          310          315          320
Cys Asp Leu His Asp Phe Trp Ala Phe
           325

```

<210> 1119

<211> 296

<212> PRT

<213> Unknown (H38g35 protein)

<220>

<223> Synthetic construct

<400> 1119

```

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met
  1           5           10           15
Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His
           20           25           30
Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu
           35           40           45
Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg
           50           55           60
Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr
           65           70           75           80
Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Thr Val Met Ser Tyr
           85           90           95
Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met

```

```

      100      105      110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
      115      120      125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
      130      135      140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
      145      150      155      160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
      165      170      175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
      180      185      190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
      195      200      205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
      210      215      220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
      225      230      235      240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
      245      250      255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
      260      265      270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
      275      280      285
Glu Lys Arg Met Arg Ala Val Leu
      290      295

```

<210> 1120

<211> 310

<212> PRT

<213> Unknown (H38g36 protein)

<220>

<223> Synthetic construct

<400> 1120

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
  1      5      10      15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
      20      25      30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
      35      40      45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
      50      55      60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
      65      70      75      80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
      85      90      95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu
      100      105      110
Leu Val Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg
      115      120      125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly
      130      135      140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu
      145      150      155      160
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys
      165      170      175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn
      180      185      190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala
      195      200      205

```

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly
 210                215                220
Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser
225                230                235                240
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser
                245                250                255
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr
                260                265                270
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile
                275                280                285
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe
290                295                300
Ser Gly Gln Ser Arg Ala
305                310

```

<210> 1121

<211> 332

<212> PRT

<213> Unknown (H38g37 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(332)

<223> Xaa = Any Amino Acid

<400> 1121

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1                5                10                15
Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                20                25                30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile
35                40                45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
50                55                60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65                70                75                80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser
                85                90                95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys
100                105                110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
115                120                125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys
130                135                140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                150                155                160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu
165                170                175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
180                185                190
Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
210                215                220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg
245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

	260		265		270
Asn Gly Val Val Ala Ser Leu Ile Tyr Ala Val Val Thr Pro Met Leu					
275		280		285	
Asn Leu Phe Ile Tyr S r Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu					
290		295		300	
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro					
305		310		315	320
Phe Ser Trp Trp Val Arg Lys Gly Asn His Ile Lys					
	325		330		

<210> 1122

<211> 310

<212> PRT

<213> Unknown (H38g38 protein)

<220>

<223> Synthetic construct

<400> 1122

Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe					
1	5	10	15		
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu					
20	25	30			
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile					
35	40	45			
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His					
50	55	60			
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met					
65	70	75	80		
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg					
85	90	95			
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu					
100	105	110			
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro					
115	120	125			
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala					
130	135	140			
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val					
145	150	155	160		
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe					
165	170	175			
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His					
180	185	190			
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly					
195	200	205			
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile					
210	215	220			
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys					
225	230	235	240		
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile					
245	250	255			
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr					
260	265	270			
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile					
275	280	285			
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu					
290	295	300			
Gly Val Glu Arg Ala Leu					
305	310				

<210> 1123

<211> 323
 <212> PRT
 <213> Unknown (H38g39 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(323)
 <223> Xaa = Any Amino Acid

<400> 1123
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu
 50 55 60
 Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg
 290 295 300
 Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe
 305 310 315 320
 Leu Cys Leu

<210> 1124
 <211> 320
 <212> PRT
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

His	Thr	Glu	Pro	Gln	Asn	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Ile	Leu	Ala	Gly	Leu	Ser
			20					25					30		
Leu	Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ile	Ile	Leu
		35				40						45			
Ala	Val	Ser	Ser	Asp	Pro	His	Leu	His	Thr	Pro	Met	Cys	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Cys	Trp	Ala	Asp	Ile	Gly	Phe	Thr	Leu	Ala	Thr	Val	Pro
65					70					75					80
Lys	Met	Ile	Val	Asp	Met	Gln	Ser	His	Thr	Arg	Val	Ile	Ser	Tyr	Glu
				85					90					95	
Gly	Cys	Leu	Thr	Arg	Ile	Ser	Phe	Leu	Val	Leu	Phe	Ala	Cys	Ile	Glu
			100					105					110		
Asp	Met	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Ala	Ile	Cys
		115				120						125			
Arg	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135						140			
Phe	Leu	Leu	Val	Tyr	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His
145					150					155					160
Ser	Trp	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn	Val	Glu	Ile	Ser
				165					170					175	
Asn	Phe	Val	Cys	Asp	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp
			180					185					190		
Ser	Val	Ile	Asn	Ser	Ile	Phe	Met	Tyr	Phe	His	Ser	Thr	Met	Phe	Gly
		195					200					205			
Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Pro
	210				215						220				
Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
225					230					235					240
Thr	Cys	Gly	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe	Tyr	Gly	Thr	Gly
				245					250					255	
Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Val	Ser	Pro	Pro	Pro	Arg	Asn	Gly
			260					265					270		
Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Asn	Leu
		275					280					285			
Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu	Arg	Arg
	290					295					300				
Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro	Phe	Ser
305					310					315					320

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125


```

Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
20     25     30
Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu
35     40     45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
50     55     60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
65     70     75     80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
85     90     95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
100    105    110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
115    120    125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
130    135    140
Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn
145    150    155    160
Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn
165    170    175
Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr
180    185    190
Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
195    200    205
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser
210    215    220
Ile Leu Arg Val Ser Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His
225    230    235    240
Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu
245    250    255
Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val
260    265    270
Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu
275    280    285
Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr
290    295    300
Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp
305    310    315    320
Val Lys Lys Gly Ser Lys Val
325

```

<210> 1126

<211> 313

<212> PRT

<213> Unknown (H38g42 protein)

<220>

<223> Synthetic construct

<400> 1126

```

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro
1      5      10      15
Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr
20     25     30
Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp
35     40     45
Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
50     55     60
Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

65					70					75				80	
Ala	Cys	Leu	Leu	Gly	Glu	Glu	Lys	Thr	Ile	Ser	Phe	Ala	Gly	Cys	Met
				85					90					95	
Ile	Gln	Thr	Tyr	Phe	Tyr	Phe	Phe	Leu	Gly	Thr	Val	Glu	Phe	Ile	Leu
			100					105					110		
Leu	Ala	Val	Met	Ser	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asp	Pro	Leu
			115				120					125			
His	Tyr	Thr	Val	Ile	Met	Asn	Ser	Arg	Ala	Cys	Leu	Leu	Leu	Val	Leu
			130			135					140				
Gly	Cys	Trp	Val	Gly	Ala	Phe	Leu	Ser	Val	Leu	Phe	Pro	Thr	Ile	Val
145					150					155					160
Val	Thr	Arg	Leu	Pro	Tyr	Cys	Arg	Lys	Glu	Ile	Asn	His	Phe	Phe	Cys
				165					170					175	
Asp	Ile	Ala	Pro	Leu	Leu	Gln	Val	Ala	Cys	Ile	Asn	Thr	His	Leu	Ile
			180					185				190			
Glu	Lys	Ile	Asn	Phe	Leu	Leu	Ser	Ala	Leu	Val	Ile	Leu	Ser	Ser	Leu
			195				200					205			
Ala	Phe	Thr	Thr	Gly	Ser	Tyr	Val	Tyr	Ile	Ile	Ser	Thr	Ile	Leu	Arg
			210			215					220				
Ile	Pro	Ser	Thr	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser
225				230						235					240
His	Ile	Thr	Val	Val	Ser	Ile	Ala	His	Gly	Ser	Asn	Ile	Phe	Val	Tyr
				245					250					255	
Val	Arg	Pro	Asn	Gln	Asn	Ser	Ser	Leu	Asp	Tyr	Asp	Lys	Val	Ala	Ala
			260					265					270		
Val	Leu	Ile	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Ile	Tyr	Ser
			275				280					285			
Leu	Arg	Asn	Glu	Lys	Val	Gln	Glu	Val	Leu	Arg	Glu	Thr	Val	Asn	Arg
			290			295					300				
Ile	Met	Thr	Leu	Ile	Gln	Arg	Lys	Thr							
305					310										

<210> 1127

<211> 247

<212> PRT

<213> Unknown (H38g43 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(247)

<223> Xaa = Any Amino Acid

<400> 1127

Met	Gly	Asn	Ile	Asn	Ile	Ser	Leu	Glu	Asn	Tyr	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Ser	Asn	Xaa	Pro	Pro	Leu	Glu	Ile	Val	Ile	Phe	Val	Val	Leu	Leu
			20					25					30		
Ile	Phe	Cys	Phe	Met	Thr	Leu	Ile	Gly	Lys	Leu	Phe	Ser	Ile	Ile	Leu
			35				40					45			
Ser	Tyr	Leu	Asp	Ser	His	Pro	His	Thr	Pro	Arg	Tyr	Leu	Phe	Ser	Phe
			50			55					60				
Leu	Asp	Phe	Cys	Tyr	Thr	Ile	Ser	Ser	Ile	Phe	Xaa	Leu	Gln	Tyr	Asn
65					70					75					80
Leu	Trp	Gly	Pro	Gln	Lys	Asn	Ile	Ser	Tyr	Ala	Ser	Gly	Met	Ile	Gln
				85					90					95	
Ile	Tyr	Phe	Val	Leu	Thr	Leu	Gly	Thr	Met	Asp	Cys	Ala	Leu	Leu	Val
			100					105					110		
Val	Met	Ser	Arg	Thr	Val	Tyr	Ala	Ala	Gly	His	Arg	His	Leu	Pro	Tyr
			115				120						125		

```

Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
130 135 140
Ala Phe Asp Ser Ph Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145 150 155 160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
165 170 175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
180 185 190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
195 200 205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
210 215 220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225 230 235 240
Arg Pro Ile Leu Gly Asn Ser
245

```

<210> 1128

<211> 316

<212> PRT

<213> Unknown (H38g44 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
1 5 10 15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
20 25 30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
35 40 45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
50 55 60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65 70 75 80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
85 90 95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
100 105 110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
115 120 125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
130 135 140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145 150 155 160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
165 170 175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
180 185 190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
195 200 205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210 215 220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225 230 235 240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```

				245					250				255				
Tyr	Val	Arg	Pro	Ser	Gln	Ser	His	Ser	Met	Gly	Phe	Asp	Lys	Val	Thr		
			260					265					270				
Ala	Val	Pro	Thr	Met	Val	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Thr	Tyr	Ser		
		275					280					285					
Leu	Arg	Asn	Glu	Lys	Val	Lys	Ala	Val	Leu	Lys	Glu	Ala	Val	Ser	Lys		
	290					295					300						
Ile	Met	Ser	Ser	Trp	His	Arg	Arg	Thr	Xaa	Asn	Phe						
305					310					315							

<210> 1129

<211> 310

<212> PRT

<213> Unknown (H38g45 protein)

<220>

<223> Synthetic construct

<400> 1129

Met	Glu	Pro	Gln	Asn	Thr	Thr	Gln	Val	Ser	Met	Phe	Val	Leu	Leu	Gly		
1				5					10					15			
Phe	Ser	Gln	Thr	Gln	Glu	Leu	Gln	Lys	Phe	Leu	Phe	Leu	Leu	Phe	Leu		
		20						25					30				
Leu	Val	Tyr	Val	Thr	Thr	Ile	Val	Gly	Asn	Leu	Leu	Ile	Met	Val	Thr		
	35					40						45					
Val	Thr	Phe	Asp	Cys	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Arg		
	50				55						60						
Asn	Leu	Ala	Leu	Ile	Asp	Leu	Cys	Tyr	Ser	Thr	Val	Thr	Ser	Pro	Lys		
65				70					75					80			
Met	Leu	Val	Asp	Phe	Leu	His	Glu	Thr	Lys	Thr	Ile	Ser	Tyr	Gln	Gly		
			85						90					95			
Cys	Met	Ala	Gln	Ile	Phe	Phe	Phe	His	Leu	Leu	Gly	Gly	Gly	Thr	Val		
		100						105					110				
Phe	Phe	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Ser	Gln		
	115						120					125					
Pro	Leu	Arg	Tyr	Val	Thr	Ile	Met	Asn	Thr	Gln	Leu	Cys	Val	Gly	Leu		
	130					135					140						
Val	Val	Ala	Ala	Trp	Val	Gly	Gly	Phe	Val	His	Ser	Ile	Val	Gln	Leu		
145				150					155					160			
Ala	Leu	Ile	Leu	Pro	Leu	Pro	Phe	Cys	Asp	Pro	Asn	Ile	Ile	Asp	Asn		
			165						170					175			
Phe	Tyr	Cys	Asp	Val	Pro	Gln	Val	Leu	Arg	Leu	Ala	Cys	Thr	Asp	Thr		
	180							185					190				
Ser	Leu	Leu	Glu	Phe	Leu	Met	Ile	Phe	Asn	Ser	Gly	Leu	Leu	Val	Ile		
	195					200					205						
Ile	Trp	Phe	Leu	Leu	Leu	Leu	Ile	Ser	Tyr	Thr	Val	Ile	Leu	Val	Met		
	210					215					220						
Leu	Arg	Ser	His	Ser	Gly	Lys	Ala	Arg	Arg	Lys	Ala	Ala	Ser	Thr	Cys		
225				230					235					240			
Thr	Thr	His	Ile	Ile	Val	Val	Ser	Met	Ile	Phe	Ile	Pro	Cys	Ile	Tyr		
			245						250					255			
Ile	Tyr	Thr	Trp	Pro	Phe	Thr	Pro	Phe	Leu	Met	Asp	Lys	Ala	Val	Ser		
	260							265					270				
Ile	Ser	Tyr	Thr	Val	Met	Thr	Pro	Met	Leu	Asn	Pro	Met	Ile	Tyr	Thr		
	275					280						285					
Leu	Arg	Asn	Gln	Asp	Met	Lys	Ala	Ala	Met	Arg	Arg	Leu	Gly	Lys	Cys		
	290					295					300						
Leu	Val	Ile	Cys	Arg	Glu												
305					310												

<210> 1130

<211> 311
 <212> PRT
 <213> Unknown (H38g46 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(311)
 <223> Xaa = Any Amino Acid

<400> 1130
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr
 20 25 30
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile
 35 40 45
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Leu Ser His
 50 55 60
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu
 65 70 75 80
 Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys
 85 90 95
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe
 100 105 110
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro
 115 120 125
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val
 130 135 140
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa
 145 150 155 160
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe
 165 170 175
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys
 180 185 190
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser
 195 200 205
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro
 210 215 220
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu
 225 230 235 240
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val
 245 250 255
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe
 260 265 270
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
 275 280 285
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu
 290 295 300
 Leu Cys Leu Ile Leu Xaa Asn
 305 310

<210> 1131
 <211> 334
 <212> PRT
 <213> Unknown (H38g47 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
          65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
          145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
          165          170          175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
          225          230          235          240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
          275          280          285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
          290          295          300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
          305          310          315          320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
          325          330

```

<210> 1132

<211> 307

<212> PRT

<213> Unknown (H38g48 protein)

<220>

<223> Synthetic construct

<400> 1132

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Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
 1          5          10          15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
          20          25          30

```

Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Il Ile Thr
 35 40 45
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg
 115 120 125
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu
 130 135 140
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val
 195 200 205
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr
 245 250 255
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser
 260 265 270
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His
 290 295 300
 Arg Leu Val
 305

<210> 1133

<211> 316

<212> PRT

<213> Unknown (H38g49 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys
 50 55 60
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 65 70 75 80
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

```
<210> 1134
<211> 123
<212> PRT
<213> Unknown (H38g50 protein)
```

<400> 1134															
Met	Ser	Gly	Ser	Pro	Thr	Gln	Leu	Thr	Ala	Gly	Pro	Arg	Thr	Ala	Ser
1				5					10					15	
Gly	Cys	Val	Ile	Met	Ile	Cys	Phe	Ala	Leu	Thr	Val	Leu	Ser	Tyr	Ile
			20					25					30		
Arg	Ile	Leu	Ala	Thr	Val	Val	Gln	Ile	Arg	Ser	Ala	Ala	Ser	Arg	Arg
		35					40					45			
Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Gly	Met	Val	Leu	Leu	Phe
	50					55					60				
Tyr	Gly	Thr	Gly	Ser	Ser	Thr	Tyr	Met	Arg	Pro	Thr	Thr	Arg	Tyr	Ser
65					70					75				80	
Pro	Leu	Glu	Gly	Arg	Leu	Ala	Ala	Val	Phe	Tyr	Ser	Ile	Leu	Ile	Pro
				85					90					95	
Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Asp	Met	Lys	Arg
			100					105					110		
Ala	Leu	Trp	Lys	Leu	Tyr	Leu	Gln	Val	Pro	Tyr					
		115					120								

480

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
 20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
 35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
 65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
 85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
 100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
 115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
 130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
 145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
 165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
 180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
 195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
 210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
 225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
 245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
 260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
 275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
 290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
 305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
 325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
 340          345          350
Arg Xaa Tyr Pro
 355

```

<210> 1136

<211> 317

<212> PRT

<213> Unknown (H38g52 protein)

<220>

<223> Synthetic construct

<400> 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
 1           5           10           15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
          35           40           45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
          65           70           75           80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
          100          105          110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
          115          120          125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
          130          135          140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
          145          150          155          160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
          165          170          175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
          180          185          190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile
          195          200          205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
          210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
          225          230          235          240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
          245          250          255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
          260          265          270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
          275          280          285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
          290          295          300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
          305          310          315

```

<210> 1137

<211> 312

<212> PRT

<213> Unknown (H38g53 protein)

<220>

<223> Synthetic construct

<400> 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
          35           40           45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
          50           55           60

```

```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65          70          75          80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
          85          90          95
Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
          100          105          110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
          115          120          125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
          130          135          140
Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser
          145          150          155          160
Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
          165          170          175
Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
          180          185          190
Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
          195          200          205
Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
          210          215          220
Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser
          225          230          235          240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
          245          250          255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe
          260          265          270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr
          275          280          285
Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly
          290          295          300
Lys Glu Met Gly Leu Thr Gln Ser
305          310

```

<210> 1138

<211> 343

<212> PRT

<213> Unknown (H38g54 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 1138

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20          25          30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
          35          40          45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
          50          55          60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
          85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
          100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```

```

      115              120              125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
  130              135              140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
  145              150              155              160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165              170              175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180              185              190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195              200              205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210              215              220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
  225              230              235              240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245              250              255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260              265              270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275              280              285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
  290              295              300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
  305              310              315              320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325              330              335
Tyr Leu Ser Tyr Thr His His
      340

```

<210> 1139

<211> 291

<212> PRT

<213> Unknown (H38g55 protein)

<220>

<223> Synthetic construct

<400> 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1           5           10           15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg Leu His Thr
      20           25           30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35           40           45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50           55           60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
  65           70           75           80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85           90           95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100          105          110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115          120          125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130          135          140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
  145          150          155          160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165          170          175

```

Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala
 180 185 190
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly
 195 200 205
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val
 210 215 220
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln
 225 230 235 240
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val
 245 250 255
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys
 260 265 270
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln
 275 280 285
 Ala Gly Gln
 290

<210> 1140

<211> 307

<212> PRT

<213> Unknown (H38g56 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile
 1 5 10 15
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile
 20 25 30
 Thr Gly Asn Gly Ala Ile Ala Phe Leu Trp Cys Asp Arg Arg Leu
 35 40 45
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile
 50 55 60
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser
 65 70 75 80
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe
 85 90 95
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala
 100 105 110
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile
 115 120 125
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys
 130 135 140
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro
 165 170 175
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys
 180 185 190
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile
 195 200 205
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser
 210 215 220
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
 225 230 235 240
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

				245					250					255					
Leu	Gly	His	Ser	Thr	Glu	Met	Gln	Lys	Ile	Val	Thr	L	u	Phe	Tyr	Ala			
			260					265						270					
Met	Val	Thr	Ser	Leu	Phe	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Gln	Asn	Lys				
		275					280						285						
Glu	Ile	Lys	Ala	Ala	Leu	Arg	Lys	Val	Leu	Val	Ser	Ser	Asn	Ile	Ile				
	290					295					300								
Xaa	Gly	Ile																	
305																			

<210> 1141

<211> 221

<212> PRT

<213> Unknown (H38g57 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400> 1141

Ala	Cys	Lys	His	Asp	Met	Ile	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Leu				
1				5					10					15					
Val	Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His				
			20					25					30						
Leu	Cys	Val	Phe	Phe	Val	Leu	Val	Ser	Phe	Phe	Ile	Ser	Met	Xaa	Asp				
		35				40						45							
Ser	Gln	Leu	His	Ser	Xaa	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn				
	50					55					60								
Val	Glu	Ile	Ser	Asn	Phe	Val	Cys	Asp	Pro	Ser	Gln	Phe	Leu	Lys	Leu				
65				70					75					80					
Ala	Cys	Ser	Asp	Ser	Val	Ile	Asn	Ser	Ile	Phe	Thr	Tyr	Phe	His	Ser				
			85					90					95						
Thr	Met	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Phe				
		100						105					110						
Lys	Ile	Val	Thr	Phe	Ile	Leu	Trp	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr				
	115					120						125							
Lys	Ala	Phe	Ser	Thr	Cys	Asp	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe				
	130				135						140								
Tyr	Gly	Thr	Gly	Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Pro				
145				150					155					160					
Pro	Arg	Asn	Gly	Val	Met	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro				
			165					170						175					
Met	Leu	Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser				
		180						185					190						
Ala	Leu	Trp	Arg	Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe				
	195					200						205							
His	Pro	Phe	Ser	Cys	Val	Gly	Lys	Gly	Asn	His	Ile	Lys							
	210					215						220							

<210> 1142

<211> 314

<212> PRT

<213> Unknown (H38g58 protein)

<220>

<223> Synthetic construct

<400> 1142

```

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1          5          10          15
Ph Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
 20          25          30
Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
 35          40          45
Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
 65          70          75          80
Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
 85          90          95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
 100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
 115          120          125
Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
 130          135          140
Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
 145          150          155          160
Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
 165          170          175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180          185          190
Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
 195          200          205
Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
 210          215          220
Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
 225          230          235          240
Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
 245          250          255
Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
 260          265          270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
 290          295          300
Ala Arg Arg Leu Gln Val Ser Leu Ser Met
305          310

```

<210> 1143

<211> 315

<212> PRT

<213> Unknown (H38g59 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1143

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
 20          25          30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35          40          45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

50		55		60
Phe Phe Leu Ser Thr	Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser			
65	70	75	80	
Trp Glu Leu Xaa Val	Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile			
	85	90	95	
Ser Tyr Asn Ser Cys	Ser Val Gln Met Ile Thr His Leu Phe Leu Gly			
	100	105	110	
Thr Ala Gln Cys Leu	Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val			
	115	120	125	
Glu Ile Ser Tyr Leu	Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val			
	130	135	140	
Cys Ile Gln Leu Ala	Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala			
145	150	155	160	
Val Thr Leu Ile Ile	Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val			
	165	170	175	
Ile Asn His Phe Thr	Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys			
	180	185	190	
Ser Asp Thr Leu Val	Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe			
	195	200	205	
Thr Leu Pro Leu Pro	Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile			
	210	215	220	
Phe Val Arg Ala Val	Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly			
225	230	235	240	
Ser His Leu Thr Gly	Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met			
	245	250	255	
Tyr Leu Lys Pro Gln	Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val			
	260	265	270	
Ser Lys Leu Tyr Gly	Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr			
	275	280	285	
Ile Gln Arg Asn Lys	Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys			
	290	295	300	
Gly Asn Glu Lys Ser	Xaa Gln Phe Ser Leu Asn			
305	310	315		

<210> 1144

<211> 351

<212> PRT

<213> Unknown (H38g61 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 1144

Met Asp Ile Leu Val	Ile Asp Asn Gly Ser Glu Val Thr Glu Phe Ile
1	5 10 15
Leu Val Gly Leu Tyr	Asn His Pro Lys Phe Gln Ile Ala Phe Tyr Arg
	20 25 30
Thr Met Val Val Val	Tyr Leu Ile Thr Phe Val Gly Ser Ser Leu Ile
	35 40 45
Ile Val Val Val Lys	Val Asp Gly Trp Leu His Thr Pro Met Cys Phe
	50 55 60
Phe Leu Ser Asn Leu	Ser Phe Leu Asp Ile Cys Tyr Ser Ser Asn Ser
65	70 75 80
Val Pro Phe Leu Leu	Phe Asn Gly Leu Arg Asp Tyr Pro Thr Ile Ser
	85 90 95
Tyr Asn Ser Cys Tyr	Ala Gln Met Thr Ser Ala Phe Phe Leu Gly Met
	100 105 110


```

Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val
  115                      120                      125
Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys
  130                      135                      140
Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile
  145                      150                      155                      160
Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met
  165                      170                      175
Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn
  180                      185                      190
His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp
  195                      200                      205
Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu
  210                      215                      220
Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala
  225                      230                      235                      240
Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala
  245                      250                      255
Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile
  260                      265                      270
Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg
  275                      280                      285
Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val
  290                      295                      300
Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val
  305                      310                      315                      320
Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala
  325                      330                      335
Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys
  340                      345                      350

```

<210> 1145

<211> 318

<212> PRT

<213> Unknown (H38g62 protein)

<220>

<223> Synthetic construct

<400> 1145

```

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly
  1           5           10           15
Leu Ser Gly Tyr Pro Lys Leu Glu Ile Phe Phe Ala Leu Ile Leu
  20           25           30
Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
  35           40           45
Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly
  50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser
  65           70           75           80
Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
  85           90           95
Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
  100          105          110
Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
  115          120          125
Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu
  130          135          140
Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr
  145          150          155          160
Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

```
<210> 1146
<211> 319
<212> PRT
<213> Unknown (H38g63 protein)
```

<400> 1146

490

Ser Met His Leu Lys Pro Ser Ala Val Asp Ser Gln Glu Ile Asp Lys
 260 265 270
 Phe Met Ala Leu Val Tyr Ala Gly Gln Thr Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser L u Arg Asn Lys Glu Val Lys Val Ala Leu Lys Lys Leu
 290 295 300
 Leu Ile Arg Asn His Phe Asn Thr Ala Phe Ile Ser Ile Leu Lys
 305 310 315

<210> 1147

<211> 310

<212> PRT

<213> Unknown (H38g64 protein)

<220>

<223> Synthetic construct

<400> 1147

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala
 1 5 10 15
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu
 35 40 45
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln
 65 70 75 80
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg
 85 90 95
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys
 100 105 110
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln
 115 120 125
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu
 130 135 140
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr
 145 150 155 160
 Val Ser Ala Phe Thr Leu Ser Phe Cys Gly Thr Ser Glu Ile Asp Phe
 165 170 175
 Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Thr Cys Gly Glu Ser
 180 185 190
 Tyr Thr Gln Glu Val Leu Ile Ile Met Phe Ala Ile Phe Val Ile Pro
 195 200 205
 Ala Ser Met Val Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
 210 215 220
 Ile Met Gly Ile Pro Ala Gly Ser Gln Ala Lys Thr Phe Ser Thr Cys
 225 230 235 240
 Thr Ser His Leu Thr Ala Val Ser Leu Phe Phe Gly Thr Leu Ile Phe
 245 250 255
 Met Tyr Leu Arg Gly Asn Ser Asp Gln Ser Ser Glu Lys Asn Arg Val
 260 265 270
 Val Ser Val Leu Tyr Thr Glu Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile Leu
 290 295 300
 Asn Arg Ala Lys Leu Ser
 305 310

<210> 1148

<211> 321

<212> PRT

<213> Unknown (H38g65 protein)

<220>

<223> Synthetic construct

<400> 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1           5           10           15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
 20           25           30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
 35           40           45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
 50           55           60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
 65           70           75           80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
 85           90           95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
100           105           110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
115           120           125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
130           135           140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145           150           155           160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
165           170           175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
180           185           190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
195           200           205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
210           215           220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225           230           235           240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
245           250           255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
260           265           270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
275           280           285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys
290           295           300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305           310           315           320
Ile

```

<210> 1149

<211> 311

<212> PRT

<213> Unknown (H38g66 protein)

<220>

<223> Synthetic construct

<400> 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser
 20 25 30
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile
 35 40 45
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met
 100 105 110
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe
 130 135 140
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu
 145 150 155 160
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr
 180 185 190
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu
 195 200 205
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly
 210 215 220
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr
 245 250 255
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser
 260 265 270
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg
 290 295 300
 His Val Asn Ser Trp Lys Asn
 305 310

<210> 1150

<211> 312

<212> PRT

<213> Unknown (H38g67 protein)

<220>

<223> Synthetic construct

<400> 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu
 20 25 30
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
 35 40 45
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
 65 70 75 80
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

<400> 1151																
Met	Cys	Ser	Gly	Asn	Gln	Thr	Ser	Gln	Asn	Gln	Thr	Ala	Ser	Thr	Asp	
1				5					10					15		
Phe	Thr	Leu	Thr	Gly	Leu	Phe	Ala	Glu	Ser	Lys	His	Ala	Ala	Leu	Leu	
			20					25					30			
Tyr	Thr	Val	Thr	Phe	Leu	Leu	Phe	Leu	Met	Ala	Leu	Thr	Gly	Asn	Ala	
		35					40					45				
Leu	Leu	Ile	Leu	Leu	Ile	His	Ser	Glu	Pro	Arg	Leu	His	Thr	Pro	Met	
	50					55					60					
Tyr	Phe	Phe	Ile	Ser	Gln	Leu	Ala	Leu	Met	Asp	Leu	Met	Tyr	Leu	Cys	
65					70					75					80	
Val	Thr	Val	Pro	Lys	Met	Leu	Val	Gly	Gln	Val	Thr	Gly	Asp	Asp	Thr	
				85					90					95		
Ile	Ser	Pro	Ser	Gly	Cys	Gly	Ile	Gln	Met	Phe	Phe	His	Leu	Thr	Leu	
			100					105					110			
Ala	Gly	Ala	Glu	Val	Phe	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	
		115					120					125				
Ala	Ala	Val	Cys	Arg	Pro	Leu	His	Tyr	Pro	Leu	Leu	Met	Asn	Gln	Arg	
	130					135					140					
Val	Cys	Gln	Leu	Leu	Val	Ser	Ala	Cys	Trp	Val	Leu	Gly	Met	Val	Asp	
145					150					155					160	
Gly	Leu	Leu	Leu	Thr	Pro	Ile	Thr	Met	Ser	Phe	Pro	Phe	Cys	Gln	Ser	
				165					170					175		
Arg	Lys	Ile	Leu	Ser	Phe	Phe	Cys	Glu	Thr	Pro	Ala	Leu	Leu	Lys	Leu	
		180						185					190			

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys
 195 200 205
 Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr
 210 215 220
 Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg
 225 230 235 240
 Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu
 245 250 255
 Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
 260 265 270
 Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro
 275 280 285
 Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg
 290 295 300
 Ala Met Arg Ser Met Met Gln Ser Arg
 305 310

<210> 1152

<211> 314

<212> PRT

<213> Unknown (H38g69 protein)

<220>

<223> Synthetic construct

<400> 1152

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser
 20 25 30
 Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr
 35 40 45
 Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr
 50 55 60
 Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
 65 70 75 80
 Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly
 85 90 95
 Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
 100 105 110
 Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu
 130 135 140
 Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val
 145 150 155 160
 Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr
 180 185 190
 Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu
 195 200 205
 Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr
 210 215 220
 Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Phe Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

275	280	285
Leu Arg Asn Gln Glu Val Lys Ile Ala Met Arg Lys Leu Lys Asn Arg		
290	295	300
Phe Leu Asn Phe Asn Lys Ala Met Pro Ser		
305	310	

<210> 1153
 <211> 310
 <212> PRT
 <213> Unknown (H38g70 protein)

<220>
 <223> Synthetic construct

<400> 1153

Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe	
1	15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu	
20	30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile	
35	45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His	
50	60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met	
65	80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg	
85	95
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu	
100	110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro	
115	125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala	
130	140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val	
145	160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe	
165	175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His	
180	190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly	
195	205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile	
210	220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys	
225	240
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile	
245	255
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr	
260	270
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile	
275	285
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu	
290	300
Gly Val Glu Arg Ala Leu	
305	310

<210> 1154
 <211> 323
 <212> PRT
 <213> Unknown (H38g71 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
          50           55           60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
          65           70           75           80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
          85           90           95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
          100          105          110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
          115          120          125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
          130          135          140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
          145          150          155          160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
          165          170          175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
          180          185          190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
          195          200          205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
          210          215          220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
          225          230          235          240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
          245          250          255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
          260          265          270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
          275          280          285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
          290          295          300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
          305          310          315          320
Phe Leu Cys

```

<210> 1155

<211> 315

<212> PRT

<213> Unknown (H38g72 protein)

<220>

<223> Synthetic construct

<400> 1155

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

```

1           5           10           15
Leu Ser Ser Ser Leu Glu Leu Gln Ile Phe Tyr Phe Leu Phe Phe Ser
20           25           30
Ile Val Tyr Ala Ala Thr Val Leu Gly Asn Leu Leu Ile Val Val Thr
35           40           45
Ile Ala Ser Glu Pro His Leu His Ser Pro Thr Tyr Phe Leu Leu Gly
50           55           60
Asn Leu Ser Phe Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
65           70           75           80
Met Ile Ala Asp Phe Leu Arg Glu His Lys Ala Ile Ser Phe Glu Gly
85           90           95
Cys Met Thr Gln Met Phe Phe Leu His Leu Leu Gly Gly Ala Glu Ile
100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Arg Arg Met Cys Val Gly Leu
130          135          140
Val Ile Leu Ser Trp Ile Val Gly Ile Phe His Ala Leu Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Val Asp Thr
180          185          190
Tyr Ile Leu Gly Val Phe Met Ile Ser Thr Ser Gly Met Ile Ala Leu
195          200          205
Val Cys Phe Ile Leu Leu Val Ile Ser Tyr Thr Ile Ile Leu Val Thr
210          215          220
Val Arg Gln Arg Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Thr Val Val Thr Leu Phe Phe Gly Pro Cys Thr Phe
245          250          255
Ile Tyr Val Trp Pro Phe Thr Asn Phe Pro Ile Asp Lys Val Leu Ser
260          265          270
Val Phe Tyr Thr Ile Tyr Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr
275          280          285
Val Arg Asn Lys Asp Val Lys Tyr Ser Met Arg Lys Leu Ser Ser His
290          295          300
Ile Phe Lys Ser Arg Lys Thr Asp His Thr Pro
305          310          315

```

<210> 1156

<211> 321

<212> PRT

<213> Unknown (H38g73 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1156

```

Met Lys Lys Tyr Met Glu Arg Thr Asn Xaa Thr Thr Glu Phe Glu Leu
1           5           10           15
Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu Phe
20           25           30
Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg Ile
35           40           45
Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His Gly
50           55           60

```

```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65          70          75          80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85          90          95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115        120        125
Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys Lys
      130        135        140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145          150          155          160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165        170        175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180        185        190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195        200        205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
210          215          220
Ser Phe Leu Tyr Phe His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225          230          235          240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245        250        255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260        265        270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275        280        285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
      290        295        300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305          310          315          320
Trp

```

<210> 1157

<211> 325

<212> PRT

<213> Unknown (H38g74 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1157

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20          25          30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35          40          45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50          55          60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65          70          75          80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85          90          95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```

	100		105		110
Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe					
115		120		125	
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His					
130		135		140	
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp					
145		150		155	160
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn					
	165		170		175
Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu					
	180		185		190
Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser					
	195	200		205	
Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys					
210		215		220	
Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys					
225		230		235	240
Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp					
	245		250		255
Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro					
	260		265		270
Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met					
	275		280		285
Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala					
	290	295		300	
Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro					
305		310		315	320
Ser Phe Phe Leu Cys					
	325				

<210> 1158

<211> 319

<212> PRT

<213> Unknown (H38g75 protein)

<220>

<223> Synthetic construct

<400> 1158

Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe					
1	5		10		15
Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Leu Val Leu Leu Leu Pro					
	20		25		30
Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val					
	35		40		45
Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn					
	50	55		60	
Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val					
	65	70		75	80
Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys					
	85		90		95
Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu					
	100		105		110
Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro					
	115		120		125
Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val					
	130	135		140	
Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile					
	145	150		155	160
Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe					
	165		170		175

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Phe Cys Asp Ser Gly Pro Leu Leu Ala Leu Ala Cys Ala Asp Thr Thr
    180                      185                      190
Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys
    195                      200                      205
Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile
    210                      215                      220
Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys
    225                      230                      235                      240
Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe
    245                      250                      255
Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile
    260                      265                      270
Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile
    275                      280                      285
Tyr Thr Leu Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp
    290                      295                      300
Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu
    305                      310                      315

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<210> 1159

<211> 313

<212> PRT

<213> Unknown (H38g76 protein)

<220>

<223> Synthetic construct

<400> 1159

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Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
  1                      5                      10                      15
Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
    20                      25                      30
Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
    35                      40                      45
Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
    50                      55                      60
Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys
    65                      70                      75                      80
Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly
    85                      90                      95
Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met
    100                      105                      110
Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
    115                      120                      125
Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu
    130                      135                      140
Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val
    145                      150                      155                      160
Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
    165                      170                      175
Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
    180                      185                      190
Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
    195                      200                      205
Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
    210                      215                      220
Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser
    225                      230                      235                      240
Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
    245                      250                      255
Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

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260	265	270
Val Ser Val Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Ile Ile		
275	280	285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Val Val		
290	295	300
Thr Lys Tyr Ile Leu Cys Glu Glu Lys		
305	310	

<210> 1160

<211> 313

<212> PRT

<213> Unknown (H38g77 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1160

Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser	
1 5 10 15	
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn	
20 25 30	
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys	
35 40 45	
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn	
50 55 60	
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val	
65 70 75 80	
Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe	
85 90 95	
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His	
100 105 110	
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg	
115 120 125	
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Leu Gly Leu Ile	
130 135 140	
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly	
145 150 155 160	
Ser Asn Lys Val Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys	
165 170 175	
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn	
180 185 190	
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr	
195 200 205	
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys	
210 215 220	
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe	
225 230 235 240	
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu	
245 250 255	
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn	
260 265 270	
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg	
275 280 285	
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys	
290 295 300	
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr	
305 310	

<210> 1161
 <211> 304
 <212> PRT
 <213> Unknown (H38g78 pr tein)

<220>
 <223> Synthetic construct

<400> 1161
 Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1 5 10 15
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
 20 25 30
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
 35 40 45
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
 50 55 60
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
 65 70 75 80
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
 85 90 95
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
 100 105 110
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
 115 120 125
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
 130 135 140
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
 145 150 155 160
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
 165 170 175
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
 180 185 190
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
 195 200 205
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
 245 250 255
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
 260 265 270
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
 275 280 285
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
 290 295 300

<210> 1162
 <211> 321
 <212> PRT
 <213> Unknown (H38g79 protein)

<220>
 <223> Synthetic construct

<400> 1162
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1 5 10 15
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

										20											25											30
Phe	Cys	Phe	Ile	Tyr	Leu	Thr	Val	Ile	Leu	Gly	Asn	Leu	Thr	Ile	Leu																	
										35											40											45
His	Val	Ile	Cys	Thr	Asp	Ala	Thr	Leu	His	Gly	Pro	Met	Tyr	Tyr	Phe																	
										50											55											60
Leu	Gly	Met	Leu	Ala	Val	Thr	Asp	Leu	Gly	Leu	Cys	Leu	Ser	Thr	Leu																	
										65											70											75
Pro	Thr	Val	Leu	Gly	Ile	Phe	Trp	Phe	Asp	Thr	Arg	Glu	Ile	Gly	Ile																	
										85											90											95
Pro	Ala	Cys	Phe	Thr	Gln	Leu	Phe	Phe	Ile	His	Thr	Leu	Ser	Ser	Met																	
										100											105											110
Glu	Ser	Ser	Val	Leu	Leu	Ser	Met	Ser	Ile	Asp	Arg	Tyr	Val	Ala	Val																	
										115											120											125
Cys	Asn	Pro	Leu	His	Asp	Ser	Thr	Val	Leu	Thr	Pro	Ala	Cys	Ile	Val																	
										130											135											140
Lys	Met	Gly	Leu	Ser	Ser	Val	Leu	Arg	Ser	Ala	Leu	Leu	Ile	Leu	Pro																	
										145											150											155
Leu	Pro	Phe	Leu	Leu	Lys	Arg	Phe	Gln	Tyr	Cys	His	Ser	His	Val	Leu																	
										165											170											175
Ala	His	Ala	Tyr	Cys	Leu	His	Leu	Glu	Ile	Met	Lys	Leu	Ala	Cys	Ser																	
										180											185											190
Ser	Ile	Ile	Val	Asn	His	Ile	Tyr	Gly	Leu	Phe	Val	Val	Ala	Cys	Thr																	
										195											200											205
Val	Gly	Val	Asp	Ser	Leu	Leu	Ile	Phe	Leu	Ser	Tyr	Ala	Leu	Ile	Leu																	
										210											215											220
Arg	Thr	Val	Leu	Ser	Ile	Ala	Ser	His	Gln	Glu	Arg	Leu	Arg	Ala	Leu																	
										225											230											235
Asn	Thr	Cys	Val	Ser	His	Ile	Cys	Ala	Val	Leu	Leu	Phe	Tyr	Ile	Pro																	
										245											250											255
Met	Ile	Gly	Leu	Ser	Leu	Val	His	Arg	Phe	Gly	Glu	His	Leu	Pro	Arg																	
										260											265											270
Val	Val	His	Leu	Phe	Met	Ser	Tyr	Val	Tyr	Leu	Leu	Val	Pro	Pro	Leu																	
										275											280											285
Met	Asn	Pro	Ile	Ile	Tyr	Ser	Ile	Lys	Thr	Lys	Gln	Ile	Arg	Gln	Arg																	
										290											295											300
Ile	Ile	Lys	Lys	Phe	Gln	Phe	Ile	Lys	Ser	Leu	Arg	Cys	Phe	Trp	Lys																	
										305											310											315
																														320		

Asp

<210> 1163

<211> 323

<212> PRT

<213> Unknown (H38g80 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1163

Met	Gly	Asn	His	Thr	Thr	Val	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Ser																		
1											5											10											15
Glu	Thr	Cys	Glu	Leu	Gln	Met	Leu	Ile	Phe	Leu	Gly	Leu	Leu	Leu	Thr																		
										20											25											30	
Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Leu	Val	Ile	Val	Val	Ile	Thr	Leu																		
										35											40											45	
Met	Asp	Arg	Arg	Leu	His	Thr	Met	Tyr	Tyr	Phe	Leu	Arg	Asn	Phe																			
										50											55											60	

Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pr Lys Val Leu
 65 70 75 80
 Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe
 85 90 95
 Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu
 100 105 110
 Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu
 130 135 140
 Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu
 145 150 155 160
 Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe
 165 170 175
 Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu
 180 185 190
 Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr
 195 200 205
 Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu
 210 215 220
 His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser
 225 230 235 240
 Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met
 245 250 255
 Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val
 260 265 270
 Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val
 290 295 300
 Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser
 305 310 315 320
 Ile Pro Arg

<210> 1164

<211> 317

<212> PRT

<213> Unknown (H38g81 protein)

<220>

<223> Synthetic construct

<400> 1164

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile
 20 25 30
 Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe
 35 40 45
 Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro
 65 70 75 80
 Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg
 85 90 95
 Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu
 100 105 110
 Gly Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

130	135	140
Met Met Leu Ala Leu Trp	Leu Gly Gly Phe Val	His Ser Ile Ile Gln
145	150	155
Val Val Leu Ile Leu Arg	Leu Pro Phe Cys Gly	Pro Asn Gln Leu Asp
165	170	175
Asn Phe Phe Cys Asp Val	Pro Gln Val Ile Lys	Leu Ala Cys Thr Asp
180	185	190
Thr Phe Val Val Glu Leu	Leu Met Val Phe Asn	Ser Gly Leu Met Thr
195	200	205
Leu Leu Cys Phe Leu Gly	Leu Leu Ala Ser Tyr	Ala Val Ile Leu Cys
210	215	220
His Val Arg Lys Ala Ala	Ser Glu Leu Lys Asn	Lys Ala Met Ser Thr
225	230	235
Cys Thr Thr His Val Ile	Ile Ile Leu Leu Met	Phe Gly Pro Ala Ile
245	250	255
Phe Ile Tyr Met His Pro	Phe Arg Ala Leu Pro	Ala Asp Lys Val Val
260	265	270
Ser Phe Phe His Thr Val	Ile Phe Pro Leu Met	Asn Pro Met Ile Tyr
275	280	285
Thr Leu Arg Asn Gln Glu	Val Lys Thr Ser Met	Lys Arg Leu Leu Ser
290	295	300
Arg His Val Val Cys Gln	Val Asp Phe Ile Ile	Arg Asn
305	310	315

<210> 1165

<211> 287

<212> PRT

<213> Unknown (H38g82 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 1165

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu	
1	5
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu	
20	25
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr	
35	40
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys	
50	55
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe	
65	70
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys	
85	90
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys	
100	105
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe	
115	120
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys	
130	135
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln	
145	150
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa	
165	170
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr	
180	185
	190

Ala	Tyr	Ile	Ile	Ser	Thr	Leu	Leu	Cys	Ile	Pro	Ser	Ala	Gln	Gly	Cys
	195						200					205			
Gln	Glu	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Ile	Thr	Ile	Ile	Phe	Ile
	210					215					220				
Ala	Cys	Arg	Asn	Ser	Ile	Ser	Thr	Cys	Val	Arg	Pro	Asn	Pro	Arg	Tyr
225					230					235					240
Xaa	Leu	Asp	Phe	Asp	Lys	Val	Thr	Ala	Ile	Leu	Thr	Ile	Val	Val	Thr
			245						250					255	
Ser	Phe	Leu	Asn	Pro	Arg	Ile	Tyr	Ser	Leu	Arg	Xaa	Arg	Lys	Tyr	Glu
			260					265					270		
Gly	Ser	Thr	Ile	Cys	Thr	Ile	Leu	Ser	Pro	His	Ser	Lys	Gly	Thr	
		275					280					285			

<210> 1166

<211> 307

<212> PRT

<213> Unknown (H38g83 protein)

<220>

<223> Synthetic construct

<400> 1166

Met	Glu	Ser	Glu	Asn	Arg	Thr	Val	Ile	Arg	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Thr	Gln	Ser	Gln	Asp	Ile	Gln	Leu	Leu	Val	Phe	Val	Leu	Val	Leu
			20					25					30		
Ile	Phe	Tyr	Phe	Ile	Ile	Leu	Pro	Gly	Asn	Phe	Leu	Ile	Ile	Phe	Thr
		35					40					45			
Ile	Lys	Ser	Asp	Pro	Gly	Leu	Thr	Ala	Pro	Leu	Tyr	Phe	Phe	Leu	Gly
	50					55					60				
Asn	Leu	Ala	Phe	Leu	Asp	Ala	Ser	Tyr	Ser	Phe	Thr	Val	Ala	Pro	Arg
65					70					75				80	
Met	Leu	Val	Asp	Phe	Leu	Ser	Ala	Lys	Lys	Ile	Ile	Ser	Tyr	Arg	Gly
				85					90					95	
Cys	Ile	Thr	Gln	Leu	Phe	Phe	Leu	His	Phe	Leu	Gly	Gly	Gly	Glu	Gly
			100					105					110		
Leu	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Arg
			115				120					125			
Pro	Leu	His	Tyr	Pro	Thr	Val	Met	Asn	Pro	Arg	Thr	Cys	Tyr	Ala	Met
			130			135					140				
Met	Leu	Ala	Leu	Trp	Leu	Gly	Gly	Phe	Val	His	Ser	Ile	Ile	Gln	Val
145					150					155				160	
Val	Leu	Ile	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Gln	Leu	Asp	Asn
				165					170					175	
Phe	Phe	Cys	Asp	Val	Pro	Gln	Val	Ile	Lys	Leu	Ala	Cys	Thr	Asp	Thr
			180					185					190		
Phe	Val	Val	Glu	Leu	Leu	Met	Val	Phe	Asn	Ser	Gly	Leu	Met	Thr	Leu
			195				200					205			
Leu	Cys	Phe	Leu	Gly	Leu	Leu	Ala	Ser	Tyr	Ala	Val	Ile	Leu	Cys	Arg
			210				215				220				
Ile	Arg	Gly	Ser	Ser	Ser	Glu	Ala	Lys	Asn	Lys	Ala	Met	Ser	Thr	Cys
225					230					235					240
Ile	Thr	His	Ile	Ile	Val	Ile	Phe	Phe	Met	Phe	Gly	Pro	Gly	Ile	Phe
				245					250					255	
Ile	Tyr	Thr	Arg	Pro	Phe	Arg	Ala	Phe	Pro	Ala	Asp	Lys	Val	Val	Ser
			260					265					270		
Leu	Phe	His	Thr	Val	Ile	Phe	Pro	Leu	Leu	Asn	Pro	Val	Ile	Tyr	Thr
			275				280					285			
Leu	Arg	Asn	Gln	Glu	Val	Lys	Ala	Ser	Met	Lys	Lys	Val	Phe	Asn	Lys
			290			295					300				
His	Ile	Ala													

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr L u Phe Leu Gly
 50 55 60
 Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Il Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
 85 90 95
 Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu
 130 135 140
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
 145 150 155 160
 Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
 165 170 175
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
 180 185 190
 Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val
 195 200 205
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr
 210 215 220
 Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr
 225 230 235 240
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr
 245 250 255
 Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
 260 265 270
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
 290 295 300
 Phe Lys Ser Asn Val
 305

<210> 1207

<211> 308

<212> PRT

<213> Unknown (H38g124 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1207

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
 20 25 30
 Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala
 35 40 45
 Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser
 50 55 60
 Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr
 65 70 75
 Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Me
 85 90 95
 Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu

signed
 Jane
 #1/1/95

305

<210> 1167

<211> 309

<212> PRT

<213> Unknown (H38g84 protein)

<220>

<223> Synthetic construct

<400> 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
      20          25          30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
      35          40          45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
      50          55          60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
      65          70          75          80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
      85          90          95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
      100          105          110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115          120          125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
      130          135          140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
      145          150          155          160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
      165          170          175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
      180          185          190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
      195          200          205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
      210          215          220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
      225          230          235          240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
      245          250          255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
      260          265          270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275          280          285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
      290          295          300
Ala Leu Ala Gly Lys
305

```

<210> 1168

<211> 311

<212> PRT

<213> Unknown (H38g85 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1           5           10           15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
 20           25           30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
 35           40           45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
 50           55           60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
 65           70           75           80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
 85           90           95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
 100          105          110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
 115          120          125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
 130          135          140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
 145          150          155          160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
 165          170          175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
 180          185          190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Leu Ile Ser Tyr Thr
 195          200          205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
 210          215          220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
 225          230          235          240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
 245          250          255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
 260          265          270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
 275          280          285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
 290          295          300
Leu Ile Gly Leu Asp Leu Leu
305          310

```

<210> 1169

<211> 210

<212> PRT

<213> Unknown (H38g86 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1           5           10           15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

```

      20      25      30
Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu
      35      40      45
Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
      50      55      60
Ser Phe Val Ile Leu Ile Lys Met Phe Met Asn Ser Ile Ser Glu Arg
      65      70      75      80
Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
      85      90      95
Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
      100      105      110
Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
      115      120      125
Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
      130      135      140
Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
      145      150      155      160
Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
      165      170      175
Phe Val Val Ile Ala Xaa Xaa Leu Ile Phe Ile Ser Asp Ile Leu
      180      185      190
Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
      195      200      205
Ala Phe
      210

```

<210> 1170

<211> 274

<212> PRT

<213> Unknown (H38g87 protein)

<220>

<223> Synthetic construct

<400> 1170

```

Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile Asn Pro Lys Leu
  1      5      10      15
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Val Asp Phe
      20      25      30
Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu Asn Leu Val Val
      35      40      45
Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met Gln Phe Phe Phe
      50      55      60
Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu Ala Ala Met Ala
      65      70      75      80
Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala
      85      90      95
Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala Ser Tyr Ser Trp
      100      105      110
Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu Leu Thr Leu Ser
      115      120      125
Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys Glu His Ala Ala
      130      135      140
Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser Gln Lys Val Ile
      145      150      155      160
Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Ile Leu
      165      170      175
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr
      180      185      190
Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala
      195      200      205

```

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 210 215 220
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 225 230 235 240
 Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 245 250 255
 Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys
 260 265 270
 His Lys

<210> 1171
 <211> 348
 <212> PRT
 <213> Unknown (H38g88 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(348)
 <223> Xaa = Any Amino Acid

<400> 1171
 Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser
 1 5 10 15
 His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser
 20 25 30
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser
 35 40 45
 Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu
 65 70 75 80
 Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val
 85 90 95
 Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly
 130 135 140
 Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val
 145 150 155 160
 Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe
 165 170 175
 Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp
 180 185 190
 Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Pro
 195 200 205
 Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile
 210 215 220
 Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly
 225 230 235 240
 Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val
 245 250 255
 Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile
 260 265 270
 Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg

290	295	300
Asp Leu Gly Thr Xaa Lys Met Lys Gln S r Thr Gln Arg Ser Thr Phe		
305	310	315
Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys		320
	325	330
Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu		335
340	345	

<210> 1172

<211> 319

<212> PRT

<213> Unknown (H38g89 protein)

<220>

<223> Synthetic construct

<400> 1172

Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly		
1	5	10
Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser		15
	20	25
Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr		30
	35	40
Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly		45
	50	55
Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys		60
65	70	75
Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly		80
	85	90
Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met		95
	100	105
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys		110
	115	120
Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu		125
	130	135
Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu		140
145	150	155
Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser		160
	165	170
Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser		175
	180	185
Tyr Ile Ile Glu Ile Leu Ile Val Asn Ser Gly Ile Leu Ser Leu		190
	195	200
Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr		205
	210	215
Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu		220
225	230	235
Ala Ser His Ile Ala Val Val Ile Leu Phe Gly Pro Cys Ile Phe		240
	245	250
Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala		255
	260	265
Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr		270
	275	280
Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His		285
290	295	300
Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg		305
305	310	315

<210> 1173

<211> 312

<212> PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
 1           5           10          15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
          20          25          30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
          35          40          45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
          50          55          60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
          65          70          75          80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
          85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
          100         105         110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
          115         120         125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
          130         135         140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
          145         150         155         160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
          165         170         175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
          180         185         190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
          195         200         205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
          210         215         220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
          225         230         235         240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
          245         250         255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
          260         265         270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
          275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
          290         295         300
Cys Arg Lys Leu Val Ser Xaa Lys
          305         310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

```

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

1 5 10 15
 Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
 20 25 30
 Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35 40 45
 Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe L u Ser
 50 55 60
 Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
 65 70 75 80
 Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
 130 135 140
 Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
 145 150 155 160
 Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
 180 185 190
 Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu Leu
 195 200 205
 Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
 210 215 220
 Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
 245 250 255
 Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
 260 265 270
 Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
 290 295 300
 Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
 305 310 315 320
 Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
 325 330 335
 Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
 340 345 350
 Gln Arg Lys Phe Pro
 355

<210> 1175

<211> 320

<212> PRT

<213> Unknown (H38g92 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1175

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
 1 5 10 15

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pr Ile Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Ph Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala
 85 90 95
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg
 145 150 155 160
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp
 180 185 190
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser
 225 230 235 240
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly
 260 265 270
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
 290 295 300
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315 320

<210> 1176

<211> 313

<212> PRT

<213> Unknown (H38g93 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys

```

65          70          75          80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85          90          95
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115          120          125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130          135          140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
      145          150          155
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165          170          175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180          185          190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195          200          205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210          215          220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
      225          230          235          240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245          250          255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260          265          270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275          280          285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
      290          295          300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305          310

```

<210> 1177

<211> 338

<212> PRT

<213> Unknown (H38g94 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
1          5          10          15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20          25          30
Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val
      35          40          45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
      50          55          60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
      65          70          75          80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85          90          95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100          105          110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
      115          120          125

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130 135 140
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
 145 150 155 160
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
 165 170 175
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
 180 185 190
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
 195 200 205
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
 210 215 220
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
 225 230 235 240
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
 245 250 255
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
 260 265 270
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
 275 280 285
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
 290 295 300
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
 305 310 315 320
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
 325 330 335
 Phe Ile

<210> 1178

<211> 314

<212> PRT

<213> Unknown (H38g95 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1178

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1 5 10 15
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
 20 25 30
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
 100 105 110
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu
 130 135 140
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

<210> 1179

<211> 314

<212> PRT

<213> Unknown (H38g96 protein)

<220>

<223> Synthetic construct

<400> 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
20     25     30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
35     40     45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
50     55     60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65     70     75     80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
85     90     95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
100    105    110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
115    120    125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
130    135    140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145    150    155    160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
165    170    175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
180    185    190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
195    200    205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
210    215    220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225    230    235    240

```

[illegible]

<210> 1180

<211> 331

<212> PRT

<213> Unknown (H38g97 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) . . . (331)

<223> Xaa = Any Amino Acid

<400> 1180

Met	Ala	Ala	Glu	Asn	Ser	Ser	Ser	Val	Thr	Glu	Phe	Ile	Leu	Ala	Gly
1				5					10					15	
Leu	Ile	His	Gln	Pro	Gly	Leu	Gln	Val	Pro	Val	Phe	Phe	Leu	Phe	Leu
			20					25					30		
Gly	Phe	Tyr	Ala	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Leu	Ile	Ile	Leu
		35					40					45			
Ile	Gly	Leu	Asn	Ser	Arg	Leu	His	Ile	Pro	Met	Tyr	Phe	Phe	Pro	Phe
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Phe	Ser	Phe	Ser	Thr	Thr	Ile	Ile	Pro	Lys
65					70					75					80
Met	Leu	Met	Ser	Phe	Val	Ser	Arg	Lys	Asn	Ile	Ile	Ser	Phe	Thr	Gly
				85					90					95	
Cys	Met	Ser	Gln	Phe	Phe	Phe	Phe	Cys	Phe	Phe	Val	Phe	Ser	Glu	Ser
			100					105					110		
Phe	Ile	Leu	Ser	Ala	Met	Val	Xaa	Asp	Arg	Tyr	Val	Gly	Ile	Cys	Asn
		115					120					125			
Pro	Leu	Leu	Tyr	Thr	Ile	Thr	Met	Ser	Pro	Gln	Val	Cys	Leu	Leu	Leu
	130					135					140				
Leu	Leu	Gly	Val	Tyr	Gly	Met	Gly	Val	Phe	Gly	Ala	Val	Ala	His	Thr
145					150					155				160	
Gly	Asn	Ile	Val	Phe	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Leu	Val	Asn	His
				165					170					175	
Tyr	Met	Cys	Asp	Ile	Leu	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Asn	Gly	Ser
			180					185					190		
Tyr	Ile	Asn	Val	Leu	Val	Ile	Phe	Ile	Val	Val	Thr	Val	Gly	Ile	Gly
		195					200					205			
Val	Pro	Ile	Val	Ala	Val	Phe	Ile	Ser	Tyr	Gly	Phe	Ile	Leu	Ser	Ser
	210					215					220				
Ile	Leu	Arg	Val	Ser	Ser	Ala	Glu	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Ser
225					230					235					240
Cys	Ser	Ser	Tyr	Ile	Ile	Ala	Val	Ser	Leu	Phe	Phe	Gly	Ser	Gly	Ala
				245					250					255	
Phe	Thr	Tyr	Leu	Lys	Pro	Pro	Ser	Ile	Leu	Pro	Leu	Asp	Gln	Gly	Lys
			260					265					270		
Val	Ser	Ser	Leu	Phe	Tyr	Thr	Thr	Val	Val	Pro	Met	Phe	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Leu	Lys	Arg	Thr

290 295 300
 Phe Ser Arg Ile Ser Phe S r Glu Lys Asn Phe Arg Asn Arg Lys Glu
 305 310 315 320
 Ile Leu Gly Phe Ph Xaa Asn Gln Ile Ala Phe
 325 330

<210> 1181
 <211> 314
 <212> PRT
 <213> Unknown (H38g98 protein)

<220>
 <223> Synthetic construct

<400> 1181
 Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu
 1 5 10 15
 Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu
 20 25 30
 Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu
 35 40 45
 Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met
 50 55 60
 Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser
 65 70 75 80
 Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met
 85 90 95
 Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly
 100 105 110
 Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
 115 120 125
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser
 130 135 140
 Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His
 145 150 155 160
 Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser
 165 170 175
 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile
 180 185 190
 Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser
 195 200 205
 Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr
 210 215 220
 Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg
 225 230 235 240
 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
 245 250 255
 Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala
 260 265 270
 Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro
 275 280 285
 Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp
 290 295 300
 Ser Phe Thr Lys Met Val Lys Arg Asn Val
 305 310

<210> 1182
 <211> 313
 <212> PRT
 <213> Unknown (H38g99 protein)

<220>

<223> Synthetic construct

<400> 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
 20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
 115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
 130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
 165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
 195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
 210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
 225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
 260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
 290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

```

<210> 1183

<211> 310

<212> PRT

<213> Unknown (H38g100 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

	20		25		30	
Val	Ile	Tyr	Leu	Ile	Thr	Ile
	35		40		45	
Ile	Trp	Lys	Asp	Pro	His	Leu
	50		55		60	
Asn	L	u	Ala	Phe	Val	Asp
	65		70		75	
Met	Leu	Asn	Asn	Phe	Leu	Ala
			85		90	
Ser	Lys	Ile	Gln	Phe	Phe	Ser
			100		105	
Phe	Leu	Leu	Ala	Thr	Met	Ala
			115		120	
Pro	Leu	Leu	Tyr	Pro	Ala	Ile
			130		135	
Leu	Gly	Gly	Leu	Leu	His	Ala
			145		150	
Leu	Thr	Phe	Cys	Asn	Ser	Asn
			165		170	
Ile	Pro	Leu	Ser	Lys	Ile	Ser
			180		185	
Met	Val	Phe	Ile	Phe	Ser	Gly
			195		200	
Gly	Leu	Ile	Ser	Tyr	Thr	Phe
			210		215	
Ser	Val	Lys	Gly	Ile	Arg	Lys
			225		230	
Leu	Ser	Val	Ser	Leu	Tyr	His
			245		250	
Ser	Ala	Ser	Pro	Gln	Ala	Asp
			260		265	
Tyr	Thr	Val	Ile	Val	Pro	Leu
			275		280	
Asn	Lys	Gln	Val	Ile	Ala	Ser
			290		295	
Ile	Xaa	Ile	Ser	Tyr	Ser	
			305		310	

<210> 1184

<211> 231

<212> PRT

<213> Unknown (H38g101 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(231)

<223> Xaa = Any Amino Acid

<400> 1184

Phe	Cys	Leu	Phe	Pro	Ala	Thr	Val	Ser	Lys	Ala	Val	Val	Lys	Phe	Leu
1			5					10					15		
Ala	Glu	Thr	Ile	Ser	Phe	Ser	Tyr	Tyr	Val	Ile	Gln	Met	Leu	Val	Phe
			20					25					30		
Leu	Phe	Phe	Val	Thr	Thr	Glu	Cys	Asn	Leu	Leu	Ala	Ser	Leu	Gly	Lys
			35					40					45		
Asp	Ile	Tyr	Met	Pro	Ile	Arg	Gln	Pro	Met	Leu	Tyr	Pro	Val	Thr	Met
			50					55					60		
Ser	Gln	Val	Cys	Cys	Ile	Gln	Leu	Val	Ala	Ser	Cys	Tyr	Gly	His	Gly
			65					70					75		80

```

Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe
      85                      90                      95
Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu
      100                    105                    110
Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe
      115                    120                    125
Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val
      130                    135                    140
Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val
      145                    150                    155                    160
Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile
      165                    170                    175
Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser
      180                    185                    190
Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val
      195                    200                    205
Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln
      210                    215                    220
Val Ile Cys Phe Leu Glu Asn
      225                    230

```

<210> 1185

<211> 216

<212> PRT

<213> Unknown (H38g102 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400> 1185

```

Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val
  1           5           10           15
Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg
  20           25           30
Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe
  35           40           45
Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu
  50           55           60
Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala
  65           70           75           80
Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile
  85           90           95
Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser
  100          105          110
Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr
  115          120          125
Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn
  130          135          140
Asn Phe Ser Asp Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val
  145          150          155          160
Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His
  165          170          175
Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys
  180          185          190
His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn
  195          200          205
Phe Leu Met Ala His Ile His Ile

```

210

215

<210> 1186
 <211> 312
 <212> PRT
 <213> Unknown (H38g103 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 1186

Phe	Met	Glu	Asn	Arg	Asn	Ile	Val	Thr	Val	Phe	Ile	Leu	Leu	Gly	Leu
1				5				10						15	
Ser	Gln	Asn	Lys	Asn	Ile	Glu	Val	Phe	Trp	Phe	Val	Leu	Phe	Val	Phe
		20						25				30			
Cys	Tyr	Ile	Ala	Ile	Trp	Met	Glu	Asn	Phe	Ile	Ile	Met	Ile	Ser	Ile
		35					40					45			
Met	Tyr	Ile	Xaa	Leu	Ile	Asp	Gln	Pro	Met	Tyr	Phe	Phe	Leu	Asn	Tyr
	50					55					60				
Leu	Ala	Leu	Ser	Asp	Leu	Cys	Tyr	Ile	Ser	Thr	Val	Ala	Pro	Lys	Leu
65					70					75				80	
Met	Ile	Asp	Leu	Leu	Thr	Glu	Arg	Lys	Ile	Val	Ser	Tyr	Asn	Asn	Cys
				85					90					95	
Met	Ile	Gln	Leu	Phe	Ile	Thr	His	Phe	Leu	Gly	Asp	Ile	Glu	Ile	Phe
		100						105					110		
Ile	Leu	Lys	Ala	Met	Ala	Tyr	Asp	His	Tyr	Ile	Ala	Ile	Cys	Lys	His
		115					120					125			
Leu	His	Tyr	Thr	Ile	Ile	Thr	Thr	Lys	Gln	Ser	Cys	Asn	Thr	Ile	Ile
	130					135					140				
Ile	Ala	Cys	Trp	Thr	Gly	Gly	Phe	Ile	His	Ser	Ala	Ser	Gln	Phe	Leu
145					150					155				160	
Leu	Thr	Ile	Phe	Leu	Pro	Phe	Cys	Gly	Leu	Asn	Glu	Ile	Asp	Gln	Tyr
			165					170					175		
Phe	Cys	Tyr	Val	Tyr	Pro	Leu	Leu	Lys	Leu	Ala	Arg	Ile	Asp	Ile	Tyr
		180						185					190		
Arg	Ile	Gly	Phe	Leu	Val	Ile	Val	Asn	Ser	Gly	Leu	Ile	Ser	Leu	Leu
	195						200					205			
Ala	Phe	Val	Ile	Leu	Met	Val	Ser	Tyr	Tyr	Leu	Ile	Leu	Ser	Thr	Ile
	210					215					220				
Arg	Val	Tyr	Ser	Ala	Glu	Ser	His	Thr	Lys	Ala	Leu	Ser	Thr	Cys	Ser
225					230					235				240	
Ser	His	Ile	Ile	Val	Val	Val	Leu	Phe	Phe	Val	Pro	Ala	Leu	Phe	Ile
			245						250				255		
Tyr	Ile	Arg	Pro	Ala	Ile	Thr	Phe	Pro	Glu	Asp	Lys	Val	Phe	Val	Leu
		260						265					270		
Phe	Cys	Ala	Ile	Ile	Ala	Pro	Met	Phe	Ser	Leu	Leu	Ile	Tyr	Met	Leu
	275						280					285			
Arg	Lys	Val	Glu	Met	Lys	Asn	Ala	Val	Arg	Lys	Met	Trp	Cys	His	Gln
	290					295					300				
Leu	Leu	Leu	Ala	Arg	Lys	Xaa	Leu								
305						310									

<210> 1187
 <211> 308
 <212> PRT
 <213> Unknown (H38g104 protein)

<220>

<223> Synthetic construct

<400> 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1          5          10          15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
          20          25          30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
          35          40          45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
          65          70          75          80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
          85          90          95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
          100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
          115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
          130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
          145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
          165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
          180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
          195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
          210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
          225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
          245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
          260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
          290          295          300
Leu Lys Arg Thr
305

```

<210> 1188

<211> 324

<212> PRT

<213> Unknown (H38g105 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

      20      25      30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
  35      40      45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Ph Leu Ser
  50      55      60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
  65      70      75      80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
  100      105      110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
  115      120      125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
  130      135      140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
  145      150      155      160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165      170      175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
  180      185      190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
  195      200      205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
  210      215      220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
  225      230      235      240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
  260      265      270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
  275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
  290      295      300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
  305      310      315      320
Lys Arg Met Leu

```

<210> 1189

<211> 291

<212> PRT

<213> Unknown (H38g106 protein)

<220>

<223> Synthetic construct

<400> 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
  1      5      10      15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
  20      25      30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
  35      40      45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
  50      55      60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
  65      70      75      80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
      85      90      95

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
 195 200 205
 Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
 210 215 220
 Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn
 290

<210> 1190

<211> 328

<212> PRT

<213> Unknown (H38g107 protein)

<220>

<223> Synthetic construct

<400> 1190

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp
 100 105 110
 Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe
 130 135 140
 Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp
 180 185 190
 Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly


```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
  210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
  305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

<210> 1191

<211> 325

<212> PRT

<213> Unknown (H38g108 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
  65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
  145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
  225              230              235              240

```

<400>	1192														
Ile	Gln	Cys	Lys	Gly	Xaa	Xaa	Lys	Xaa	Ile	Lys	Thr	Phe	Ser	Val	Thr
1				5					10					15	
Pro	Ile	Leu	Asn	Gly	Asn	Arg	Glu	Ile	Ala	Arg	Phe	Leu	Ser	Asn	Leu
			20					25					30		
Ser	Leu	Ala	Gly	Ile	Gly	Phe	Pro	Ser	Thr	Ile	Val	Ser	Lys	Met	Ile
		35					40					45			
Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu
	50					55					60				
Thr	Gln	Val	Ser	Leu	Phe	Ala	Val	Phe	Gly	Cys	Met	Glu	Asp	Met	Leu
65					70				75					80	
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Asp	Ile	Cys	His	Pro	Leu
				85					90					95	
Asp	Tyr	Pro	Val	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu
			100					105					110		
Leu	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Asn	Trp	Ile
		115					120					125			
Ala	Leu	Gln	Ile	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe
	130					135					140				
Cys	Asp	Pro	Ser	Gln	His	Pro	Thr	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr
145					150					155					160
Asn	Asp	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro
				165					170					175	
Ile	Ser	Gly	Thr	Phe	Ser	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu
			180					185					190		
Arg	Val	Ser	Ser	Ser	Ser	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly
		195					200					205			
Ser	His	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Gly	Phe	Gly	Gly
	210					215					220				
Asp	Leu	Ser	Ser	Asp	Met	Ser	Ser	Tyr	Pro	Arg	Lys	Gly	Ala	Val	Ala
225					230					235					240
Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr
				245					250					255	
Ser	Arg	Asn	Arg	Glu	Ile	Lys	Ser	Ala	Leu	Arg	Gln	Leu	His	Cys	Arg
		260						265					270		
Ile	Val	Xaa	Ser	His	Phe	Leu	Ile	Ile	Cys	Ser	Ile	Pro	Ser	Val	Val

275 280 285
 Xaa Val Arg Lys Gly Ser Lys
 290 295

<210> 1193
 <211> 320
 <212> PRT
 <213> Unknown (H38g110 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1193

Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp
 100 105 110
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu
 130 135 140
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn
 145 150 155 160
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn
 165 170 175
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser
 210 215 220
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu
 245 250 255
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala
 260 265 270
 Val Thr Ser Val Met Tyr Thr Val Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu
 290 295 300
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser
 305 310 315 320

<210> 1194
 <211> 318
 <212> PRT

<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu Phe
 20           25           30
Leu Ser Met Cys Leu Val Thr Met Leu Gly Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
 50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
 85           90           95
Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp
 100          105          110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys
 115          120          125
His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
 130          135          140
Leu Val Leu Met Ser Phe Ile Leu Ser Leu Leu Asp Ser Xaa Leu His
 145          150          155          160
Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Val
 180          185          190
Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe Leu
 195          200          205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
 210          215          220
Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
 225          230          235          240
Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 245          250          255
Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val
 260          265          270
Ala Ser Val Leu Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe Ile
 275          280          285
Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu Cys
 290          295          300
Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
 305          310          315

```

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amin Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1           5           10           15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
      20           25           30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
      35           40           45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
      50           55           60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65           70           75           80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
      85           90           95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
      100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
      115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
      130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
      165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
      180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
      195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
      210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
      245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
      260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
      275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
      290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
      325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
      340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1           5           10           15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu Leu
      20           25           30

```

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
  35          40          45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
  50          55          60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
  65          70          75          80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
          85          90          95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
          100          105          110
Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val
          115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
          130          135          140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
          145          150          155          160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
          165          170          175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
          180          185          190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
          195          200          205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
          210          215          220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
          225          230          235          240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
          245          250          255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
          260          265          270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
          275          280          285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
          290          295          300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
          305          310          315          320

```

<210> 1197

<211> 315

<212> PRT

<213> Unknown (H38g114 protein)

<220>

<223> Synthetic construct

<400> 1197

```

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
  1          5          10          15
Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
          20          25          30
Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
          35          40          45
Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
          50          55          60
Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
          65          70          75          80
Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
          85          90          95
Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

```

```

      115              120              125
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
  130              135              140
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
 145              150              155              160
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
      165              170              175
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
      180              185              190
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
      195              200              205
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
  210              215              220
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
 225              230              235              240
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
      245              250              255
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
      260              265              270
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
      275              280              285
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly
  290              295              300
Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe
305              310              315

```

<210> 1198

<211> 289

<212> PRT

<213> Unknown (H38g115 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1198

```

Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro
  1              5              10              15
Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr
      20              25              30
Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp
      35              40              45
Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp
      50              55              60
Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe
  65              70              75              80
Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met
      85              90              95
Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser
      100              105              110
Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met
      115              120              125
Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu
  130              135              140
Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met
 145              150              155              160
Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr
      165              170              175

```

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser
 180 185 190
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala
 195 200 205
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys
 210 215 220
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala
 225 230 235 240
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val
 245 250 255
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
 260 265 270
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu
 275 280 285
 Leu

<210> 1199
 <211> 174
 <212> PRT
 <213> Unknown (H38g116 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(174)
 <223> Xaa = Any Amino Acid

<400> 1199
 Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly
 1 5 10 15
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe
 20 25 30
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys
 35 40 45
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Phe
 50 55 60
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr
 65 70 75 80
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala
 85 90 95
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr
 100 105 110
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys
 115 120 125
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile
 130 135 140
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val
 145 150 155 160
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg
 165 170

<210> 1200
 <211> 318
 <212> PRT
 <213> Unknown (H38g117 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
1      5      10      15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
20      25      30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
35      40      45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
50      55      60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
65      70      75      80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
85      90      95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
100     105     110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
115     120     125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
130     135     140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
145     150     155     160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
165     170     175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
180     185     190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
195     200     205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
210     215     220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
225     230     235     240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
245     250     255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
260     265     270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
275     280     285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
290     295     300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
305     310     315

```

<210> 1201

<211> 315

<212> PRT

<213> Unknown (H38g118 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
1      5      10      15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala
 20 25 30
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile
 35 40 45
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe
 50 55 60
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr
 65 70 75 80
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu
 85 90 95
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr
 100 105 110
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile
 115 120 125
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile
 130 135 140
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile
 145 150 155 160
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile
 165 170 175
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr
 180 185 190
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile
 195 200 205
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu
 210 215 220
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu
 245 250 255
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln
 260 265 270
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn
 275 280 285
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr
 290 295 300
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr
 305 310 315

<210> 1202

<211> 313

<212> PRT

<213> Unknown (H38g119 protein)

<220>

<223> Synthetic construct

<400> 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser
 85 90 95
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
305      310

```

<210> 1203

<211> 314

<212> PRT

<213> Unknown (H38g120 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
65      70      75      80
Met Leu Ile Asn Phe Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
145      150      155      160

```

```
<210> 1205
<211> 308
<212> PRT
<213> Unknown (H38g122 protein)
```

<220>

<223> Synthetic construct

<400> 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
1      5      10      15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
20      25      30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
35      40      45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
50      55      60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
65      70      75      80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
85      90      95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
100     105     110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
115     120     125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
130     135     140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
145     150     155     160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
165     170     175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
180     185     190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
195     200     205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
210     215     220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
225     230     235     240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
245     250     255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
260     265     270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
275     280     285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
290     295     300
Phe Phe Asn Lys
305

```

<210> 1206

<211> 309

<212> PRT

<213> Unknown (H38g123 protein)

<220>

<223> Synthetic construct

<400> 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
1      5      10      15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
20      25      30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Il Val Leu
35      40      45

```

```

      100      105      110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
115      120      125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
130      135      140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
145      150      155      160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
165      170      175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
180      185      190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
195      200      205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
210      215      220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
225      230      235      240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
245      250      255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
260      265      270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
275      280      285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
290      295      300
Ser Ser Val Lys
305

```

<210> 1208

<211> 321

<212> PRT

<213> Unknown (H38g125 protein)

<220>

<223> Synthetic construct

<400> 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
180      185      190

```

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu
  195                200                205
Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys
  210                215                220
Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser
  225                230                235                240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
  245                250                255
Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr
  260                265                270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
  275                280                285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val
  290                295                300
Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu
  305                310                315                320
Ile

```

<210> 1209

<211> 298

<212> PRT

<213> Unknown (H38g126 protein)

<220>

<223> Synthetic construct

<400> 1209

```

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro
  1          5          10          15
Glu Thr Glu Gly Leu Glu Thr Ala Leu Leu Phe Leu Phe Ser Ser Phe
  20          25          30
Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile
  35          40          45
Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu
  50          55          60
Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu
  65          70          75          80
Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val
  85          90          95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
  100         105         110
Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu
  115         120         125
Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr
  130         135         140
Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu
  145         150         155         160
Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe
  165         170         175
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu
  180         185         190
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys
  195         200         205
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile
  210         215         220
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser
  225         230         235
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pr
  245         250
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser

```

260 265 270
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275 230 285
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro
 290 295

<210> 1210
 <211> 324
 <212> PRT
 <213> Unknown (H38g127 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1210
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
 20 25 30
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
 35 40 45
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly
 50 55 60
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
 85 90 95
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys
 100 105 110
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu
 130 135 140
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
 145 150 155 160
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
 165 170 175
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
 180 185 190
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val
 195 200 205
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu Ile
 210 215 220
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr
 225 230 235 240
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val
 245 250 255
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
 260 265 270
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
 290 295 300
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr
 305 310 315 320
 Lys Ile Phe Pro

<210> 1211
 <211> 308
 <212> PRT
 <213> Unknown (H38g128 protein)

<220>
 <223> Synthetic construct

<400> 1211
 Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe
 1 5 10 15
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe
 20 25 30
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile
 35 40 45
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn
 50 55 60
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala
 65 70 75 80
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys
 85 90 95
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu
 100 105 110
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala
 130 135 140
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly
 145 150 155 160
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe
 165 170 175
 Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val
 195 200 205
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile
 210 215 220
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr
 245 250 255
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu
 260 265 270
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe
 290 295 300
 Pro Phe Phe Arg
 305

<210> 1212
 <211> 319
 <212> PRT
 <213> Unknown (H38g129 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
 20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
 35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
 50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
 65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
 85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145          150          155          160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
180          185          190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
195          200          205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
210          215          220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
245          250          255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
260          265          270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
290          295          300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305          310          315

```

<210> 1213

<211> 311

<212> PRT

<213> Unknown (H38g130 protein)

<220>

<223> Synthetic construct

<400> 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
 20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
 35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
 50          55          60

```

```

Asn L u Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
65          70          75          80
Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu
      85          90          95
Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
      100          105          110
Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115          120          125
Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
      130          135          140
Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
145          150          155          160
Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His
      165          170          175
Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
      180          185          190
Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
      195          200          205
Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
210          215          220
Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe
      245          250          255
Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile
      260          265          270
Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile
290          295          300
Leu Leu Lys Ile Lys Ser Gln
305          310

```

<210> 1214

<211> 328

<212> PRT

<213> Unknown (H38g131 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1214

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
1          5          10          15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
      20          25          30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
      35          40          45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
      50          55          60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
      85          90          95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
      100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```

```
<210> 1215
<211> 328
<212> PRT
<213> Unknown (H38a132 protein)
```

```
<220>
<223> Synthetic construct
<221> VARIANT
<222> (1)...(328)
<223> Xaa = Any Amino Acid
```

548

```

Val Ile Arg Pro Gln Pro Leu Cys Gly Pro Asn Ile Leu Asp Asn Phe
      165                      170                      175
Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr Ser
      180                      185                      190
Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile Ile
      195                      200                      205
Trp Phe Leu Leu Ser Leu Met Ser Tyr Thr Val Ile Leu Val Met Leu
      210                      215                      220
Arg Ser His Ser Gly Lys Ala Arg Ser Lys Ala Ala Ser Thr Cys Thr
      225                      230                      235                      240
Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr Ile
      245                      250                      255
Tyr Thr Trp Pro Phe Thr Pro Phe Ile Met Asp Lys Ala Val Ser Ile
      260                      265                      270
Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr Leu
      275                      280                      285
Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys Leu
      290                      295                      300
Val Ile Cys Arg Glu Leu Thr Leu Ser Lys Leu Thr Leu Asn Asp Lys
      305                      310                      315                      320
Leu Leu Trp Ile Cys Tyr Phe Pro
      325

```

<210> 1216
 <211> 129
 <212> PRT
 <213> Unknown (H38g133 protein)

<220>
 <223> Synthetic construct

```

<400> 1216
Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1      5      10      15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
      20      25      30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
      35      40      45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
      50      55      60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
      65      70      75      80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
      85      90      95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100     105     110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115     120     125
Pro

```

<210> 1217
 <211> 335
 <212> PRT
 <213> Unknown (H38g134 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(335)

<223> Xaa = Any Amin Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
          20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35           40           45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
          65           70           75           80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
          85           90           95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
          145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
          165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala
          225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
          290          295          300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
          305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
          325          330          335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38g135 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1           5           10           15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
 20 25 30
 Tyr Met Ile Thr Leu Ser Gly Asn L u Leu Leu Val Val Thr Ile Thr
 35 40 45
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
 65 70 75 80
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
 100 105 110
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
 130 135 140
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
 145 150 155 160
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
 180 185 190
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
 210 215 220
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
 225 230 235 240
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
 245 250 255
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
 260 265 270
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
 290 295 300
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
 305 310 315

<210> 1219

<211> 312

<212> PRT

<213> Unknown (H38gl36 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu
 20 25 30
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys
 35 40 45
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala
 50 55 60
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

```

65          70          75          80
Gly Phe Leu Arg Arg Gly Thr Ala Leu Pro Val Thr Ser Cys Glu Ala
      85          90          95
Gln L u Cys Ser Val Val Met Phe Gly Thr Ser Glu Cys Phe Leu Leu
      100         105         110
Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Val
      115         120         125
Asn Ser Thr His Leu Ser Pro Ile Ile Cys Ile Leu Leu Val Gly Val
      130         135         140
Cys Tyr Leu Gly Gly Trp Val Asn Ala Ser Thr Phe Thr Ser Cys Leu
145         150         155         160
Leu Ser Leu Ser Phe Cys Gly Pro Asn Gln Ile Asp His Phe Phe Cys
      165         170         175
Asp Phe Ser Pro Leu Leu Lys Leu Ser Cys Ser Asn Ile Ser Ile Pro
      180         185         190
Glu Ile Ile Pro Ser Ile Ser Ser Gly Ser Ile Ile Val Val Thr Val
      195         200         205
Phe Ala Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys
      210         215         220
Met Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys Thr Ser
225         230         235         240
His Leu Ala Ala Val Thr Leu Tyr Tyr Gly Thr Ile Thr Phe Ile Tyr
      245         250         255
Val Met Pro Lys Ser Ser Tyr Ser Thr Ser Gln Asn Arg Leu Ile Ser
      260         265         270
Leu Ser Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Phe Ile Tyr Ser
      275         280         285
Leu Arg Asn Arg Asp Val Lys Glu Ala Leu Arg Lys Ala Thr Val Arg
      290         295         300
Ile Tyr Ser Xaa Asp Gln Phe Val
305         310

```

<210> 1220

<211> 324

<212> PRT

<213> Unknown (H38g137 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1220

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Pro Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
      50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65      70      75      80
Val Ser Lys Thr Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100     105     110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115     120     125

```



```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130                135                140
Val Ph  Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                150                155                160
L u His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
                165                170                175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                180                185                190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
                195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
210                215                220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
                245                250                255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
                260                265                270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
275                280                285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290                295                300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305                310                315                320
Phe Phe Trp Cys

```

<210> 1221

<211> 318

<212> PRT

<213> Unknown (H38g138 protein)

<220>

<223> Synthetic construct

<400> 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1                5                10                15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
                20                25                30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
35                40                45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
50                55                60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu
65                70                75                80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
                85                90                95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
100                105                110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
115                120                125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
130                135                140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145                150                155                160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
                165                170                175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
180                185                190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

195	200	205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser		
210	215	220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala		
225	230	235
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu		240
245	250	255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg		
260	265	270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His		
275	280	285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys		
290	295	300
Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg		
305	310	315

<210> 1222

<211> 236

<212> PRT

<213> Unknown (H38g139 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(236)

<223> Xaa = Any Amino Acid

<400> 1222

Pro Lys Val Pro Asp Phe Phe Val Phe Gly Leu Arg Ala Ile Ser Phe	
1	5
Pro Ala Gly Phe Leu Gln Lys Tyr Ile Lys Asn Cys Phe Gln Ala Met	
20	25
Glu Phe Trp Pro Phe Lys Val Arg Ala Met Asp Arg Xaa Gly Thr Leu	
35	40
Cys His Pro Leu Lys Tyr Pro Ser Ile Ile Thr Asp Pro Phe Gly Val	
50	55
Lys Ala Ala Arg Phe Ile Leu Pro Arg Asn Val Leu Met Thr Leu Pro	
65	70
Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn Val Ile	
85	90
Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser Cys Asp	
100	105
Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp Thr Leu	
115	120
Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile Leu	
130	135
Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys Ala Leu	
145	150
Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser Thr Ile	
165	170
Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val Ser Pro	
180	185
Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro Ala Ala	
195	200
Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys Gln Gly	
210	215
Met Gln Arg Leu Leu Lys Lys Gly Cys Xaa Gln Gly	
225	230
	235

<210> 1223

<211> 308
 <212> PRT
 <213> Unknown (H38g140 protein)

<220>
 <223> Synthetic construct

<400> 1223
 Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile
 1 5 10 15
 Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met
 20 25 30
 Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Ile Leu Ile Arg Ile Ser
 35 40 45
 Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe
 50 55 60
 Ala Asp Met Ala Tyr Ser Ser Ser Val Thr Pro Asn Met Leu Val Asn
 65 70 75 80
 Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln
 85 90 95
 Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala
 100 105 110
 Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr
 115 120 125
 Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Leu Val Val
 130 135 140
 Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr
 145 150 155 160
 Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp
 165 170 175
 Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr
 180 185 190
 Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys
 195 200 205
 Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met
 210 215 220
 Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His
 225 230 235 240
 Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val
 245 250 255
 Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val
 260 265 270
 Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275 280 285
 Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys
 290 295 300
 Ile Leu Ser His
 305

<210> 1224
 <211> 335
 <212> PRT
 <213> Unknown (H38g141 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(335)
 <223> Xaa = Any Amino Acid

<400> 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
 35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
 85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
115          120          125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
130          135          140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
165          170          175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
180          185          190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
195          200          205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
245          250          255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
290          295          300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
325          330          335

```

<210> 1225

<211> 311

<212> PRT

<213> Unknown (H38g142 protein)

<220>

<223> Synthetic construct

<400> 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
 1          5          10          15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
 20          25          30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
 35          40          45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
 50          55          60

```

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val
65          70          75          80
Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly
      85          90          95
Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys
      100         105         110
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
      115         120         125
Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu
      130         135         140
Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile
145         150         155         160
Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His
      165         170         175
Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp
      180         185         190
Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val
      195         200         205
Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr
      210         215         220
Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr
225         230         235         240
Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr
      245         250         255
Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys
      260         265         270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275         280         285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu
      290         295         300
Leu Arg Ile Lys Ile Phe Ser
305          310

```

<210> 1226

<211> 314

<212> PRT

<213> Unknown (H38g143 protein)

<220>

<223> Synthetic construct

<400> 1226

```

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu
1          5          10          15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
      20          25          30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
      35          40          45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
      50          55          60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr
      65          70          75          80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly
      85          90          95
Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser
      100         105         110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
      115         120         125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
      130         135         140
Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile

```

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

<210> 1227

<211> 315

<212> PRT

<213> Unknown (H38g144 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
 1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ser Ile Gly Pro Lys
          65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Tyr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser
 210 215 220
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr
 225 230 235 240
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe
 245 250 255
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn
 260 265 270
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys
 290 295 300
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser
 305 310 315

<210> 1228

<211> 202

<212> PRT

<213> Unknown (H38g145 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
 1 5 10 15
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
 20 25 30
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
 35 40 45
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
 50 55 60
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr
 65 70 75 80
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
 85 90 95
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
 100 105 110
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
 130 135 140
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
 145 150 155 160
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Gly Thr Met Phe
 165 170 175
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp
 180 185 190
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys
 195 200

<210> 1229

<211> 203

<212> PRT

<213> Unknown (H38g146 protein)

<220>

<223> Synthetic construct

<400> 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
      20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
      35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
      50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
      65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
      85          90          95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
      100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
      130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
      145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
      165          170          175          180
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
      180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
      195          200

```

<210> 1230

<211> 304

<212> PRT

<213> Unknown (H38g147 protein)

<220>

<223> Synthetic construct

<400> 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1          5          10          15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
      20          25          30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
      35          40          45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
      50          55          60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
      65          70          75          80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
      85          90          95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
      100          105          110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
      115          120          125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
      130          135          140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
      145          150          155          160
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
      165          170          175

```



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Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180      185      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210      215      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260      265      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275      280      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290      295      300

```

<210> 1231
 <211> 110
 <212> PRT
 <213> Unknown (H38g148 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(110)
 <223> Xaa = Any Amino Acid

```

<400> 1231
Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20      25      30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35      40      45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50      55      60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85      90      95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100      105      110

```

<210> 1232
 <211> 327
 <212> PRT
 <213> Unknown (H38g149 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(327)
 <223> Xaa = Any Amino Acid

```

<400> 1232
Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1      5      10      15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```

<400> 1233
Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
 1          5          10          15
Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
          20          25          30
Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
          35          40          45
Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
          50          55          60

```

Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
 65 70 75 80
 His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
 85 90 95
 Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
 100 105 110
 Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
 115 120 125
 Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
 130 135 140
 Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
 145 150 155 160
 His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
 165 170 175
 Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
 180 185 190
 Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
 195 200 205
 Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
 210 215 220
 Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
 225 230 235 240
 Pro

<210> 1234

<211> 313

<212> PRT

<213> Unknown (H38g151 protein)

<220>

<223> Synthetic construct

<400> 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu
 1 5 10 15
 Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu
 20 25 30
 Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu
 35 40 45
 Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr
 50 55 60
 Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
 65 70 75 80
 Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser
 85 90 95
 Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr
 100 105 110
 Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val
 130 135 140
 Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu
 145 150 155 160
 Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile
 165 170 175
 Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys
 180 185 190
 Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr
 195 200 205
 Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile

```

      210              215              220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245              250              255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260              265              270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275              280              285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290              295              300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305              310

```

<210> 1235
 <211> 135
 <212> PRT
 <213> Unknown (H38g152 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(135)
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1              5              10              15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20              25              30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35              40              45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50              55              60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
65              70              75              80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85              90              95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100              105              110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115              120              125
Arg Arg Leu Xaa Lys Ile Lys
      130              135

```

<210> 1236
 <211> 319
 <212> PRT
 <213> Unknown (H38g153 protein)

<220>
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1              5              10              15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20              25              30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser M t Val Ala
      35              40              45

```

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50          55          60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65          70          75          80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
          85          90          95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
100        105        110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
115        120        125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
130        135        140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
145        150        155        160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
165        170        175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
180        185        190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
195        200        205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
210        215        220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
225        230        235        240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
245        250        255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
260        265        270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
275        280        285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
290        295        300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
305        310        315

```

<210> 1237

<211> 325

<212> PRT

<213> Unknown (H38g154 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1237

```

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
20          25          30
Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
35          40          45
Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
50          55          60
Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
65          70          75          80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
85          90          95
Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Il
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

```

<210> 1238
 <211> 319
 <212> PRT
 <213> Unknown (H38g155 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

```

<400> 1238
Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser
 180 185 190
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr
 195 200 205
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr
 245 250 255
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met
 260 265 270
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu
 275 280 285
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val
 290 295 300
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu
 305 310 315

<210> 1239

<211> 313

<212> PRT

<213> Unknown (H38g156 protein)

<220>

<223> Synthetic construct

<400> 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser
 85 90 95
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu
 100 105 110
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
 115 120 125
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
 130 135 140
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
 145 150 155 160
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
 180 185 190
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
 195 200 205
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
 210 215 220
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

```

225          230          235          240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
          245          250          255
Ile Asn Leu Ala Val Val His Arg Phe Ala Arg His Val Ser Pro Leu
          260          265          270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Thr
          275          280          285
Asn Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
          290          295          300
Val Ala Lys Leu Cys Gln Arg Lys Ile
305          310

```

<210> 1240
 <211> 308
 <212> PRT
 <213> Unknown (H38g157 protein)

<220>
 <223> Synthetic construct

```

<400> 1240
Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu Ser
          50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu Leu
          100          105          110
Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu His
          115          120          125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
          130          135          140
Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe Ile
145          150          155          160
Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met Trp
          165          170          175
Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr Leu
          180          185          190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
          195          200          205
Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg Thr
          210          215          220
His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser His
225          230          235          240
Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
          245          250          255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
          260          265          270
Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
          290          295          300
Ser Ser Val Lys
305

```


<210> 1241
 <211> 321
 <212> PRT
 <213> Unknown (H38g158 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1241
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe
 1 5 10 15
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu
 20 25 30
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile
 35 40 45
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr
 50 55 60
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser
 65 70 75 80
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn
 85 90 95
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly
 100 105 110
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu
 130 135 140
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu
 145 150 155 160
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile
 165 170 175
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys
 180 185 190
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe
 195 200 205
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu
 210 215 220
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro
 245 250 255
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His
 260 265 270
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser
 275 280 285
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg
 290 295 300
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu
 305 310 315 320
 Leu

<210> 1242
 <211> 162
 <212> PRT
 <213> Unknown (H38g159 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(162)

<223> Xaa = Any Amino Acid

<400> 1242

Gly	Thr	Val	Xaa	Ile	Leu	Ser	Pro	Val	Xaa	Leu	Pro	Phe	Tyr	Asp	Pro
1				5					10					15	
Asn	Val	Ile	Ala	His	Phe	Met	Cys	Asp	Leu	Asn	Thr	Leu	Leu	Lys	Leu
			20					25					30		
Leu	Cys	Met	Gly	Thr	Thr	Asn	Thr	Leu	Gly	Phe	Phe	Val	Ala	Ala	Asn
		35					40					45			
Gly	Gly	Phe	Asn	Tyr	Leu	Leu	Asn	Ile	Ile	Phe	Leu	Met	Val	Ser	Xaa
	50					55					60				
Val	Ala	Ile	Leu	Cys	Thr	Leu	Lys	Thr	His	Ser	Leu	Glu	Glu	Arg	Cys
65					70					75				80	
Lys	Ala	Leu	Ser	Thr	Cys	Ile	Ser	His	Thr	Thr	Val	Val	Ile	Leu	Phe
				85					90					95	
Phe	Gly	Phe	Cys	Ile	Ser	Val	Tyr	Leu	Cys	Pro	Val	Thr	Leu	Leu	Pro
			100					105					110		
Ile	Asn	Lys	Ala	Val	Ala	Val	Phe	Tyr	Thr	Met	Ile	Asn	Pro	Met	Leu
	115						120					125			
Lys	Pro	Leu	Val	Tyr	Thr	Leu	Arg	Asn	Ala	Glu	Val	Lys	Ser	Ala	Leu
	130					135					140				
Arg	Lys	Leu	Trp	Val	Lys	Arg	Xaa	Thr	Glu	Glu	Arg	Asn	Asn	Pro	Asn
145					150					155					160
Ile	Arg														

<210> 1243

<211> 311

<212> PRT

<213> Unknown (H38g160 protein)

<220>

<223> Synthetic construct

<400> 1243

Met	Phe	Tyr	His	Asn	Lys	Ser	Ile	Phe	His	Pro	Val	Thr	Phe	Phe	Leu
1				5					10					15	
Ile	Gly	Ile	Pro	Gly	Leu	Glu	Asp	Phe	His	Met	Trp	Ile	Ser	Gly	Pro
			20					25					30		
Phe	Cys	Ser	Val	Tyr	Leu	Val	Ala	Leu	Leu	Gly	Asn	Ala	Thr	Ile	Leu
	35						40					45			
Leu	Val	Ile	Lys	Val	Glu	Gln	Thr	Leu	Arg	Glu	Pro	Met	Phe	Tyr	Phe
	50					55					60				
Leu	Ala	Ile	Leu	Ser	Thr	Ile	Asp	Leu	Ala	Leu	Ser	Ala	Thr	Ser	Val
65					70					75				80	
Pro	Arg	Met	Leu	Gly	Ile	Phe	Trp	Phe	Asp	Ala	His	Glu	Ile	Asn	Tyr
				85					90					95	
Gly	Ala	Cys	Val	Ala	Gln	Met	Phe	Leu	Ile	His	Ala	Phe	Thr	Gly	Met
			100					105					110		
Glu	Ala	Glu	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
	115					120					125				
Cys	Ala	Pro	Leu	His	Tyr	Ala	Thr	Ile	Leu	Thr	Ser	Leu	Val	Leu	Val
	130					135					140				
Gly	Ile	Ser	Met	Cys	Ile	Val	Ile	Arg	Pro	Val	Leu	Leu	Thr	Leu	Pro
145					150					155					160

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Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile
      165                      170                      175
Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly
      180                      185                      190
Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe
      195                      200                      205
Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg
      210                      215                      220
Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser
      225                      230                      235                      240
Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser
      245                      250                      255
Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr
      260                      265                      270
Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu
      275                      280                      285
Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
      290                      295                      300
Leu Tyr Val Phe Thr Lys Lys
      305                      310

```

<210> 1244

<211> 315

<212> PRT

<213> Unknown (H38g161 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1244

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Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
  1                      5                      10                      15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
      20                      25                      30
Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr
      35                      40                      45
Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu
      50                      55                      60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
      65                      70                      75                      80
Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met
      85                      90                      95
Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu
      100                      105                      110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115                      120                      125
His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly
      130                      135                      140
Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
      145                      150                      155                      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
      165                      170                      175
Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met
      180                      185                      190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195                      200                      205
Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

```

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      210              215              220
Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser
225              230              235              240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
      245              250              255
Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe
      260              265              270
Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275              280              285
Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp
      290              295              300
Ile Ser Gly Asn Lys Xaa Met Xaa Leu Glu Leu
305              310              315

```

<210> 1245
 <211> 322
 <212> PRT
 <213> Unknown (H38g162 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(322)
 <223> Xaa = Any Amino Acid

```

<400> 1245
Ser Asn Thr Gly Met Ser Ile Leu Asn Thr Ser Glu Met Glu Ile Ser
 1              5              10              15
Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp
      20              25              30
Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn
      35              40              45
Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro
      50              55              60
Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser
      65              70              75              80
Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro
      85              90              95
Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly
      100              105              110
Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg
      115              120              125
Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser
      130              135              140
Ala Arg Val Ile Gln Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu
      145              150              155              160
Leu Ile Leu Pro Phe Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys
      165              170              175
Lys Asn Leu Leu Ser Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys
      180              185              190
Leu Ala Cys Thr Asp Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val
      195              200              205
Ala Leu Thr Gly Ile Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met
      210              215              220
Leu Ile Leu Lys Ala Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu
      225              230              235              240
Lys Val Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe
      245              250              255
Tyr Val Pro Ile Ile Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His
      260              265              270

```

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val
 275 280 285
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile
 290 295 300
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly
 305 310 315 320
 Cys Leu

<210> 1246

<211> 319

<212> PRT

<213> Unknown (H38g163 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu
 20 25 30
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile
 35 40 45
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys
 100 105 110
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys
 130 135 140
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Asp Ser Xaa Leu
 145 150 155 160
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

<210> 1247

<211> 320

<212> PRT

<213> Unknown (H38g164 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1247

Met	Arg	Leu	Ile	Xaa	Asp	Glu	Glu	Met	Ser	Arg	Arg	Asn	Tyr	Thr	Glu
1				5					10					15	
Leu	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Thr	Ser	Arg	Pro	Glu	Leu	Arg
		20						25					30		
Val	Ala	Phe	Leu	Ala	Leu	Phe	Leu	Phe	Val	Tyr	Ile	Ala	Thr	Val	Val
		35					40					45			
Gly	Asn	Leu	Gly	Met	Ile	Ile	Leu	Ile	Lys	Val	Asp	Ser	Arg	Leu	His
	50					55					60				
Thr	Pro	Met	Xaa	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Asp	Leu	Cys
65					70					75				80	
Phe	Ser	Thr	Asn	Phe	Thr	Pro	Lys	Met	Leu	Glu	Asn	Phe	Leu	Ser	Glu
			85						90					95	
Lys	Lys	Thr	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Met	Gln	Cys	Tyr	Val	Val
		100						105					110		
Ile	Ala	Val	Val	Leu	Ala	Glu	His	Cys	Met	Leu	Ala	Val	Met	Ala	Tyr
		115					120					125			
Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Ser	Ser	Lys	Met
	130					135					140				
Ser	Gln	Gly	Val	Cys	Val	His	Leu	Val	Ile	Val	Pro	Tyr	Val	Tyr	Gly
145					150					155					160
Phe	Leu	Leu	Ser	Val	Met	Glu	Thr	Leu	Arg	Thr	Tyr	Asn	Leu	Ser	Phe
			165						170					175	
Cys	Gly	Thr	Asn	Glu	Ile	Asn	His	Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu
		180						185				190			
Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	Ser	Lys	Glu	Leu	Ser	Met	Tyr
	195						200					205			
Ile	Val	Ala	Gly	Tyr	Ser	Asn	Val	Gln	Ser	Leu	Leu	Ile	Ile	Leu	Thr
	210					215					220				
Ser	Tyr	Met	Phe	Ile	Leu	Val	Ala	Ile	Leu	Arg	Ser	His	Ser	Ala	Glu
225					230					235					240
Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val
			245						250					255	
Thr	Ile	Phe	Tyr	Gly	Thr	Leu	Phe	Cys	Met	His	Leu	Arg	Arg	Pro	Thr
		260						265					270		
Asp	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met	Val	Ala	Val	Phe	Tyr	Thr	Thr
		275					280					285			
Val	Ile	Leu	Met	Leu	Asn	Ser	Met	Ile	Tyr	Gly	Leu	Arg	Asn	Lys	Asp
	290					295					300				
Val	Lys	Glu	Ala	Leu	Lys	Lys	Ala	Ile	Gly	Lys	Gln	Thr	Leu	Gly	Lys
305					310					315					320

<210> 1248

<211> 316

<212> PRT

<213> Unknown (H38g165 protein)

<220>

<223> Synthetic construct

<400> 1248

Arg Arg Met Gly Asn His Thr Ala Val S r Leu Phe Leu Leu Trp Gly
 1 5 10 15
 Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
 20 25 30
 Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
 35 40 45
 Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Ile Pro Arg
 65 70 75 80
 Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
 100 105 110
 Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
 115 120 125
 Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
 130 135 140
 Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
 145 150 155 160
 Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
 165 170 175
 Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
 180 185 190
 Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
 195 200 205
 Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
 210 215 220
 Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
 245 250 255
 Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
 260 265 270
 Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
 275 280 285
 Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
 290 295 300
 Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
 305 310 315

<210> 1249

<211> 319

<212> PRT

<213> Unknown (H38g166 protein)

<220>

<223> Synthetic construct

<400> 1249

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
 1 5 10 15
 Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

50	55	60
Leu Cys Met Leu Ala Val Val Asp Leu Val Val Cys Ser Thr Ala Val		
65	70	75
Pro Lys Leu Leu Ser Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe		
85	90	95
Glu Thr Cys Leu Thr Gln Met Phe Leu Ile His Ser Cys Ser Thr Met		
100	105	110
Glu Ser Gly Phe Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile		
115	120	125
Cys Asn Pro Leu Arg His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly		
130	135	140
Arg Val Gly Leu Ala Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro		
145	150	155
His Ser Phe Leu Leu Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile		
165	170	175
Ser His Thr Tyr Cys Glu Phe Met Ala Leu Ile Arg Ile Ala Cys Ala		
180	185	190
Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile Val Ala Phe Leu Thr		
195	200	205
Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser Tyr Val Leu Ile Leu		
210	215	220
His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala Arg Leu Lys Ser Leu		
225	230	235
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Val Ser Tyr Thr Pro		
245	250	255
Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Ala Pro		
260	265	270
His Phe His Ile Phe Val Ala Asn Ile Tyr Leu Leu Val Pro Pro Met		
275	280	285
Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Arg Ile Trp Asp Arg		
290	295	300
Phe Leu Lys Val Phe Ser Phe Ser Lys Pro Leu Ser Lys Ser Phe		
305	310	315

<210> 1250

<211> 307

<212> PRT

<213> Unknown (H38g167 protein)

<220>

<223> Synthetic construct

<400> 1250

Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr		
1	5	10
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val		
20	25	30
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys		
35	40	45
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu		
50	55	60
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu		
65	70	75
Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu		
85	90	95
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile		
100	105	110
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu		
115	120	125
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr		
130	135	140

Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
 180 185 190
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
 210 215 220
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser
 290 295 300
 Arg Ser Cys
 305

<210> 1251

<211> 322

<212> PRT

<213> Unknown (H38g168 protein)

<220>

<223> Synthetic construct

<400> 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe
 1 5 10 15
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe
 20 25 30
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu
 35 40 45
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr
 50 55 60
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val
 85 90 95
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu
 100 105 110
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg
 130 135 140
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His
 145 150 155 160
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro
 165 170 175
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu
 180 185 190
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile
 195 200 205
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile
 210 215 220
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

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225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

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```

<210> 1252
<211> 322
<212> PRT
<213> Unknown (H38g169 protein)

```

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<220>
<223> Synthetic construct

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<221> VARIANT
<222> (1)...(322)
<223> Xaa = Any Amino Acid

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```

<400> 1252
Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
 65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
 130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
 145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
 210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
 225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys
          260          265          270

```

Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val
 290 295 300
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Ph
 305 310 315 320
 Val Phe

<210> 1253

<211> 311

<212> PRT

<213> Unknown (H38g170 protein)

<220>

<223> Synthetic construct

<400> 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1 5 10 15
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val
 20 25 30
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35 40 45
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50 55 60
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65 70 75 80
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
 85 90 95
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
 100 105 110
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
 115 120 125
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
 130 135 140
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
 145 150 155 160
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
 165 170 175
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
 180 185 190
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly
 195 200 205
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
 210 215 220
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys
 225 230 235 240
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val
 245 250 255
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala
 260 265 270
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
 290 295 300
 Val Ala His Pro Gln Arg Lys
 305 310

<210> 1254

<211> 320

<212> PRT
 <213> Unknown (H38g171 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1254

Gly	Val	Gly	Leu	Xaa	Lys	Leu	Xaa	Trp	Gln	Ile	Ile	Phe	Ser	Gly	Asp	1	5	10	15
Ser	Phe	Ser	Thr	Trp	Glu	Met	Phe	Ser	Leu	Ser	Ile	Leu	Gln	Leu	Pro	20	25	30	
Xaa	Met	Tyr	Thr	Val	Ala	Leu	Ser	Gly	Thr	Ser	Ile	Leu	Ile	Phe	Leu	35	40	45	
Ile	Xaa	Thr	Asp	Phe	Xaa	Val	His	Thr	Ser	Leu	Tyr	Ser	Phe	Xaa	Val	50	55	60	
Leu	Ile	Asp	Ile	Ala	Ile	Ser	Val	Val	Lys	Ile	Gly	Ile	Glu	Val	Phe	65	70	75	80
Ser	Gly	Lys	Ile	Asn	Phe	Ser	His	Thr	Gly	Cys	Gly	Thr	Gln	Ile	Phe	85	90	95	
Phe	Phe	Leu	Thr	Ala	Gly	Ile	Phe	Lys	Tyr	Val	Leu	Leu	Thr	Tyr	Met	100	105	110	
Ala	Tyr	Asp	His	Asn	Val	Ala	Ile	Cys	Asp	Leu	Arg	Xaa	Pro	Thr	Phe	115	120	125	
Met	Ser	Asp	Gln	Val	Phe	Xaa	Gln	Trp	Ala	Val	Glu	Ser	Trp	Ile	Gly	130	135	140	
Gly	Lys	Leu	Ser	Ser	Leu	Ala	His	Thr	Ile	Tyr	Ile	Phe	His	Leu	Phe	145	150	155	160
Ser	Tyr	Lys	Ala	Lys	Glu	Ile	Ser	His	Leu	Trp	Pro	Lys	Leu	Phe	Xaa	165	170	175	
Ser	Ser	Ser	Val	Gly	Ile	Pro	Tyr	Ile	Gln	Asn	Asp	Val	Phe	Phe	Thr	180	185	190	
Ile	Ile	Thr	Phe	Leu	Phe	Thr	Leu	Leu	Pro	Leu	Thr	Leu	Thr	Leu	Ser	195	200	205	
Ser	Lys	Leu	Ile	Val	Phe	Thr	Ile	Leu	His	Met	Asn	Ser	Ser	Asn	Gly	210	215	220	
Gly	Ala	Lys	Ser	Trp	His	Thr	Tyr	Cys	Phe	His	Leu	Ser	Val	Leu	Ile	225	230	235	240
Pro	Cys	Cys	Gly	Gln	Ala	Ile	Phe	Val	Tyr	Met	Thr	Ser	Ser	Ser	Phe	245	250	255	
Xaa	Thr	Val	Asn	Lys	Tyr	Gln	Thr	Met	Ser	Val	Leu	Thr	Ala	Xaa	Leu	260	265	270	
Tyr	Pro	Leu	Lys	Pro	Leu	Ile	Asp	Ile	Leu	Lys	Asn	Ala	Glu	Val		275	280	285	
Ala	Gly	Ala	Trp	Ser	Lys	Phe	Leu	Xaa	Lys	Lys	Ala	Leu	Lys	Ser	Gln	290	295	300	
His	Leu	Ile	Thr	Arg	Ser	Cys	Glu	Asn	Lys	Xaa	Thr	Thr	Glu	Gln	Ser	305	310	315	320

<210> 1255
 <211> 320
 <212> PRT
 <213> Unknown (H38g172 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1           5           10           15
Glu Phe Ile Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
      20           25           30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
      35           40           45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
 50           55           60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
65           70           75           80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85           90           95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100          105          110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115          120          125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130          135          140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
145           150           155           160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165          170          175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180          185          190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195          200          205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210          215          220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
225           230           235           240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245          250          255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260          265          270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275          280          285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290          295          300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
305           310           315           320

```

<210> 1256

<211> 235

<212> PRT

<213> Unknown (H38g173 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1           5           10           15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

```
<210> 1257
<211> 307
<212> PRT
<213> Unknown (H38q174 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(307)
<223> Xaa = Any Amino Acid
```

<400> 1257															
Met	Ile	Thr	Glu	Phe	Ile	Leu	Ile	Gly	Phe	Ser	Asn	Leu	Gly	Asp	Leu
1				5					10					15	
Gln	Ile	Leu	Leu	Phe	Phe	Ile	Phe	Leu	Leu	Val	Tyr	Leu	Thr	Thr	Leu
			20					25					30		
Met	Ala	Asn	Thr	Thr	Ile	Met	Thr	Val	Ile	His	Leu	Asp	Arg	Ala	Leu
		35					40					45			
His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Val	Leu	Ser	Cys	Ser	Glu	Thr
	50					55					60				
Cys	Tyr	Thr	Leu	Val	Ile	Val	Pro	Lys	Met	Leu	Thr	Asn	Leu	Leu	Ser
65					70					75				80	
Ala	Ile	Pro	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Val	Val	Gln	Leu	Tyr	Leu
				85					90					95	
Phe	Val	Gly	Leu	Ala	Cys	Thr	Asn	Cys	Phe	Leu	Ile	Ala	Val	Met	Gly
			100					105					110		
Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro	Leu	Asn	Tyr	Thr	Leu	Ile
		115					120					125			
Val	Ser	Xaa	Ala	Thr	Cys	Met	Gln	Leu	Val	Leu	Ala	Ser	Ser	Phe	Cys
	130					135					140				
Gly	Phe	Leu	Thr	Ser	Val	Ile	Val	Asn	Ile	Leu	Val	Phe	Ser	Val	Leu
145					150					155					160

```

Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
      165      170      175
Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
      180      185      190
Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
      195      200      205
Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
      210      215      220
Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
      225      230      235      240
Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      245      250      255
Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
      260      265      270
Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
      275      280      285
Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
      290      295      300
Lys Thr Val
305

```

<210> 1258
 <211> 157
 <212> PRT
 <213> Unknown (H38g175 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(157)
 <223> Xaa = Any Amino Acid

```

<400> 1258
Ile Cys His Asn Arg Lys Val Ile Pro Ala Ser Met Xaa Asn Met Cys
1      5      10      15
Xaa Phe Leu Leu Lys Val Ala Xaa Asp Asn Phe Leu His Val Leu Phe
      20      25      30
Ile Leu Ala Lys Thr Ala Pro Pro Leu Leu Phe Leu Xaa Glu Ile Pro
      35      40      45
Ser Tyr Phe Ser Ser Pro Ser Xaa Ile Ile Val Leu Xaa Cys Leu Pro
      50      55      60
Xaa Phe Leu Lys Gln Leu Val Ile Leu Phe Val Phe Leu Leu Leu Asn
      65      70      75      80
Xaa Ser Tyr Leu Thr Leu Ile Phe Met Leu Leu Thr Met Lys Ile Thr
      85      90      95
Ser Ser Phe Lys Ala Ser Thr Val Ile Ser Cys Leu Gln Phe Pro Ser
      100      105      110
Lys Ala Thr Cys Met His Gly Val Phe Ser Ala Val Cys Ala Gln Met
      115      120      125
Xaa Pro Tyr Tyr Asn Gly Xaa Ile Ile Xaa His Pro Glu Ser Ile Thr
      130      135      140
Glu Ser Lys Xaa Leu Thr Cys Val Asn Pro Xaa Phe Asn
145      150      155

```

<210> 1259
 <211> 321
 <212> PRT
 <213> Unknown (H38g176 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amin Acid

<400> 1259

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
          20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr
          35           40           45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
          50           55           60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
65           70           75           80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
          85           90           95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
          100          105          110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
          115          120          125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
          130          135          140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
145          150          155          160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
          165          170          175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
          180          185          190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
          195          200          205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
          210          215          220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
225          230          235          240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
          245          250          255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
          260          265          270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
          275          280          285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
          290          295          300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
305          310          315          320
Pro

```

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1260

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1           5           10           15
Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
      20           25           30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
      35           40           45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50           55           60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
      65           70           75           80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
      85           90           95
Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
      100          105          110
Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
      115          120          125
Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
      130          135          140
Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
      145          150          155          160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
      165          170          175
Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
      180          185          190
Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
      195          200          205
Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
      210          215          220
Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
      225          230          235          240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
      245          250          255
Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
      260          265          270
Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
      290          295          300
Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu
      305          310          315

```

<210> 1261

<211> 317

<212> PRT

<213> Unknown (H38g178 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1261

```

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1           5           10           15
Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
      20           25           30
Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

```

```

      35              40              45
Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
  50              55              60
Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys M t Ile Val Asp
  65              70              75              80
Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
      85              90              95
Met Ser Phe Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
      100              105              110
Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
      115              120              125
Pro Ile Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
      130              135              140
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
      145              150              155              160
Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
      165              170              175
Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
      180              185              190
Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
      195              200              205
Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
      210              215              220
Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
      225              230              235              240
Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Leu Tyr Leu
      245              250              255
Thr Ser Ala Gly Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
      260              265              270
Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
      275              280              285
Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Ser Arg Ala
      290              295              300
Val Glu Tyr Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
      305              310              315

```

<210> 1262

<211> 314

<212> PRT

<213> Unknown (H38g179 protein)

<220>

<223> Synthetic construct

<400> 1262

```

Met Arg Gly Phe Asn Lys Thr Thr Val Val Thr Gln Phe Ile Leu Val
  1              5              10              15
Gly Phe Ser Ser Leu Gly Glu Leu Gln Leu Leu Leu Phe Val Ile Phe
      20              25              30
Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
      35              40              45
Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
      50              55              60
Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
      65              70              75              80
Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
      85              90              95
Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
      100              105              110
Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
      115              120              125

```

His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
 130 135 140
 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
 145 150 155 160
 Thr Asn L u Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
 165 170 175
 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
 180 185 190
 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
 195 200 205
 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
 210 215 220
 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
 245 250 255
 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
 260 265 270
 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val
 290 295 300
 Leu Gly Met Pro Val Ala Thr Lys Met Ser
 305 310

<210> 1263

<211> 314

<212> PRT

<213> Unknown (H38g180 protein)

<220>

<223> Synthetic construct

<400> 1263

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser

```

      210              215              220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245              250              255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260              265              270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
      290              295              300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu
305              310

```

<210> 1264
 <211> 275
 <212> PRT
 <213> Unknown (H38g181 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(275)
 <223> Xaa = Any Amino Acid

```

<400> 1264
Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
 1              5              10              15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20              25              30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35              40              45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
 50              55              60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
 65              70              75              80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85              90              95
Ser Pro Ser Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100              105              110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115              120              125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130              135              140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
 145              150              155              160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165              170              175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180              185              190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195              200              205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210              215              220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
 225              230              235              240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245              250              255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260              265              270

```

Gln Tyr Ser
275

<210> 1265

<211> 312

<212> PRT

<213> Unknown (H38g182 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1265

Met	Arg	Arg	Asn	Phe	Thr	Leu	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly	Leu	1	5	10	15
Thr	Asn	His	Gln	Glu	Leu	Gln	Ile	Leu	Leu	Phe	Met	Leu	Phe	Leu	Ala	20	25	30	
Ile	Tyr	Met	Val	Thr	Val	Ala	Gly	Asn	Leu	Ser	Met	Ile	Ala	Leu	Ile	35	40	45	
Gln	Ala	Asn	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His	50	55	60	
Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Ser	Ser	Asn	Val	Thr	Pro	Lys	Met	65	70	75	80
Leu	Glu	Ile	Phe	Leu	Ser	Glu	Lys	Lys	Ser	Ile	Ser	Tyr	Pro	Ala	Cys	85	90	95	
Leu	Val	Gln	Cys	Tyr	Leu	Tyr	Ile	Ile	Leu	Val	His	Val	Glu	Ile	Tyr	100	105	110	
Ile	Leu	Ala	Val	Met	Ala	Phe	Asp	Xaa	Tyr	Met	Ala	Ile	Xaa	Asn	Pro	115	120	125	
Leu	Leu	Tyr	Gly	Ser	Lys	Met	Ser	Lys	Ser	Val	Cys	Ser	Phe	Leu	Ile	130	135	140	
Thr	Val	Pro	Tyr	Val	Tyr	Gly	Ala	Leu	Thr	Gly	Leu	Met	Glu	Thr	Met	145	150	155	160
Trp	Thr	Tyr	Asn	Leu	Ala	Phe	Cys	Gly	Pro	Asn	Glu	Ile	Asn	His	Phe	165	170	175	
Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	180	185	190	
Asn	Lys	Glu	Leu	Ser	Met	Phe	Val	Val	Ala	Gly	Trp	Asn	Leu	Ser	Phe	195	200	205	
Ser	Leu	Phe	Ile	Ile	Phe	Ile	Ser	Tyr	Phe	Tyr	Ile	Phe	Pro	Ala	Ile	210	215	220	
Leu	Arg	Ile	Arg	Ser	Thr	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys	225	230	235	240
Gly	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Ala	Thr	Leu	Phe	Phe	245	250	255	
Met	Cys	Leu	Arg	Pro	Pro	Ser	Glu	Glu	Ser	Met	Glu	Gln	Gly	Gln	Met	260	265	270	
Val	Ala	Val	Leu	Tyr	Thr	Thr	Val	Ile	Pro	Met	Leu	Asn	Pro	Met	Ile	275	280	285	
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Lys	Ala	Leu	Ser	Lys	Glu	Leu	290	295	300	
Phe	Lys	Arg	Lys	Leu	Phe	Pro	Lys									305	310		

<210> 1266

<211> 315

<212> PRT

<213> Unknown (H38g183 protein)

<220>

<223> Synthetic construct

<400> 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
          20           25           30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
          35           40           45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
          50           55           60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65           70           75           80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
          85           90           95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
          100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
          115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
          165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
          180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
          195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
          245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
          260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
305          310          315

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<210> 1267

<211> 317

<212> PRT

<213> Unknown (H38g184 protein)

<220>

<223> Synthetic construct

<400> 1267

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Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
          20           25           30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Phe Ile
          35           40           45

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Thr Ser Trp Thr Asp Pro Lys Leu Asn S r Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
 65 70 75 80
 Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val
 85 90 95
 Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu
 100 105 110
 Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
 130 135 140
 Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
 145 150 155 160
 Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
 165 170 175
 Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
 180 185 190
 Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
 195 200 205
 Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
 210 215 220
 Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
 245 250 255
 Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
 260 265 270
 Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
 290 295 300
 Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
 305 310 315

<210> 1268

<211> 324

<212> PRT

<213> Unknown (H38g185 protein)

<220>

<223> Synthetic construct

<400> 1268

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr
 1 5 10 15
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile
 20 25 30
 Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu
 35 40 45
 Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu
 50 55 60
 His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr
 65 70 75 80
 Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
 85 90 95
 Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
 100 105 110
 Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
 115 120 125
 Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

130	135	140
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Cys Ala Ile Gly		
145	150	155
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro		
	165	170
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala		
	180	185
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile		
	195	200
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys		
	210	215
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala		
225	230	235
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val		
	245	250
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr		
	260	265
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr		
	275	280
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys		
	290	295
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu		
305	310	315
Lys Leu Tyr Asn		

<210> 1269

<211> 327

<212> PRT

<213> Unknown (H38g186 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1269

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile	
1	5
Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe	
	20
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val	
	35
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu	
	50
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro	
65	70
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu	
	85
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu	
	100
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr	
	115
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro	
	130
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His	
145	150
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg	
	165


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His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
      180      185      190
Thr His Val Ile Gln Leu L u Phe Phe Tyr Phe Val Gly Ser Ile Glu
      195      200      205
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
      210      215      220
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
225      230      235      240
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
      245      250      255
Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
      260      265      270
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
      290      295      300
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
305      310      315      320
Val Lys Leu Gln Ile Ile Leu
      325

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<210> 1270

<211> 319

<212> PRT

<213> Unknown (H38g187 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1270

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1      5      10      15
Leu Ser Lys Pro Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
      20      25      30
Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
      35      40      45
Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
      50      55      60
Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
65      70      75      80
Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
      85      90      95
Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
      100      105      110
Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
      115      120      125
Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
      130      135      140
Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
145      150      155      160
Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
      165      170      175
Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
      180      185      190
Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
      195      200      205
Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

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210	215	220
Ser Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr		
225	230	235
Val Gly Ile Leu Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro		
	245	250
Leu Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu		255
	260	265
Ser Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val		270
	275	280
Ser Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser		285
	290	295
Xaa Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro		300
305	310	315

<210> 1271

<211> 324

<212> PRT

<213> Unknown (H38g188 protein)

<220>

<223> Synthetic construct

<400> 1271

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg		
1	5	10
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe		15
	20	25
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu		30
	35	40
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met		45
	50	55
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr		60
	65	70
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser		75
	85	90
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe		95
	100	105
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr		110
	115	120
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln		125
	130	135
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr		140
	145	150
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met		155
	165	170
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val		175
	180	185
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala		190
	195	200
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala		205
	210	215
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln		220
	225	230
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe		235
	245	250
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala		255
	260	265
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro		270
	275	280
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala		285
	290	295
		300

Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
 305 310 315 320
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
 130 135 140
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
 145 150 155 160
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
 165 170 175
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
 195 200 205
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
 210 215 220
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
 225 230 235 240
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
 305 310 315 320
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

<220>

<223> Synthetic construct

<400> 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1      5      10      15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
      20      25      30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
      35      40      45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
      65      70      75      80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
      85      90      95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
      100     105     110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
      115     120     125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
      130     135     140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
      145     150     155     160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
      165     170     175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
      180     185     190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
      195     200     205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
      210     215     220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
      225     230     235     240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
      245     250     255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
      260     265     270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
      275     280     285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
      290     295     300
Gln Arg Arg Gln Asp Ser Arg
305      310

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<210> 1274

<211> 305

<212> PRT

<213> Unknown (H38g191 protein)

<220>

<223> Synthetic construct

<400> 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1      5      10      15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20      25      30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35      40      45

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His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1275

<211> 312

<212> PRT

<213> Unknown (H38g192 protein)

<220>

<223> Synthetic construct

<400> 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20 25 30
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ser Thr
 35 40 45
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
 100 105 110
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

130	135	140
Val Ala Ala Ala Cys	Ala Cys Gly Phe Thr Val	Ala Gln Ile Ile Thr
145	150	155
Ser Leu Val Phe His	Leu Pro Phe Tyr Ser Ser	Asn Gln Leu His His
165	170	175
Phe Phe Cys Asp Ile	Ala Pro Val Leu Lys Leu	Ala Ser His His Asn
180	185	190
His Phe Ser Gln Ile	Val Ile Phe Met Leu Cys Thr	Leu Val Leu Ala
195	200	205
Ile Pro Leu Leu Leu	Ile Leu Val Ser Tyr Val	His Ile Leu Ser Ala
210	215	220
Ile Leu Gln Phe Pro	Ser Thr Leu Gly Arg Cys	Lys Ala Phe Ser Thr
225	230	235
Cys Val Ser His Leu	Ile Ile Val Thr Val	His Tyr Gly Cys Ala Ser
245	250	255
Phe Ile Tyr Leu Arg	Pro Gln Ser Asn Tyr Ser	Ser Ser Gln Asp Ala
260	265	270
Leu Ile Ser Val Ser	Tyr Thr Ile Ile Thr Pro	Leu Phe Asn Pro Met
275	280	285
Ile Tyr Ser Leu Arg	Asn Lys Glu Phe Lys Ser	Ala Leu Cys Lys Ile
290	295	300
Val Arg Arg Thr Ile	Ser Leu Leu	
305	310	

<210> 1276

<211> 244

<212> PRT

<213> Unknown (H38g193 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(244)

<223> Xaa = Any Amino Acid

<400> 1276

Met Met Ile Ser Ser	Asp Glu Glu Asn Asp Thr	Asn Met Met Glu Phe
1	5	10
Ile Leu Val Gly Leu	Ser Arg Gln Pro Ala Ser	Gln Leu Leu Phe Phe
20	25	30
Xaa Ala Ile Leu Phe	Ile Tyr Ser Val Thr Leu	Val Gly Asn Ile Leu
35	40	45
Ile Ile Val Ile Ile	Gln Ile Asp Ser His Leu	Gln Thr Pro Met Tyr
50	55	60
Phe Phe Leu Ile Gln	Val Ser Phe Leu Asp Ile	Cys Ser Thr Pro Thr
65	70	75
Val Leu Val Asn Cys	Xaa Lys Asp Phe Pro Ser	Val Ser Tyr Ser Gly
85	90	95
Cys Leu Phe Xaa Met	Thr Ile Phe Leu Tyr Leu	Gly Val Thr Glu Cys
100	105	110
Val Phe Phe Leu Phe	Cys Phe Glu Cys Phe Leu	Ile Ala Val Met Ala
115	120	125
Tyr Asp Arg Phe Val	Ala Ile Ser Lys Pro Leu	Cys Tyr Pro Phe Ile
130	135	140
Ile Asn Ser Asn Val	Cys Ile Trp Met Val Ala	Gly Val Trp Ala His
145	150	155
Pro Gly Arg Thr Asn	Pro Ile Leu Trp Pro Gln	Cys Ser Gln His Phe
165	170	175
Thr Cys Glu Leu Gln	Val Ile Phe Lys Leu Thr	Cys Ser Pro Val Leu
180	185	190

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala
 195 200 205
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr
 210 215 220
 His Pro Arg S r Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile
 225 230 235 240
 Ile Gly Val His

<210> 1277

<211> 306

<212> PRT

<213> Unknown (H38g194 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(306)

<223> Xaa = Any Amino Acid

<400> 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1 5 10 15
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu
 20 25 30
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu
 35 40 45
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn
 115 120 125
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val
 130 135 140
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val
 145 150 155 160
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp
 165 170 175
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu
 180 185 190
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu
 195 200 205
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn
 210 215 220
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His
 225 230 235 240
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu
 245 250 255
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val
 260 265 270
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys
 290 295 300
 Leu Phe

305

<210> 1278
 <211> 251
 <212> PRT
 <213> Unknown (H38g195 protein)

<220>
 <223> Synthetic construct

<400> 1278

Met	Ala	Asn	Ser	Ser	Val	Thr	Glu	Phe	Leu	Val	Leu	Gly	Phe	Ser
1			5					10					15	
Ser	Leu	Gly	Glu	Leu	Gln	Leu	Val	Leu	Phe	Ala	Val	Phe	Leu	Cys
		20					25					30		Leu
Tyr	Leu	Ile	Ile	Leu	Ser	Gly	Asn	Ile	Ile	Ile	Ile	Ser	Val	Ile
		35				40						45		His
Leu	Asp	His	Ser	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Ile
	50					55					60			Leu
Ser	Ile	Ser	Glu	Ile	Phe	Tyr	Thr	Thr	Val	Ile	Leu	Pro	Lys	Met
65				70					75					80
Ile	Asn	Leu	Phe	Ser	Val	Phe	Arg	Thr	Leu	Ser	Phe	Val	Ser	Cys
			85						90					95
Thr	Gln	Met	Phe	Phe	Phe	Leu	Gly	Phe	Ala	Val	Thr	Asn	Cys	Leu
			100					105					110	Leu
Leu	Gly	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	Gln	Pro
		115				120						125		Leu
Gln	Tyr	Ala	Val	Leu	Met	Ser	Trp	Arg	Val	Cys	Gly	Gln	Leu	Ile
	130					135					140			Ala
Thr	Cys	Ile	Ile	Ser	Gly	Phe	Leu	Ile	Ser	Leu	Val	Gly	Thr	Thr
145					150					155				160
Val	Phe	Ser	Leu	Pro	Phe	Cys	Gly	Ser	Asn	Lys	Val	Asn	His	Tyr
				165					170					175
Cys	Asp	Ile	Ser	Pro	Val	Ile	Arg	Leu	Ala	Cys	Ala	Asp	Ser	Tyr
		180						185				190		Ile
Ser	Glu	Leu	Val	Ile	Phe	Ile	Phe	Gly	Val	Leu	Val	Leu	Val	Pro
		195					200					205		
Leu	Ile	Phe	Ile	Cys	Ile	Ser	Tyr	Gly	Phe	Ile	Val	Arg	Thr	Ile
	210					215					220			Leu
Lys	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Ser	Thr	Cys
225					230					235				240
Ser	His	Leu	Ile	Val	Val	Ile	Val	His	Tyr	Gly				
			245						250					

<210> 1279
 <211> 315
 <212> PRT
 <213> Unknown (H38g196 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1279

Met	Gly	Gly	Leu	Lys	Arg	Asp	Asn	Ala	Ser	Glu	Met	Thr	Glu	Leu
1			5						10				15	
Leu	Val	Gly	Phe	Ala	Gln	His	Pro	Glu	Ile	Gln	Thr	Ala	Phe	Phe
		20						25					30	Leu

Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35 40 45
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe
 50 55 60
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser
 65 70 75 80
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile
 85 90 95
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly
 100 105 110
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val
 115 120 125
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val
 130 135 140
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala
 145 150 155 160
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val
 165 170 175
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys
 180 185 190
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe
 195 200 205
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile
 210 215 220
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met
 245 250 255
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val
 260 265 270
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr
 275 280 285
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys
 290 295 300
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn
 305 310 315

<210> 1280

<211> 319

<212> PRT

<213> Unknown (H38g197 protein)

<220>

<223> Synthetic construct

<400> 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr
 1 5 10 15
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro
 20 25 30
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn
 35 40 45
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser
 65 70 75 80
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn
 85 90 95
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile
 100 105 110
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

115	120	125
Tyr Val Ala Ile Cys Lys	Pro Leu Leu Tyr Val Ile	Ile Met Ala Glu
130	135	140
Lys Val Leu Trp Val Leu Val Ile Val	Pro Tyr Leu Tyr Ser Thr Phe	
145	150	155
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe	Lys Leu Ser Phe Cys Gly	
165	170	175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp	Cys Ile Pro Leu Met Ser	
180	185	190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu	Leu Ile Ile Leu Ile Phe	
195	200	205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser	Ile Val Leu Ile Ser Tyr	
210	215	220
Met Phe Ile Leu Val Ala Ile Leu Arg Met	Asn Ser Arg Lys Gly Arg	
225	230	235
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His	Leu Thr Val Val Ile Met	
245	250	255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu	Gln Pro Lys Ser Ser His	
260	265	270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val	Phe Tyr Thr Leu Leu Ile	
275	280	285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu	Arg Asn Lys Glu Val Lys	
290	295	300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg	Phe Lys Ile Pro Ile	
305	310	315

<210> 1281

<211> 157

<212> PRT

<213> Unknown (H38g198 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1281

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met	
1	5
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe	
20	25
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg	
35	40
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro	
50	55
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu	
65	70
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg	
85	90
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His	
100	105
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln	
115	120
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu	
130	135
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu	
145	150
	155

<210> 1282

<211> 317
 <212> PRT
 <213> Unknown (H38g199 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1282

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
 1      5      10      15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
 20      25      30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Ile Leu
 35      40      45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
 50      55      60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
 65      70      75      80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
 85      90      95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
100      105      110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
115      120      125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
130      135      140
Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
145      150      155      160
Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
165      170      175
Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
180      185      190
Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
195      200      205
Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
210      215      220
Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
225      230      235      240
Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
245      250      255
Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
260      265      270
Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
275      280      285
Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
290      295      300
Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
305      310      315

```

<210> 1283
 <211> 302
 <212> PRT
 <213> Unknown (H38g200 protein)

<220>
 <223> Synthetic construct

<400> 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1           5           10           15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
      20           25           30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Leu Gly Asn Gly Thr Ile Leu
      35           40           45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
      50           55           60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
      65           70           75           80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
      85           90           95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
      100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
      115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
      130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
      145          150          155          160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
      165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
      180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
      195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
      210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
      225          230          235          240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
      245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
      260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
      275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
      290          295          300

```

<210> 1284

<211> 324

<212> PRT

<213> Unknown (H38g201 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35           40           45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
      50           55           60

```

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100         105         110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115         120         125
Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130         135         140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165         170         175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
          180         185         190
Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
          195         200         205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
210          215          220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
          245         250         255
Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
          260         265         270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275         280         285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290          295         300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310         315         320
Phe Phe Trp Cys

```

<210> 1285

<211> 144

<212> PRT

<213> Unknown (H38g202 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(144)

<223> Xaa = Any Amino Acid

<400> 1285

```

Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
1          5          10          15
Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
          20          25          30
Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
          35          40          45
Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
          50          55          60
Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
65          70          75          80
Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
          85          90          95
Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

```

	100		105		110										
Asp	Leu	Ala	Leu	Lys	Gln	Asn	Phe	Ala	Ile	Leu	Arg	Ser	Ile	Pro	Ser
	115		120		125										
Phe	Ser	Ser	Xaa	Asp	Leu	Glu	Ile	His	Asn	Val	Arg	Tyr	Gln	His	Phe
	130				135						140				

<210> 1286
 <211> 314
 <212> PRT
 <213> Unknown (H38g203 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1286

Thr	His	Gly	Tyr	Thr	Phe	Ser	Leu	Arg	Leu	Phe	Leu	His	Cys	Leu	Thr
1				5				10					15		
Tyr	Val	Xaa	Val	Ser	His	Cys	Leu	Leu	Ile	Trp	Leu	Ile	Thr	Phe	Ser
			20				25						30		
Pro	Phe	Asn	Leu	Leu	Phe	Lys	Xaa	Asn	Leu	Xaa	Phe	Thr	Ile	Xaa	Leu
		35				40					45				
Ile	Thr	Xaa	Ile	Glu	Ser	Arg	Tyr	Ser	Lys	His	Trp	Pro	Phe	Phe	Leu
	50				55						60				
Leu	Xaa	Cys	Phe	Cys	Asn	Val	Leu	Phe	His	Leu	Asp	Cys	Asp	Ser	Pro
65				70				75						80	
Val	Cys	Asn	Thr	Lys	Arg	Ile	Arg	Ser	Phe	Phe	Val	Leu	Glu	Arg	Xaa
			85				90						95		
Lys	Ser	Ser	Xaa	Lys	Ser	Glu	Lys	Ile	His	Phe	Xaa	Thr	Arg	Asn	Lys
			100				105						110		
Val	Ser	Cys	Phe	Xaa	Asp	Phe	Gly	Ile	Lys	Tyr	Thr	Val	Tyr	Leu	Leu
		115				120					125				
Leu	Leu	Lys	His	Phe	Leu	Leu	Ile	His	Ser	Ile	Leu	Arg	Tyr	Leu	Xaa
	130				135						140				
Val	Ala	Gly	Tyr	Gly	Thr	Ser	Xaa	Phe	Leu	Ser	Arg	Ile	Ser	Ser	Ile
145				150					155					160	
Thr	Leu	Lys	Thr	Ile	Ile	Cys	Ile	Leu	Lys	Lys	Ser	Tyr	His	Phe	Phe
			165					170					175		
Ser	Val	Gln	Tyr	Thr	Ile	Ser	Tyr	Ile	Asp	Pro	Phe	Ile	Asn	Ser	Leu
		180					185					190			
Val	Met	Phe	Val	Val	Phe	Thr	Ala	Phe	Ile	Gln	Ala	Phe	Ala	Phe	Met
	195					200					205				
Ile	Ile	Ile	Val	Ser	Tyr	Thr	Gln	Val	Leu	Phe	Ala	Leu	Leu	Lys	Lys
	210				215					220					
Asn	Ser	Glu	Lys	Gly	Arg	Ser	Lys	Ser	Phe	Leu	Met	Cys	Ser	Ala	His
225				230					235					240	
Leu	Leu	Ser	Val	Ser	Leu	Phe	Tyr	Ser	Ser	Val	Phe	Phe	Met	Tyr	Gly
			245				250						255		
Cys	Pro	Arg	Ser	Gly	Pro	Asp	Xaa	Gln	Trp	Asn	Glu	Met	Tyr	Phe	Pro
		260				265						270			
Phe	Tyr	Met	Ile	Ile	Ile	Pro	Leu	Gln	Thr	Pro	Phe	Ile	Tyr	Ser	Met
	275				280						285				
Lys	Asn	Lys	Glu	Val	Leu	Gly	Thr	Leu	Arg	Thr	Met	Ile	Lys	Lys	Tyr
	290				295					300					
Phe	Trp	Arg	Thr	Leu	Ser	Xaa	Phe	Phe	Pro						
305				310											

<210> 1287

<211> 253
 <212> PRT
 <213> Unknown (H38g204 protein)

<220>
 <223> Synthetic construct

<400> 1287
 Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser
 1 5 10 15
 Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg
 20 25 30
 Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe
 35 40 45
 Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg
 50 55 60
 Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His
 65 70 75 80
 Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile
 85 90 95
 His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly
 100 105 110
 Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg
 115 120 125
 Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp
 130 135 140
 Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr
 145 150 155 160
 Gly Tyr Ile Val Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg
 165 170 175
 Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val
 180 185 190
 Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu
 195 200 205
 Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu
 210 215 220
 Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala
 225 230 235 240
 Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His
 245 250

<210> 1288
 <211> 311
 <212> PRT
 <213> Unknown (H38g205 protein)

<220>
 <223> Synthetic construct

<400> 1288
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20 25 30
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
 35 40 45
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65 70 75 80
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

```

      85      90      95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115      120      125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
      130      135      140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
      145      150      155      160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
      165      170      175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
      180      185      190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
      195      200      205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
      210      215      220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
      225      230      235      240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
      245      250      255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
      260      265      270
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
      275      280      285
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
      290      295      300
Trp Arg Gly Arg Asp Ser Gly
      305      310

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<210> 1289

<211> 311

<212> PRT

<213> Unknown (H38g206 protein)

<220>

<223> Synthetic construct

<400> 1289

```

Met Lys Ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly
1      5      10      15
Ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu
      20      25      30
Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Leu Ala
      35      40      45
Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50      55      60
Asn Leu Ser Val Phe Asp Ile Phe Phe Pro Ser Val Ser Ser Pro Lys
      65      70      75      80
Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr Ile Ser Phe Gln Gly
      85      90      95
Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys
      100      105      110
Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
      115      120      125
Pro Leu Pro Tyr Thr Val Ile Met Lys Arg Arg Val Cys Ala Leu Leu
      130      135      140
Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr
      145      150      155      160
Leu Leu Ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn
      165      170      175

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Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr
    180                      185                      190
Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu
    195                      200                      205
Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser
    210                      215                      220
Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser Thr
    225                      230                      235                      240
Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val
    245                      250                      255
Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val
    260                      265                      270
Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr
    275                      280                      285
Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile
    290                      295                      300
Gln Gly Val His Asn Cys Gly
    305                      310

```

<210> 1290

<211> 298

<212> PRT

<213> Unknown (H38g207 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400> 1290

```

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe
  1          5          10          15
Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe
  20          25          30
Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Val Gly Ser His Met
  35          40          45
Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly
  50          55          60
Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln
  65          70          75          80
Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala
  85          90          95
Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser
  100         105         110
Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln
  115         120         125
Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu
  130         135         140
Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser
  145         150         155         160
Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His
  165         170         175
Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr
  180         185         190
Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala
  195         200         205
His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val
  210         215         220
Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

```

225					230					235					240
Ala	His	Leu	Ala	Met	Ile	Gly	Leu	Phe	Tyr	Val	Thr	Ser	Val	Pr	Cys
				245					250					255	
Tyr	Ile	Leu	Pro	Asn	Ser	Ala	Tyr	Ser	Gly	Leu	Gly	Asp	Trp	Val	Leu
			260					265					270		
Ser	Val	Leu	Cys	Val	Val	Leu	Thr	His	Met	Leu	Asn	Pro	Ile	Phe	Pro
		275					280					285			
Ser	Met	Leu	Gly	Xaa	Gln	Cys	Met	Ser	His						
	290					295									

<210> 1291

<211> 312

<212> PRT

<213> Unknown (H38g208 protein)

<220>

<223> Synthetic construct

<400> 1291

Met	Gly	Val	Lys	Asn	His	Ser	Thr	Val	Thr	Glu	Phe	Leu	Leu	Ser	Gly
1				5					10					15	
Leu	Thr	Glu	Gln	Ala	Glu	Leu	Gln	Leu	Pro	Leu	Phe	Cys	Leu	Phe	Leu
			20					25					30		
Gly	Ile	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Ser	Met	Ile	Ser	Ile
		35					40					45			
Ile	Arg	Leu	Asn	Arg	Gln	Leu	His	Thr	Pro	Met	Tyr	Tyr	Phe	Leu	Ser
	50					55					60				
Ser	Leu	Ser	Phe	Leu	Asp	Phe	Cys	Tyr	Ser	Ser	Val	Ile	Thr	Pro	Lys
65					70					75				80	
Met	Leu	Ser	Gly	Phe	Leu	Cys	Arg	Asp	Arg	Ser	Ile	Ser	Tyr	Ser	Gly
			85					90					95		
Cys	Met	Ile	Gln	Leu	Phe	Phe	Phe	Cys	Val	Cys	Val	Ile	Ser	Glu	Cys
			100					105					110		
Tyr	Met	Leu	Ala	Ala	Met	Ala	Cys	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser
		115					120					125			
Pro	Leu	Leu	Tyr	Arg	Val	Ile	Met	Ser	Pro	Arg	Val	Cys	Ser	Leu	Leu
	130					135					140				
Val	Ala	Ala	Val	Phe	Ser	Val	Gly	Phe	Thr	Asp	Ala	Val	Ile	His	Gly
145					150					155				160	
Gly	Cys	Ile	Leu	Arg	Leu	Ser	Phe	Cys	Gly	Ser	Asn	Ile	Ile	Lys	His
			165						170					175	
Tyr	Phe	Cys	Asp	Ile	Val	Pro	Leu	Ile	Lys	Leu	Ser	Cys	Ser	Ser	Thr
			180					185					190		
Tyr	Ile	Asp	Glu	Leu	Leu	Ile	Phe	Val	Ile	Gly	Gly	Phe	Asn	Met	Val
		195					200					205			
Ala	Thr	Ser	Leu	Thr	Ile	Ile	Ile	Ser	Tyr	Ala	Phe	Ile	Leu	Thr	Ser
	210					215					220				
Ile	Leu	Arg	Ile	His	Ser	Lys	Lys	Gly	Arg	Cys	Lys	Ala	Phe	Ser	Thr
225				230					235					240	
Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Leu	Met	Phe	Tyr	Gly	Ser	Leu	Met
			245						250				255		
Ser	Met	Tyr	Leu	Lys	Pro	Ala	Ser	Ser	Ser	Ser	Leu	Thr	Gln	Glu	Lys
		260						265					270		
Val	Ser	Ser	Val	Phe	Tyr	Thr	Thr	Val	Ile	Leu	Met	Leu	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Asn	Glu	Val	Arg	Asn	Ala	Leu	Met	Lys	Leu
	290				295						300				
Leu	Arg	Arg	Lys	Ile	Ser	Leu	Ser								
305					310										

<210> 1292

<211> 251
 <212> PRT
 <213> Unknown (H38g209 protein)

<220>
 <223> Synthetic construct

<400> 1292
 Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1 5 10 15
 Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
 20 25 30
 Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
 35 40 45
 Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
 50 55 60
 Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
 65 70 75 80
 Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
 85 90 95
 Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
 100 105 110
 Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
 115 120 125
 Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
 130 135 140
 Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
 145 150 155 160
 Ile Phe Ile Ile Ala Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
 165 170 175
 His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
 180 185 190
 Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
 195 200 205
 Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
 210 215 220
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
 225 230 235 240
 Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
 245 250

<210> 1293
 <211> 311
 <212> PRT
 <213> Unknown (H38g210 protein)

<220>
 <223> Synthetic construct

<400> 1293
 Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1 5 10 15
 His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
 20 25 30
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35 40 45
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50 55 60
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65 70 75 80
 Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys

```
<210> 1294
<211> 278
<212> PRT
<213> Unknown (H38g211 protein)
```

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<220>
<223> Synthetic construct
<221> VARIANT
<222> (1)...(278)
<223> Xaa = Any Amino Acid

```

<400> 1294																
His	Ser	Ser	Leu	Leu	Phe	Ala	Val	Phe	Leu	Leu	Thr	Tyr	Ser	Val	Thr	
1				5					10					15		
Leu	Val	Gly	Asn	Leu	Gly	Met	Thr	Asp	Leu	Ile	Cys	Gln	Ser	Arg	Thr	
			20					25					30			
Ser	Ser	Ala	Leu	His	Thr	Pro	Met	Cys	Phe	Leu	Leu	Ser	Val	Phe	Ser	
		35					40					45				
Phe	Leu	Asp	Ile	Cys	Ser	Ser	Ser	Ile	Val	His	Pro	Arg	Leu	Leu	Ile	
50						55				60						
His	Phe	Leu	Thr	Thr	Arg	Pro	Ser	Ile	Ser	Phe	Ala	Gly	Gly	Ile	Ile	
65					70					75					80	
Gln	Met	Ala	Leu	Met	Thr	Phe	Tyr	Gly	Thr	Gly	Glu	Cys	Leu	Leu	Leu	
				85					90					95		
Ala	Ile	Val	Ala	Tyr	Asp	Xaa	Val	Val	Ala	Ile	Cys	His	Pro	Phe	Pro	
			100					105					110			
Xaa	His	Ile	Ile	Met	Ser	Lys	Gly	Leu	Cys	Ala	Gln	Leu	Val	Val	Val	
		115					120					125				
Thr	Ser	Ala	Val	Gly	Val	Leu	Ile	Ser	Ala	His	Arg	Gln	Asp	Ala	Phe	
	130					135					140					

```

Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser
145          150          155          160
Val Thr Ph  Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr
          165          170          175
Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro
          180          185          190
Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu
          195          200          205
Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg
          210          215          220
Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu
225          230          235          240
Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile
          245          250          255
Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu
          260          265          270
Arg Asn Lys Asp Val Lys
          275

```

<210> 1295

<211> 312

<212> PRT

<213> Unknown (H38g212 protein)

<220>

<223> Synthetic construct

<400> 1295

```

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu
1          5          10          15
Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe
          20          25          30
Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met
          35          40          45
Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro
65          70          75          80
Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr
          85          90          95
Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu
          100          105          110
Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu
          130          135          140
Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr
145          150          155          160
Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His
          165          170          175
Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr
          180          185          190
His Val Lys Glu Leu Met Leu Leu Ile Ile Ala Gly Phe Asn Thr Leu
          195          200          205
Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala
          210          215          220
Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile
          245          250          255
Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

```

	260		265		270										
Val	Ala	Ser	Val	Phe	Asn	Val	Val	Val	Ile	Pr	Thr	Leu	Asn	Pro	Leu
	275					280						285			
Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Glu	Val	Lys	Asn	Ala	Leu	Lys	Arg	Ile
	290					295						300			
Ile	Glu	Lys	Leu	Cys	Leu	Ala	Val								
305					310										

<210> 1296

<211> 232

<212> PRT

<213> Unknown (H38g213 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(232)

<223> Xaa = Any Amino Acid

<400> 1296

Ser	Gly	Leu	Val	Pro	Lys	Ser	Phe	Pro	Gly	Cys	Leu	Thr	Gln	Leu	Phe
1				5				10					15		
Phe	Leu	His	Tyr	Ser	Phe	Val	Leu	Asp	Ser	Ala	Ile	Leu	Leu	Ala	Met
		20						25					30		
Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Ser	Pro	Leu	Arg	Tyr	Thr	Thr
		35					40					45			
Ile	Leu	Thr	Pro	Lys	Thr	Ile	Val	Lys	Ile	Ala	Val	Gly	Ile	Cys	Phe
	50					55					60				
Arg	Ser	Phe	Cys	Val	Phe	Val	Pro	Cys	Val	Phe	Leu	Val	Asn	Arg	Leu
65					70					75				80	
Pro	Phe	Cys	Arg	Thr	His	Ile	Ile	Ser	His	Thr	Tyr	Cys	Glu	His	Ile
				85					90					95	
Gly	Val	Ala	Gln	Leu	Ala	Cys	Ala	Asp	Ile	Ser	Ile	Asn	Ile	Trp	Cys
			100					105					110		
Gly	Phe	Cys	Val	Pro	Ile	Met	Thr	Val	Met	Thr	Asp	Val	Ile	Leu	Ile
		115					120					125			
Ala	Val	Ser	Tyr	Thr	Leu	Ile	Leu	Cys	Ala	Val	Phe	Cys	Leu	Pro	Ser
	130					135					140				
Gln	Asp	Ala	Arg	Gln	Lys	Ala	Leu	Cys	Ser	Cys	Gly	Ser	His	Val	Cys
145					150					155				160	
Val	Ile	Leu	Ile	Phe	Tyr	Ile	Pro	Ala	Phe	Phe	Ser	Ile	Leu	Ala	His
				165					170					175	
Cys	Phe	Gly	His	Asn	Val	Pro	His	Thr	Phe	His	Ile	Met	Phe	Ala	Asn
			180					185					190		
Leu	Tyr	Val	Ile	Ile	Pro	Pro	Ala	Leu	Asn	Ser	Ile	Val	Tyr	Arg	Ile
	195						200					205			
Lys	Thr	Lys	Gln	Ile	Gln	Asn	Arg	Ile	Leu	Leu	Leu	Phe	Pro	Lys	Gly
	210					215						220			
Ser	Gln	Xaa	Xaa	Val	Pro	Glu	Leu								
225					230										

<210> 1297

<211> 310

<212> PRT

<213> Unknown (H38g214 protein)

<220>

<223> Synthetic construct

<400> 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
 1          5          10          15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
 20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35          40          45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
 50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
 65          70          75          80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
 85          90          95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
100          105          110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
115          120          125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
180          185          190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
195          200          205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
210          215          220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
260          265          270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
290          295          300
Val Ala His Ser Gln Ser
305          310

```

<210> 1298

<211> 311

<212> PRT

<213> Unknown (H38g215 protein)

<220>

<223> Synthetic construct

<400> 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
 20          25          30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
 35          40          45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
 65          70          75          80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

				85					90					95					
Leu	Val	Gln	Cys	Tyr	Leu	Phe	Ile	Ala	Leu	Val	His	Val	Glu	Ile	Tyr				
			100					105					110						
Ile	Leu	Ala	Val	Met	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro				
		115					120					125							
Leu	Leu	Tyr	Gly	Ser	Arg	Met	Ser	Lys	Ser	Val	Cys	Ser	Phe	Leu	Ile				
	130					135					140								
Thr	Val	Pro	Tyr	Val	Tyr	Gly	Ala	Leu	Thr	Gly	Leu	Met	Glu	Thr	Met				
145					150					155					160				
Trp	Thr	Tyr	Asn	Leu	Ala	Phe	Cys	Gly	Pro	Asn	Glu	Ile	Asn	His	Phe				
			165					170					175						
Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr				
		180						185					190						
Asn	Lys	Glu	Leu	Ser	Met	Phe	Ile	Val	Ala	Gly	Trp	Asn	Leu	Ser	Phe				
	195						200					205							
Ser	Leu	Phe	Ile	Ile	Cys	Ile	Ser	Tyr	Leu	Tyr	Ile	Phe	Pro	Ala	Ile				
	210					215					220								
Leu	Lys	Ile	Arg	Ser	Thr	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys				
225					230				235						240				
Gly	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Ala	Thr	Leu	Phe	Phe				
			245				250					255							
Met	Tyr	Leu	Arg	Pro	Pro	Ser	Lys	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met				
		260					265					270							
Val	Ala	Val	Phe	Tyr	Thr	Thr	Val	Ile	Pro	Met	Leu	Asn	Leu	Ile	Ile				
		275					280				285								
Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys	Glu	Ala	Leu	Ile	Lys	Glu	Leu				
	290				295				300										
Ser	Met	Lys	Ile	Tyr	Phe	Ser													
305					310														

<210> 1299

<211> 315

<212> PRT

<213> Unknown (H38g216 protein)

<220>

<223> Synthetic construct

<400> 1299

Met	Leu	Leu	Ser	Asn	Ile	Thr	Gln	Phe	Ser	Pro	Ile	Phe	Tyr	Leu	Thr				
1				5				10					15						
Ser	Phe	Pro	Gly	Leu	Glu	Gly	Ile	Lys	His	Trp	Ile	Phe	Ile	Pro	Phe				
		20					25					30							
Phe	Phe	Met	Tyr	Met	Val	Ala	Ile	Ser	Gly	Asn	Cys	Phe	Ile	Leu	Ile				
	35					40					45								
Ile	Ile	Lys	Thr	Asn	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Tyr	Leu	Leu				
	50				55					60									
Ser	Leu	Leu	Ala	Leu	Thr	Asp	Leu	Gly	Leu	Cys	Val	Ser	Thr	Leu	Pro				
65				70				75					80						
Thr	Thr	Met	Gly	Ile	Phe	Trp	Phe	Asn	Ser	Gln	Ser	Ile	Tyr	Phe	Gly				
			85				90					95							
Ala	Cys	Gln	Ile	Gln	Met	Phe	Cys	Ile	His	Ser	Phe	Ser	Phe	Met	Glu				
		100					105					110							
Ser	Ser	Val	Leu	Leu	Met	Met	Ser	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys				
		115				120					125								
His	Pro	Leu	Arg	Tyr	Ser	Val	Ile	Ile	Thr	Gly	Gln	Gln	Val	Val	Arg				
	130				135					140									
Ala	Gly	Leu	Ile	Val	Ile	Phe	Arg	Gly	Pro	Val	Ala	Thr	Ile	Pro	Ile				
145				150				155						160					
Val	Leu	Leu	Leu	Lys	Ala	Phe	Pro	Tyr	Cys	Gly	Ser	Val	Val	Leu	Ser				
			165					170						175					


```

His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp
      180                      185                      190
Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val
      195                      200                      205
Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His
      210                      215                      220
Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln
      225                      230                      235                      240
Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met
      245                      250                      255
Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala
      260                      265                      270
Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu
      275                      280                      285
Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile
      290                      295                      300
Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys
      305                      310                      315

```

<210> 1300

<211> 323

<212> PRT

<213> Unknown (H38g217 protein)

<220>

<223> Synthetic construct

<400> 1300

```

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly
  1          5          10          15
Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met
      20          25          30
Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Val Leu
      35          40          45
Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg
      50          55          60
Asn Phe Ser Phe Leu Glu Leu Leu Leu Val Thr Val Val Val Pro Lys
      65          70          75          80
Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser
      85          90          95
Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe
      100          105          110
Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg
      115          120          125
Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu
      130          135          140
Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr
      145          150          155          160
Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His
      165          170          175
Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr
      180          185          190
His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu
      195          200          205
Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr
      210          215          220
Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr
      225          230          235          240
Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile
      245          250          255
Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

```

	260		265		270										
Gly	Ala	Ser	Val	Leu	Ser	Cys	Ile	Ile	Thr	Pro	Leu	Leu	Asn	Pro	Phe
	275						280						285		
Ile	Phe	Thr	Leu	Arg	Asn	Asp	Lys	Val	Gln	Gln	Ala	Leu	Arg	Glu	Ala
	290					295					300				
Leu	Gly	Trp	Pro	Arg	Leu	Thr	Ala	Val	Met	Lys	Leu	Arg	Val	Thr	Ser
305					310					315					320
Gln	Arg	Lys													

<210> 1301

<211> 338

<212> PRT

<213> Unknown (H38g218 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1301

Met	Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu
1				5					10					15	
Glu	Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val
			20					25					30		
His	Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile
		35					40					45			
Thr	Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe
	50					55					60				
Leu	Asn	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile
65					70					75					80
Pro	Lys	Leu	Leu	Val	Ile	Phe	Leu	Ser	Gly	Arg	Gln	Ile	Ile	Pro	Phe
				85					90					95	
Thr	Thr	Cys	Leu	Met	Gln	Ser	Phe	Ser	Phe	Leu	Phe	Leu	Gly	Ser	Thr
			100					105					110		
Val	Phe	Phe	Leu	Met	Ala	Val	Met	Ser	Leu	Asp	Xaa	Tyr	Leu	Ala	Ile
		115					120					125			
Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	Thr	Ser	Phe
	130					135					140				
His	Leu	Val	Thr	Val	Cys	Phe	Val	Val	Gly	Phe	Thr	Leu	Ile	Thr	Gly
145					150					155					160
Leu	Met	Val	Lys	Val	Ser	Gln	Leu	Ser	Phe	Cys	Gly	Pro	His	Val	Ile
				165					170					175	
Pro	His	Phe	Phe	Arg	Asp	Leu	Gly	Pro	Leu	Ile	Gln	Leu	Ser	Cys	Ser
			180					185					190		
Asp	Thr	Arg	Ser	Thr	Glu	Thr	Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Val
		195					200					205			
Leu	Phe	Thr	Ser	Leu	Ile	Ile	Thr	Ile	Ile	Ala	Tyr	Gly	Asn	Ile	Val
	210					215						220			
Val	Thr	Ile	Val	Arg	Leu	Pro	Ser	Ala	Lys	Glu	Arg	Gln	Lys	Ala	Phe
225					230					235					240
Ser	Thr	Cys	Ser	Ser	His	Leu	Ile	Val	Leu	Ser	Leu	Val	Tyr	Gly	Ser
				245					250					255	
Cys	Val	Phe	Ile	Tyr	Val	Lys	Pro	Lys	Gln	Met	Asp	Arg	Leu	Asp	Ser
		260						265					270		
Asn	Arg	Met	Ala	Ala	Leu	Val	Asn	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn
		275					280					285			
Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Gln	Val	His	Gln	Ala	Leu	Arg
	290					295						300			

Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln
 305 310 315 320
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe
 325 330 335
 Trp Asn

<210> 1302
 <211> 309
 <212> PRT
 <213> Unknown (H38g219 protein)

<220>
 <223> Synthetic construct

<400> 1302
 Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe
 1 5 10 15
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val
 20 25 30
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
 35 40 45
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu
 50 55 60
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile
 65 70 75 80
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu
 85 90 95
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu
 100 105 110
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala
 130 135 140
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val
 145 150 155 160
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met
 180 185 190
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser
 195 200 205
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg
 210 215 220
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser
 225 230 235 240
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr
 245 250 255
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu
 290 295 300
 Asn Pro Gly Arg Glu
 305

<210> 1303
 <211> 322
 <212> PRT
 <213> Unknown (H38g220 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
 20          25          30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
 35          40          45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65          70          75          80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
 85          90          95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
 100          105          110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115          120          125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
 130          135          140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
 145          150          155          160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
 165          170          175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
 180          185          190
Val Lys Glu Leu Met Leu Phe Ile Ile Ala Ala Phe Asn Val Phe Cys
 195          200          205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
 210          215          220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225          230          235          240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
 245          250          255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
 260          265          270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
 275          280          285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
 290          295          300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
 305          310          315          320
Glu Ile

```

<210> 1304

<211> 317

<212> PRT

<213> Unknown (H38g221 protein)

<220>

<223> Synthetic construct

<400> 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1          5          10          15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20          25          30
Val Cys Cys Leu Tyr Thr Il Ser Ile Met Gly Asn Thr Thr Ile Leu
          35          40          45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
          50          55          60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65          70          75          80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85          90          95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145          150          155          160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Leu Ile
          195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
          210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225          230          235          240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
          290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305          310          315

```

<210> 1305

<211> 315

<212> PRT

<213> Unknown (H38g222 protein)

<220>

<223> Synthetic construct

<400> 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20          25          30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35          40          45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50          55          60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
65          70          75          80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

```

```
<210> 1306
<211> 320
<212> PRT
<213> Unknown (H38g223 protein)
```

<220>
<223> Synthetic construct

622

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
 180 185 190
 Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
 195 200 205
 Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
 210 215 220
 Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
 245 250 255
 Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro
 260 265 270
 Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro
 275 280 285
 Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu
 290 295 300
 Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe
 305 310 315 320

<210> 1307

<211> 305

<212> PRT

<213> Unknown (H38g224 protein)

<220>

<223> Synthetic construct

<400> 1307

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
 1 5 10 15
 Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
 20 25 30
 Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
 35 40 45
 Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
 50 55 60
 Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
 65 70 75 80
 Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
 85 90 95
 Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
 100 105 110
 Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
 130 135 140
 Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
 165 170 175
 Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
 180 185 190
 Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
 195 200 205
 Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
 210 215 220
 Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser
 225 230 235 240
 His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
 245 250 255
 Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

260 265 270
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val
 290 295 300
 Ile
 305

<210> 1308
 <211> 313
 <212> PRT
 <213> Unknown (H38g225 protein)

<220>
 <223> Synthetic construct

<400> 1308
 Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu
 35 40 45
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu
 85 90 95
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val
 100 105 110
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu
 130 135 140
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser
 145 150 155 160
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His
 165 170 175
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val
 195 200 205
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser
 210 215 220
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu
 245 250 255
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg
 290 295 300
 Phe Met Thr Asn Leu Cys Tyr Ser Phe
 305 310

<210> 1309
 <211> 326
 <212> PRT

<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

```

Met Lys Ile Ser Asn Asn Ser Leu Gly Phe Leu Pro Thr Thr Phe Ile
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Ser Glu His Leu Trp Ile Ser Val
           20           25           30
Pro Phe Ser Leu Ile Tyr Ile Ile Phe Leu Gly Asn Gly Ile Ile
           35           40           45
Leu His Val Ile Arg Thr Asp Ile Ala Leu His Gln Pro Met Tyr Leu
           50           55           60
Phe Leu Ala Met Leu Ala Leu Ala Glu Val Arg Val Ser Ala Ser Thr
65           70           75           80
Leu Pro Thr Val Leu Gly Ile Phe Leu Phe Gly Asn Thr Glu Ile Ser
           85           90           95
Leu Glu Ala Phe Phe Phe Gln Met Phe Ser Ile His Ser Leu Ser Met
           100          105          110
Met Glu Ser Ala Val Leu Leu Ala Met Ser Leu Asp Arg Phe Ile Ala
           115          120          125
Ile Tyr Ser Pro Leu Ser Tyr Thr Ala Ile Leu Thr Leu Pro Arg Val
           130          135          140
Phe Gly Thr Gly Ala Ile Ile Val Leu Lys Ser Ile Met Leu Met Ala
145          150          155          160
Pro Leu Pro Ile Leu Leu Trp Arg Leu Pro Phe Cys Gly His Asn Ala
           165          170          175
Leu Ser His Ser Tyr Cys Leu His Pro Asn Leu Ile Tyr Leu Ser Cys
           180          185          190
Gly Asn Ile Ser Val Asn Asn Ile Tyr Gly Ile Phe Ile Val Thr Ser
           195          200          205
Thr Phe Gly Leu Asp Ser Leu Leu Ile Val Ile Ser Tyr Gly Leu Ile
           210          215          220
Leu His Thr Val Leu Gly Ile Ala Thr Gly Glu Gly Arg Lys Lys Ala
225          230          235          240
Leu Asn Thr Cys Gly Ser His Val Cys Ala Val Leu Ala Tyr Tyr Val
           245          250          255
Pro Met Ile Gly Leu Ser Ile Val His Arg Leu Gly His Arg Val Ser
           260          265          270
Pro Leu Leu Gln Ala Met Met Ala Asn Ala Tyr Leu Phe Phe Pro Pro
           275          280          285
Val Val Asn Pro Ile Val Tyr Ser Ile Lys Thr Lys Glu Ile His Gly
           290          295          300
Ala Ile Val Arg Met Leu Leu Glu Lys Arg Arg Arg Val Xaa Pro Lys
305          310          315          320
Thr Ile Val Gly Arg Asn
           325

```

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

<400> 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1      5      10      15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
 20      25      30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35      40      45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50      55      60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65      70      75      80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
 85      90      95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
100      105      110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
115      120      125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
130      135      140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
145      150      155      160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
165      170      175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
180      185      190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
195      200      205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
210      215      220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
225      230      235      240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
245      250      255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
260      265      270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
275      280      285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
290      295      300
Val Ala His Ser Gln Gly Glu
305      310

```

<210> 1311

<211> 312

<212> PRT

<213> Unknown (H38g228 protein)

<220>

<223> Synthetic construct

<400> 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
 20      25      30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
 35      40      45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
 50      55      60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
 65      70      75      80

```

```

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe
      85                      90                      95
Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met
      100                    105                    110
Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115                    120                    125
Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser
      130                    135                    140
Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro
      145                    150                    155                    160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val
      165                    170                    175
Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala
      180                    185                    190
Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile
      195                    200                    205
Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg
      210                    215                    220
Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn
      225                    230                    235                    240
Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala
      245                    250                    255
Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr
      260                    265                    270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
      275                    280                    285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Gln Ile
      290                    295                    300
Val Lys Ile Phe Val Gln Lys Glu
      305                    310

```

<210> 1312

<211> 303

<212> PRT

<213> Unknown (H38g229 protein)

<220>

<223> Synthetic construct

<400> 1312

```

Met Thr Glu Phe Ile Phe Leu Val Leu Ser Pro Asn Gln Glu Val Gln
  1                      5                      10                      15
Arg Val Cys Phe Val Ile Phe Leu Phe Leu Tyr Thr Ala Ile Val Leu
      20                    25                    30
Gly Asn Phe Leu Ile Val Leu Thr Val Met Thr Ser Arg Ser Leu Gly
      35                    40                    45
Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu Ser Phe Met Glu Ile Cys
      50                    55                    60
Tyr Ser Ser Ala Thr Ala Pro Lys Leu Ile Ser Asp Leu Leu Ala Glu
      65                    70                    75                    80
Arg Lys Val Ile Ser Trp Trp Gly Cys Met Ala Gln Leu Phe Phe Leu
      85                    90                    95
His Phe Phe Gly Gly Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr
      100                    105                    110
Asp His Tyr Val Ala Ile Cys Lys Pro Leu Ser Tyr Thr Thr Ile Met
      115                    120                    125
Asn Trp Gln Val Cys Thr Val Leu Val Gly Ile Ala Trp Val Gly Gly
      130                    135                    140
Phe Met His Ser Phe Ala Gln Ile Leu Leu Ile Phe His Leu Leu Phe
      145                    150                    155                    160
Cys Gly Pro Asn Val Ile Asn His Tyr Phe Cys Asp Leu Val Pro Leu

```

				165					170					175	
Leu	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Phe	Leu	Ile	Gly	Leu	Leu	Ile	Val
			180					185					190		
Ala	Asn	Gly	Gly	Thr	Leu	Ser	Val	Ile	Ser	Phe	Gly	Val	Leu	Leu	Ala
		195					200					205			
Ser	Tyr	Met	Val	Ile	Leu	Leu	His	Leu	Arg	Thr	Trp	Ser	Ser	Glu	Gly
	210					215					220				
Trp	Cys	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Phe	Ala	Val	Val	Ile
225					230					235				240	
Leu	Phe	Phe	Gly	Pro	Cys	Val	Phe	Asn	Ser	Leu	Arg	Pro	Ser	Thr	Thr
			245					250						255	
Leu	Pro	Ile	Asp	Lys	Met	Val	Ala	Val	Phe	Tyr	Thr	Val	Ile	Thr	Ala
			260					265					270		
Ile	Leu	Asn	Pro	Val	Ile	Tyr	Ser	Leu	Arg	Asn	Ala	Glu	Met	Arg	Lys
		275					280					285			
Ala	Met	Lys	Arg	Leu	Trp	Ile	Arg	Thr	Leu	Arg	Leu	Asn	Glu	Lys	
	290						295				300				

<210> 1313

<211> 316

<212> PRT

<213> Unknown (H38g230 protein)

<220>

<223> Synthetic construct

<400> 1313

Leu	Ile	Ala	Thr	Gly	Asn	Trp	Thr	Arg	Ile	Ser	Glu	Phe	Ile	Leu	Met
1				5					10					15	
Ser	Phe	Ser	Ser	Leu	Pro	Thr	Glu	Ile	Gln	Ser	Leu	Leu	Phe	Leu	Thr
			20					25					30		
Phe	Leu	Thr	Ile	Tyr	Leu	Val	Thr	Leu	Met	Gly	Asn	Cys	Leu	Ile	Ile
		35					40					45			
Leu	Val	Thr	Leu	Ala	Asp	Pro	Met	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe
	50					55					60				
Leu	Arg	Asn	Leu	Ser	Phe	Leu	Glu	Ile	Gly	Phe	Asn	Leu	Val	Ile	Val
65					70					75				80	
Pro	Lys	Met	Leu	Gly	Thr	Leu	Leu	Ala	Gln	Asp	Thr	Thr	Ile	Ser	Phe
				85					90					95	
Leu	Gly	Cys	Ala	Thr	Gln	Met	Tyr	Phe	Phe	Phe	Phe	Phe	Gly	Val	Ala
			100					105					110		
Glu	Cys	Phe	Leu	Gln	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile
		115					120					125			
Cys	Ser	Pro	Leu	His	Tyr	Pro	Val	Ile	Met	Asn	Gln	Arg	Thr	Arg	Ala
		130				135					140				
Lys	Leu	Ala	Ala	Ala	Ser	Trp	Phe	Pro	Gly	Phe	Pro	Val	Ala	Thr	Val
145					150					155				160	
Gln	Thr	Thr	Trp	Leu	Phe	Ser	Phe	Pro	Phe	Cys	Gly	Thr	Asn	Lys	Val
			165					170					175		
Asn	His	Phe	Phe	Cys	Asp	Ser	Pro	Pro	Val	Leu	Arg	Leu	Val	Cys	Ala
			180					185					190		
Asp	Thr	Ala	Leu	Phe	Glu	Ile	Tyr	Ala	Ile	Val	Gly	Thr	Ile	Leu	Val
		195					200					205			
Val	Met	Ile	Pro	Cys	Leu	Leu	Ile	Leu	Cys	Ser	Tyr	Thr	Arg	Ile	Ala
	210					215					220				
Ala	Ala	Ile	Leu	Lys	Ile	Pro	Ser	Ala	Lys	Gly	Lys	Asn	Lys	Ala	Phe
225					230					235				240	
Ser	Thr	Cys	Ser	Ser	His	Leu	Leu	Val	Val	Ser	Leu	Phe	Tyr	Ile	Ser
				245					250					255	
Leu	Ser	Leu	Thr	Tyr	Phe	Arg	Pro	Lys	Ser	Asn	Asn	Ser	Pro	Glu	Gly
			260					265					270		

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser
 290 295 300
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu
 305 310 315

<210> 1314
 <211> 309
 <212> PRT
 <213> Unknown (H38g231 protein)

<220>
 <223> Synthetic construct

<400> 1314
 Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr
 1 5 10 15
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val
 20 25 30
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser
 35 40 45
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu
 65 70 75 80
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu
 85 90 95
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu
 115 120 125
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser
 130 135 140
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile
 180 185 190
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu
 210 215 220
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr
 290 295 300
 Lys Thr Tyr Val Arg
 305

<210> 1315
 <211> 320
 <212> PRT
 <213> Unknown (H38g232 protein)

<220>

<223> Synthetic construct

<400> 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Leu
 35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
 50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
 65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
          145          150          155          160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
          225          230          235          240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
          305          310          315          320

```

<210> 1316

<211> 312

<212> PRT

<213> Unknown (H38g233 protein)

<220>

<223> Synthetic construct

<400> 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Thr Val Gly Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe
 85 90 95
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu
 100 105 110
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu
 130 135 140
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr
 145 150 155 160
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His
 165 170 175
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr
 180 185 190
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile
 195 200 205
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala
 210 215 220
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe
 245 250 255
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val
 260 265 270
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp
 290 295 300
 Asn Asn Leu Cys Asn Ile Phe Val
 305 310

<210> 1317

<211> 315

<212> PRT

<213> Unknown (H38g234 protein)

<220>

<223> Synthetic construct

<400> 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser
 1 5 10 15
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe
 20 25 30
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu
 35 40 45
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu
 50 55 60
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Ala Ala Glu
 100 105 110
 Cys Cys Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

130	135	140
Leu Ala Ala Ala Ser Trp	Phe Ser Gly Phe Ser	Val Ala Thr Val Gln
145	150	155
Thr Thr Trp Ile Phe Ser	Phe Pro Phe Cys Gly	Pro Asn Arg Val Asn
165	170	175
His Phe Phe Cys Asp Ser	Pro Pro Val Ile Ala	Leu Val Cys Ala Asp
180	185	190
Thr Ser Val Phe Glu Leu	Glu Ala Leu Thr Ala	Thr Val Pro Phe Ile
195	200	205
Leu Phe Pro Phe Leu Leu	Ile Leu Gly Ser Tyr	Val Arg Ile Leu Ser
210	215	220
Thr Ile Phe Arg Met Pro	Ser Ala Glu Gly Lys	His Gln Ala Phe Ser
225	230	235
Thr Cys Ser Ala His Leu	Leu Val Val Ser Leu	Phe Tyr Ser Thr Ala
245	250	255
Ile Leu Thr Tyr Phe Arg	Pro Gln Ser Ser Ala	Ser Ser Glu Ser Lys
260	265	270
Lys Leu Leu Ser Leu Ser	Ser Thr Val Val Thr	Pro Met Leu Asn Pro
275	280	285
Ile Ile Tyr Ser Ser Arg	Asn Lys Glu Val Lys	Ala Ala Leu Lys Arg
290	295	300
Leu Ile His Arg Thr Leu	Gly Ser Gln Lys Leu	
305	310	315

<210> 1318

<211> 310

<212> PRT

<213> Unknown (H38g235 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1318

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
1 5 10 15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
20 25 30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
35 40 45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
50 55 60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ile Thr Pro Asn
65 70 75 80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
85 90 95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
100 105 110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115 120 125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
130 135 140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
145 150 155 160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
165 170 175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
180 185 190

His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Ph
 195 200 205
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly
 245 250 255
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp
 260 265 270
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile
 275 280 285
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met
 290 295 300
 Glu Asn Leu Cys Leu Thr
 305 310

<210> 1319

<211> 184

<212> PRT

<213> Unknown (H38g236 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(184)

<223> Xaa = Any Amino Acid

<400> 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
 1 5 10 15
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
 20 25 30
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
 35 40 45
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
 50 55 60
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
 65 70 75 80
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His
 85 90 95
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile
 100 105 110
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His
 115 120 125
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val
 130 135 140
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys
 145 150 155 160
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr
 165 170 175
 Val Tyr Leu Gln Pro Asp Phe Phe
 180

<210> 1320

<211> 321

<212> PRT

<213> Unknown (H38g237 protein)

<220>

<223> Synthetic construct

<400> 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
 20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
 35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
 50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
 65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
 85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
 100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
 130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
 145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
 165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
 180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
 195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
 210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
 225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
 245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
 260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
 275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
 290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
 305          310          315          320
Lys

```

<210> 1321

<211> 134

<212> PRT

<213> Unknown (H38g238 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```

Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg
 20 25 30
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln
 35 40 45
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser
 50 55 60
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly
 65 70 75 80
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln
 85 90 95
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser
 100 105 110
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Lys Xaa Ser Gly Glu Arg
 115 120 125
 Ser Ser Phe Pro Arg Glu
 130

<210> 1322

<211> 318

<212> PRT

<213> Unknown (H38g239 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr
 1 5 10 15
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro
 20 25 30
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn
 35 40 45
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser
 65 70 75 80
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys
 85 90 95
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val
 100 105 110
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro
 130 135 140
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile
 145 150 155 160
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala
 180 185 190
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe
 195 200 205
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr
 210 215 220
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg
 225 230 235 240
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

<210> 1324

<211> 313
 <212> PRT
 <213> Unknown (H38g241 protein)

<220>
 <223> Synthetic construct

<400> 1324

```

Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys
          50           55           60
Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe
          85           90           95
Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met
          100          105          110
Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
          130          135          140
Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro
145          150          155          160
Leu Val Phe Leu Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
          180          185          190
Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu
          195          200          205
Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr
          210          215          220
Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225          230          235          240
Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala
          245          250          255
Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr
          260          265          270
Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu
          275          280          285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val
          290          295          300
Leu Arg Ile Phe Phe Lys Thr Asp His
305          310

```

<210> 1325
 <211> 328
 <212> PRT
 <213> Unknown (H38g242 protein)

<220>
 <223> Synthetic construct

<400> 1325

```

Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr
 1           5           10           15
Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

```

      20      25      30
Gln Thr Ile Phe Phe Phe Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu
      35      40      45
Met Gly Asn Leu Gly Leu Ile Leu Val Val Ile Arg Asp Ser Gln Leu
      50      55      60
His Lys Pro Met Tyr Tyr Phe Leu Ser Met Leu Ser Ser Val Asp Ala
      65      70      75      80
Cys Tyr Ser Ser Val Ile Thr Pro Asn Met Leu Val Asp Phe Thr Thr
      85      90      95
Lys Asn Lys Val Ile Ser Phe Leu Gly Cys Val Ala Gln Val Phe Leu
      100      105      110
Ala Cys Ser Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala
      115      120      125
Tyr Asp Arg Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser
      130      135      140
Met Ser Pro Arg Val Tyr Met Pro Leu Ile Asn Ala Ser Tyr Val Ala
      145      150      155      160
Gly Ile Leu His Ala Thr Ile His Thr Val Ala Thr Phe Ser Leu Ser
      165      170      175
Phe Cys Gly Ala Asn Glu Ile Arg Arg Val Phe Cys Asp Ile Pro Pro
      180      185      190
Leu Leu Ala Ile Ser Tyr Ser Asp Thr His Thr Asn Gln Leu Leu Leu
      195      200      205
Phe Tyr Phe Val Gly Ser Ile Glu Leu Val Thr Ile Leu Ile Val Leu
      210      215      220
Ile Ser Tyr Gly Leu Ile Leu Leu Ala Ile Leu Lys Met Tyr Ser Ala
      225      230      235      240
Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly
      245      250      255
Val Ser Ile Tyr Tyr Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser
      260      265      270
Ser Ser Tyr Ala Ser Asp His Asp Met Ile Val Ser Ile Phe Tyr Thr
      275      280      285
Ile Val Ile Pro Leu Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys
      290      295      300
Asp Val Lys Asp Ser Met Lys Lys Met Phe Gly Lys Asn Gln Val Ile
      305      310      315      320
Asn Lys Val Tyr Phe His Thr Lys
      325

```

<210> 1326

<211> 329

<212> PRT

<213> Unknown (H38g243 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1326

```

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
  1           5           10           15
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
      20      25      30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile
      35      40      45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe
      50      55      60

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```

Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val
65          70          75          80
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe
      85          90          95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met
      100        105        110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
      115        120        125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr
      130        135        140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro
145          150          155          160
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile
      165        170        175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly
      180        185        190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile
      195        200        205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile
      210        215        220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro
      245        250        255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
      260        265        270
His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
      275        280        285
Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
      290        295        300
Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
305          310          315          320
Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
      325

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<210> 1327

<211> 301

<212> PRT

<213> Unknown (H38g244 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 1327

```

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
1          5          10          15
Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
      20          25          30
Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
      35          40          45
Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
      50          55          60
Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
65          70          75          80
Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
      85          90          95
Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

```

100	105	110
Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr		
115	120	125
Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe		
130	135	140
Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val		
145	150	155
Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp		
165	170	175
Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly		
180	185	190
Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile		
195	200	205
Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser		
210	215	220
Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val		
225	230	235
Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr		
245	250	255
Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu		
260	265	270
Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met		
275	280	285
Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu		
290	295	300

<210> 1328

<211> 324

<212> PRT

<213> Unknown (H38g245 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1328

Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr	
1 5 10 15	
Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe	
20 25 30	
Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala	
35 40 45	
Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu	
50 55 60	
Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro	
65 70 75 80	
Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp	
85 90 95	
Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu	
100 105 110	
Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr	
115 120 125	
Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys	
130 135 140	
Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu	
145 150 155 160	
Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser	
165 170 175	


```

His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp
      180      185      190
Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe
      195      200      205
Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr
      210      215      220
Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn
      225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met
      245      250      255
Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile
      260      265      270
Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu
      275      280      285
Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile
      290      295      300
Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg
      305      310      315      320
Ser Gln Glu Leu

```

<210> 1329

<211> 292

<212> PRT

<213> Unknown (H38g246 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(292)

<223> Xaa = Any Amino Acid

<400> 1329

```

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu
  1           5           10           15
Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln
      20           25           30
Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr
      35           40           45
Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe
      50           55           60
Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu
      65           70           75           80
Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg
      85           90           95
Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile
      100          105          110
Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu
      115          120          125
Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His
      130          135          140
Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val
      145          150          155          160
Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile
      165          170          175
Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu
      180          185          190
Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys
      195          200          205
Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

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210	215	220
Xaa Tyr Thr Ala Trp	Xaa Lys His Pro Cys Tyr	Ile Arg Ile Phe Leu
225	230	235
Ala Asn Val Tyr Thr	Val Val Leu Pro Val Phe	Asn Pro Val Ile Tyr
245	250	255
Gly Ile Arg Lys Lys	Gln Ile Pro Asp Xaa	Gly Ile Asp Leu Lys Thr
260	265	270
Phe Asp Asp Gln Ser	Leu Leu Val Met Met	Ile Tyr Ile Leu Gly Tyr
275	280	285
Ile Cys Lys Tyr		
290		

<210> 1330

<211> 312

<212> PRT

<213> Unknown (H38g247 protein)

<220>

<223> Synthetic construct

<400> 1330

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly	
1	5 10 15
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Phe Leu Phe Phe Ser	
20	25 30
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr	
35	40 45
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala	
50	55 60
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys	
65	70 75 80
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly	
85	90 95
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met	
100	105 110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys	
115	120 125
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe	
130	135 140
Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu	
145	150 155 160
Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser	
165	170 175
Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr	
180	185 190
Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu	
195	200 205
Ala Ser Phe Leu Ile Leu Ile Ser Tyr Ile Phe Ile Leu Val Thr	
210	215 220
Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu	
225	230 235 240
Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe	
245	250 255
Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala	
260	265 270
Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr	
275	280 285
Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln	
290	295 300
Phe Val Asn Tyr Ser Lys Ile Phe	
305	310

<210> 1331
 <211> 168
 <212> PRT
 <213> Unknown (H38g248 protein)

<220>
 <223> Synthetic construct

<400> 1331
 Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1 5 10 15
 Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
 20 25 30
 Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
 35 40 45
 Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
 65 70 75 80
 Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
 85 90 95
 Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
 100 105 110
 Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
 115 120 125
 Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
 130 135 140
 Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
 145 150 155 160
 Thr Met Ala Leu Ala Ala Pro Leu
 165

<210> 1332
 <211> 321
 <212> PRT
 <213> Unknown (H38g249 protein)

<220>
 <223> Synthetic construct

<400> 1332
 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu
 1 5 10 15
 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro
 20 25 30
 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu
 35 40 45
 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile
 65 70 75 80
 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe
 85 90 95
 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met
 100 105 110
 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala
 130 135 140
 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro

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145          150          155          160
Phe Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu
      165      170
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly
      180      185      190
Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
      195      200      205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
      210      215      220
Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
225      230      235      240
Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
      245      250      255
Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
      260      265      270
Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
      275      280      285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
      290      295      300
Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
305      310      315      320
Met

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<210> 1333

<211> 315

<212> PRT

<213> Unknown (H38g250 protein)

<220>

<223> Synthetic construct

<400> 1333

```

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
 1          5          10          15
Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
      20      25      30
Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
      35      40      45
Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
      50      55      60
Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr
65      70      75      80
Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
      85      90      95
Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
      100      105      110
Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
      130      135      140
Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
145      150      155      160
Leu Pro Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn
      165      170      175
Val Ile Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser
      180      185      190
Cys Asp Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp
      195      200      205
Thr Leu Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe
210      215      220

```

Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys
 225 230 235 240
 Ala Leu Ser Thr Cys Gly Ser His Phe M t Leu Ile Leu Phe Phe Ser
 245 250 255
 Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val
 260 265 270
 Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro
 275 280 285
 Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys
 290 295 300
 Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys
 305 310 315

<210> 1334

<211> 302

<212> PRT

<213> Unknown (H38g251 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(302)

<223> Xaa = Any Amino Acid

<400> 1334

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu
 1 5 10 15
 Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu
 20 25 30
 Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu
 35 40 45
 Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val
 65 70 75 80
 Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe
 85 90 95
 Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr
 100 105 110
 Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val
 115 120 125
 Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu
 130 135 140
 Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile
 145 150 155 160
 Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys
 165 170 175
 Tyr Phe Ser Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met
 180 185 190
 Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser
 195 200 205
 Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro
 210 215 220
 Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu
 225 230 235 240
 Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys
 245 250 255
 Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
 260 265 270
 Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

275 280 285
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pr Leu Leu
 290 295 300

<210> 1335
 <211> 324
 <212> PRT
 <213> Unknown (H38g252 protein)

<220>
 <223> Synthetic construct

<400> 1335
 Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
 1 5 10 15
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His
 20 25 30
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
 35 40 45
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
 50 55 60
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
 65 70 75 80
 Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
 85 90 95
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
 100 105 110
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala
 115 120 125
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg
 145 150 155 160
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn
 275 280 285
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320
 Lys Gly Ala Gly

<210> 1336
 <211> 274
 <212> PRT
 <213> Unknown (H38g253 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 1336

```

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1          5          10          15
Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
 20          25          30
Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
 35          40          45
Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
 50          55          60
Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
 65          70          75          80
Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
 85          90          95
Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
100          105          110
Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
115          120          125
Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
130          135          140
Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
145          150          155          160
Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
165          170          175
Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
180          185          190
Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
195          200          205
Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
210          215          220
Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
225          230          235          240
Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
245          250          255
Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
260          265          270
Ile Leu

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<210> 1337

<211> 315

<212> PRT

<213> Unknown (H38g254 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1337

```

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

```

Val 1	Glu	Asn	Ser	Pro 5	Met	Val	Thr	Asp	Phe 10	Ile	Phe	Leu	Gly	Met 15	Thr
Asp	Asn	Ser	Gln 20	Leu	Glu	Val	Leu	Leu 25	Phe	Gly	Val	Phe	Leu 30	Ile	Ala
Tyr	Ile	Ile 35	Thr	Val	Leu	Glu	Asn 40	Leu	Gly	Leu	Val	Val 45	Leu	Ile	Arg
Val	Ser 50	Ser	Arg	Leu	His	Thr 55	Pro	Met	Tyr	Phe	Phe 60	Leu	Ser	Asn	Gln
Ser 65	Phe	Leu	Asp	Val	Cys 70	Phe	Ser	Ser	Ile	Thr 75	Ile	Pro	Gln	Asn 80	Leu

Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr
 85 90 95
 Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe
 100 105 110
 Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu
 115 120 125
 Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala
 130 135 140
 Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser
 145 150 155 160
 Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe
 165 170 175
 Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile
 180 185 190
 Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr
 195 200 205
 Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile
 210 215 220
 Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr
 245 250 255
 Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile
 260 265 270
 Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu
 290 295 300
 Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile
 305 310 315 320
 Leu Xaa Arg

<210> 1339

<211> 311

<212> PRT

<213> Unknown (H38g256 protein)

<220>

<223> Synthetic construct

<400> 1339

Trp Leu Asp Glu Lys Lys Gln Asp Ser Asn Val Thr Glu Leu Val Leu
 1 5 10 15
 Leu Gly Leu Ser Ser Ser Trp Glu Leu Gln Leu Phe Leu Leu Leu Leu
 20 25 30
 Phe Leu Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val
 35 40 45
 Val Thr Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr
 50 55 60
 Phe Leu Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr
 65 70 75 80
 Leu Pro Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser
 85 90 95
 Phe Ser Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala
 100 105 110
 Ser Glu Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu Arg Tyr Leu Ile Ile Met Asn Pro Gln Leu Cys
 130 135 140
 Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
          165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
          180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
          195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
          210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
          225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
          245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
          260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
          290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

<210> 1340

<211> 318

<212> PRT

<213> Unknown (H38g257 protein)

<220>

<223> Synthetic construct

<400> 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1      5      10      15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20     25     30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35     40     45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50     55     60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65     70     75     80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85     90     95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100    105    110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115    120    125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130    135    140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145    150    155    160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165    170    175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180    185    190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195    200    205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210    215    220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225    230    235    240

```

```
<210> 1341
<211> 320
<212> PRT
<213> Unknown (H38g258 protein)
```

```
<221> VARIANT
<222> (1)...(320)
<223> Xaa = Any Amino Acid
```

651

290 295 300
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile
 305 310 315 320

<210> 1342
 <211> 309
 <212> PRT
 <213> Unknown (H38g259 protein)

<220>
 <223> Synthetic construct

<400> 1342
 Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1 5 10 15
 Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
 20 25 30
 Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile
 35 40 45
 Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu
 65 70 75 80
 Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
 130 135 140
 Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met
 145 150 155 160
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe
 165 170 175
 Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu
 180 185 190
 Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu
 195 200 205
 Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser
 210 215 220
 Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met
 225 230 235 240
 Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His
 245 250 255
 Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr
 260 265 270
 Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 275 280 285
 Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp
 290 295 300
 Pro Lys Glu Ile Leu
 305

<210> 1343
 <211> 331
 <212> PRT
 <213> Unknown (H38g260 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Leu Val Phe Val Leu Val Leu
           20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
           35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
           50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
           85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
           100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
           115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
           130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
           165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
           180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
           195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
           210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
           245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
           260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
           275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
           290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
           325          330

```

<210> 1344

<211> 315

<212> PRT

<213> Unknown (H38g261 protein)

<220>

<223> Synthetic construct

<400> 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

```

      20      25      30
Ph  Thr Ala Val Tyr Val Phe Ile Ile Gly Asn Met Leu Ile Ile
   35      40      45
Val Ala Val Val Ser Ser Gln Arg Leu His Lys Pro Met Tyr Ile Phe
   50      55      60
Leu Ala Asn Leu Ser Phe Leu Asp Ile Leu Tyr Thr Ser Ala Val Met
  65      70      75      80
Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser Val Ala
      85      90      95
Gly Cys Leu Leu Gln Phe Phe Ile Phe Gly Ser Leu Ala Thr Ala Glu
   100      105      110
Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
   115      120      125
Tyr Pro Leu His Tyr Pro Leu Leu Met Gly Pro Arg Arg Tyr Met Gly
   130      135      140
Leu Val Val Thr Thr Trp Leu Ser Gly Phe Val Val Asp Gly Leu Val
  145      150      155      160
Val Ala Leu Val Ala Gln Leu Arg Phe Cys Gly Pro Asn His Ile Asp
      165      170      175
Gln Phe Tyr Cys Asp Phe Met Leu Phe Val Gly Leu Ala Cys Ser Asp
   180      185      190
Pro Arg Val Ala Gln Val Thr Thr Leu Ile Leu Ser Val Phe Cys Leu
   195      200      205
Thr Ile Pro Phe Gly Leu Ile Leu Thr Ser Tyr Ala Arg Ile Val Val
  210      215      220
Ala Val Leu Arg Val Pro Ala Gly Ala Ser Arg Arg Arg Ala Phe Ser
  225      230      235      240
Thr Cys Ser Ser His Leu Ala Val Val Thr Thr Phe Tyr Gly Thr Leu
      245      250      255
Met Ile Phe Tyr Val Ala Pro Ser Ala Val His Ser Gln Leu Leu Ser
   260      265      270
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Phe Asn Pro
   275      280      285
Val Ile Tyr Thr Met Arg Asn Lys Glu Val His Gln Ala Leu Arg Lys
   290      295      300
Ile Leu Cys Ile Lys Gln Thr Glu Thr Leu Asp
  305      310      315

```

<210> 1345

<211> 312

<212> PRT

<213> Unknown (H38g262 protein)

<220>

<223> Synthetic construct

<400> 1345

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
  1      5      10      15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
   20      25      30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
   35      40      45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
   50      55      60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
  65      70      75      80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
      85      90      95
Ala Leu Gln Met Phe Phe Ph Leu Phe Phe Gly Ala Thr Glu Cys Cys
   100      105      110

```

```

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
  115                      120                      125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
  130                      135                      140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
  145                      150                      155                      160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
  165                      170                      175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
  180                      185                      190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
  195                      200                      205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
  210                      215                      220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
  225                      230                      235                      240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
  245                      250                      255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
  260                      265                      270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
  275                      280                      285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
  290                      295                      300
Gln Lys Thr Val Pro Met Glu Ile
  305                      310

```

<210> 1346

<211> 316

<212> PRT

<213> Unknown (H38g263 protein)

<220>

<223> Synthetic construct

<400> 1346

```

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
  1           5           10           15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
  20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val
  35           40           45
Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
  50           55           60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
  65           70           75           80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
  85           90           95
Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
  100          105          110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
  115          120          125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
  130          135          140
Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
  145          150          155          160
Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
  165          170          175
Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
  180          185          190
Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

```

195	200	205
Leu Ser Leu Ile Leu Ala Ser	Tyr Gly Ala Thr Ala Gln Ala Val Leu	
210	215	220
Arg Ile Asn Ser Ala Thr	Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser	
225	230	235
Ser His Leu Thr Val Val Thr	Leu Phe Tyr Ser Ser Val Ile Ala Val	
245	250	255
Tyr Leu Gln Pro Lys Asn Pro	Tyr Ala Gln Gly Arg Gly Lys Phe Phe	
260	265	270
Gly Leu Phe Tyr Ala Val Gly	Thr Pro Ser Leu Asn Pro Leu Val Tyr	
275	280	285
Thr Leu Arg Asn Lys Glu Ile	Lys Arg Ala Leu Arg Arg Leu Leu Gly	
290	295	300
Lys Glu Arg Asp Ser Arg Glu	Ser Trp Arg Ala Ala	
305	310	315

<210> 1347

<211> 318

<212> PRT

<213> Unknown (H38g264 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1347

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile	
1	15
Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe	
20	30
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met	
35	45
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe	
50	60
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile	
65	80
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr	
85	95
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr	
100	110
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile	
115	125
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Ala Cys Val	
130	140
Cys Leu Val Val Gly Ser Ile Cys Gly Cys Ile Asn Ser Met Ile	
145	160
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu	
165	175
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile	
180	190
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile	
195	205
Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser	
210	220
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser	
225	240
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val	
245	255

Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Il
 260 265 270
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys
 290 295 300
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile
 305 310 315

<210> 1348

<211> 177

<212> PRT

<213> Unknown (H38g265 protein)

<220>

<223> Synthetic construct

<400> 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu
 1 5 10 15
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro
 20 25 30
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 35 40 45
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val
 50 55 60
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu
 65 70 75 80
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly
 85 90 95
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val
 100 105 110
 Leu Leu Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro
 115 120 125
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr
 130 135 140
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys
 145 150 155 160
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile
 165 170 175
 Ser

<210> 1349

<211> 322

<212> PRT

<213> Unknown (H38g266 protein)

<220>

<223> Synthetic construct

<400> 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65          70          75          80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
          85          90          95
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
          130          135          140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145          150          155          160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
          165          170          175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
          180          185          190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Gly Val
          195          200          205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
          210          215          220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
          245          250          255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
          260          265          270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
          290          295          300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
305          310          315          320
Lys Arg

```

<210> 1350
 <211> 322
 <212> PRT
 <213> Unknown (H38g267 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(322)
 <223> Xaa = Any Amino Acid

```

<400> 1350
Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
  1          5          10          15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
          20          25          30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
          85          90          95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
          100          105          110

```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Gln Val Il Met Ser Pro Arg Leu Cys Gly Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp
 180 185 190
 Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly
 195 200 205
 Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
 210 215 220
 Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala
 245 250 255
 Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly
 260 265 270
 Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg
 290 295 300
 Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys
 305 310 315 320
 Ser Ile

<210> 1351

<211> 308

<212> PRT

<213> Unknown (H38g268 protein)

<220>

<223> Synthetic construct

<400> 1351

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
 20 25 30
 Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ser Leu
 35 40 45
 Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln
 65 70 75 80
 Ala Leu Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu
 85 90 95
 Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
 100 105 110
 Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu
 130 135 140
 Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
 145 150 155 160
 Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
 165 170 175
 Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

180 185 190
 His Ala Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu
 195 200 205
 Ile Pro Val Phe Leu Ile Leu Val S r Tyr Gly Arg Ile Ile Val Thr
 210 215 220
 Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile
 245 250 255
 Ile Thr Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val
 260 265 270
 Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
 290 295 300
 Arg Asn Phe Pro
 305

<210> 1352

<211> 321

<212> PRT

<213> Unknown (H38g269 protein)

<220>

<223> Synthetic construct

<400> 1352

Met Pro Ile Leu Met Ala Ile Gly Asn Trp Thr Glu Ile Ser Glu Phe
 1 5 10 15
 Ile Leu Met Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu
 20 25 30
 Phe Leu Thr Phe Leu Thr Ile Tyr Leu Val Thr Leu Lys Gly Asn Ser
 35 40 45
 Leu Ile Ile Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met
 50 55 60
 Tyr Phe Phe Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu
 65 70 75 80
 Val Ile Val Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr
 85 90 95
 Ile Ser Phe Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Phe
 100 105 110
 Gly Val Ala Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
 115 120 125
 Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
 130 135 140
 Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
 145 150 155 160
 Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
 165 170 175
 Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Lys Leu
 180 185 190
 Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
 195 200 205
 Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
 210 215 220
 Arg Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys His
 225 230 235 240
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
 245 250 255
 Tyr Ile Ser Ser Ser Leu Thr Tyr Phe Trp Pro Lys Ser Asn Asn Ser
 260 265 270

Pro Glu Ser Lys Lys Leu Leu Ser L u Ser Tyr Thr Val Val Thr Pro
 275 280 285
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn
 290 295 300
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile
 305 310 315 320
 Pro

<210> 1353

<211> 260

<212> PRT

<213> Unknown (H38g270 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro
 1 5 10 15
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met
 20 25 30
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu
 35 40 45
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys
 50 55 60
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly
 65 70 75 80
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gln Leu Leu Gly His
 85 90 95
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp
 100 105 110
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser
 115 120 125
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val
 130 135 140
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg
 145 150 155 160
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly
 165 170 175
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile
 180 185 190
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly
 195 200 205
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg
 225 230 235 240
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His
 245 250 255
 Leu Thr Ser Leu
 260

<210> 1354

<211> 329

<212> PRT

<213> Unknown (H38g271 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1354

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Glu Glu Ile Leu Xaa Ile Ile Ser Gln His Val His Thr Gly Cys Val
 1           5           10           15
Gln Asn Xaa Glu Leu Gln Pro Ile Leu Phe Gly Leu Phe Leu Ser Met
 20           25           30
Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser
 35           40           45
Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe Phe Leu Ser Asn Leu
 50           55           60
Ser Leu Ala Asp Ile Gly Phe Pro Ser Thr Thr Val Pro Lys Met Ile
 65           70           75           80
Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
 85           90           95
Thr Gln Ile Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
 100          105          110
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 115          120          125
Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 130          135          140
Leu Ser Phe Phe Leu Ser Leu Leu Asp Phe Gln Leu His Asn Trp Ile
 145          150          155          160
Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Ser Phe Phe
 165          170          175
Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
 180          185          190
Asn Asn Ile Val Met Tyr Phe Leu Ala Ala Ile Leu Gly Phe Leu Pro
 195          200          205
Ile Ser Gly Ile Phe Tyr Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
 210          215          220
Lys Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
 225          230          235          240
Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly
 245          250          255
Tyr Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
 260          265          270
Ser Val Met Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Tyr
 275          280          285
Ser Leu Arg Lys Arg Asp Ile Lys Ser Ala Leu Gln Gln Leu His Gly
 290          295          300
Arg Ile Val Xaa Ser His Asp Leu Ile Ile Gly Ser Ile Leu Xaa Pro
 305          310          315          320
Trp Val Gly Lys Gly Ser Lys Val Lys
 325

```

<210> 1355

<211> 321

<212> PRT

<213> Unknown (H38g272 protein)

<220>

<223> Synthetic construct

<400> 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
          20          25          30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
          35          40          45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
65          70          75          80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
          85          90          95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
          100          105          110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
          130          135          140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
145          150          155          160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
          165          170          175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
          180          185          190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
          195          200          205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
          210          215          220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
225          230          235          240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
          245          250          255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
          260          265          270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
          275          280          285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
          290          295          300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
305          310          315          320
Glu

```

<210> 1356

<211> 327

<212> PRT

<213> Unknown (H38g273 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1356

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Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Leu Phe Ala
          20          25          30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

<400> 1357																
Met	Glu	Ala	Gly	Asn	Gln	Thr	Gly	Phe	Leu	Glu	Phe	Ile	Leu	Leu	Gly	
1				5					10					15		
Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Phe	Ile	Phe	Gly	Leu	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
		50				55					60					
Asn	Leu	Ser	Trp	Val	Asp	Ile	Cys	Phe	Ser	Thr	Cys	Ile	Val	Pro	Lys	
65					70					75					80	
Met	Leu	Val	Asn	Ile	Gln	Thr	Glu	Asn	Lys	Ala	Ile	Ser	Tyr	Met	Asp	
				85					90					95		
Cys	Leu	Thr	Gln	Val	Tyr	Phe	Ser	Met	Phe	Phe	Pro	Ile	Leu	Asp	Thr	
			100					105					110			

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu
 130 135 140
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile
 145 150 155 160
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val
 195 200 205
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser
 210 215 220
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu
 290 295 300
 Leu Ser Arg Ala Ala Ser Cys Leu
 305 310

<210> 1358

<211> 320

<212> PRT

<213> Unknown (H38g275 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu
 1 5 10 15
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu
 35 40 45
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu
 50 55 60
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile
 65 70 75 80
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr
 85 90 95
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met
 100 105 110
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly
 130 135 140
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro
 145 150 155 160
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

```
<210> 1359
<211> 316
<212> PRT
<213> Unknown (H38a276 protein)
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<220>
<223> Synthetic construct

Met 1	Glu	Leu	Trp	Asn 5	Phe	Thr	Leu	Gly	Ser 10	Gly	Phe	Ile	Leu	Val 15	Gly
Ile	Leu	Asn 20	Asp	Ser	Gly	Ser	Pro	Glu 25	Leu	Leu	Cys	Ala	Thr 30	Ile	Thr
Ile	Leu	Tyr 35	Leu	Leu	Ala	Leu	Ile 40	Ser	Asn	Gly	Leu	Leu	Leu	Leu	Ala
Ile	Thr 50	Met	Glu	Ala	Arg	Leu 55	His	Met	Pro	Met	Tyr 60	Leu	Leu	Leu	Gly
Gln 65	Leu	Ser	Leu	Met	Asp 70	Leu	Leu	Phe	Thr	Ser 75	Val	Val	Thr	Pro	Lys
Ala	Leu	Ala	Asp	Phe 85	Leu	Arg	Arg	Glu	Asn 90	Thr	Ile	Ser	Phe	Gly 95	Gly
Cys	Ala	Leu	Gln 100	Met	Phe	Leu	Ala 105	Leu	Thr	Met	Gly	Gly	Ala	Glu	Asp
Leu	Leu	Leu 115	Ala	Phe	Met	Ala	Tyr 120	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
Pro	Leu 130	Thr	Tyr	Met	Thr	Leu 135	Met	Ser	Ser	Arg	Ala 140	Cys	Trp	Leu	Met
Val 145	Ala	Thr	Ser	Trp	Ile 150	Leu	Ala	Ser	Leu	Ser 155	Ala	Leu	Ile	Tyr	Thr
Val	Tyr	Thr	Met	His 165	Tyr	Pro	Phe	Cys	Arg 170	Ala	Gln	Glu	Ile	Arg	His
Leu	Leu	Cys	Glu 180	Ile	Pro	His	Leu 185	Leu	Lys	Val	Ala	Cys	Ala	Asp	Thr
Ser	Arg	Tyr 195	Glu	Leu	Met	Val	Tyr 200	Val	Met	Gly	Val	Thr 205	Phe	Leu	Ile
Pro	Ser 210	Leu	Ala	Ala	Ile	Leu 215	Ala	Ser	Tyr	Thr	Gln 220	Ile	Leu	Leu	Thr
Val 225	Leu	His	Met	Pro	Ser 230	Asn	Glu	Gly	Arg	Lys 235	Lys	Ala	Leu	Val	Thr
Cys	Ser	Ser	His 245	Leu	Thr	Val	Val	Gly	Met 250	Phe	Tyr	Gly	Ala	Ala	Thr

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 1360

<211> 312

<212> PRT

<213> Unknown (H38g277 protein)

<220>

<223> Synthetic construct

<400> 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn
 100 105 110
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu
 130 135 140
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr
 145 150 155 160
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val
 180 185 190
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val
 195 200 205
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser
 210 215 220
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe
 245 250 255
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala
 260 265 270
 Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Ser Arg Ile Pro Ser Phe His
 305 310

<210> 1361

<211> 328

<212> PRT

<213> Unknown (H38g278 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1361

```

Lys Ile Ser Asn Ser Ser Lys Phe Gln Val Ser Glu Phe Ile Leu Leu
 1           5           10           15
Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu
          20           25           30
Ala Leu Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile
          35           40           45
Ile Ile Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu
          50           55           60
Gly Ile Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro
65           70           75           80
Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro
          85           90           95
Glu Cys Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu
          100          105          110
Ser Gly Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
          115          120          125
His Pro Leu Arg Tyr Pro Ser Ile Val Thr Ser Ser Leu Ile Leu Lys
          130          135          140
Ala Thr Leu Phe Met Val Leu Arg Asn Gly Leu Phe Val Thr Pro Val
145          150          155          160
Pro Val Leu Ala Ala Gln Arg Asp Tyr Cys Ser Lys Asn Glu Ile Glu
          165          170          175
His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp
          180          185          190
Arg Arg Pro Asn Ser Ile Cys Gln Leu Val Leu Ala Trp Leu Gly Met
          195          200          205
Gly Ser Asp Leu Ser Leu Ile Leu Ser Tyr Ile Leu Ile Leu Tyr
          210          215          220
Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Ala Ala Lys Ala Leu Ser
225          230          235          240
Thr Cys Ser Ser His Leu Thr Leu Ile Leu Phe Phe Tyr Thr Ile Val
          245          250          255
Val Val Ile Ser Val Thr His Leu Thr Glu Met Lys Ala Thr Leu Ile
          260          265          270
Pro Val Leu Leu Asn Val Leu His Asn Ile Ile Pro Pro Ser Leu Asn
          275          280          285
Pro Thr Val Tyr Ala Leu Gln Thr Lys Glu Leu Arg Ala Ala Phe Gln
          290          295          300
Lys Val Leu Phe Ala Leu Thr Lys Glu Ile Arg Ser Xaa Arg Pro Ser
305          310          315          320
Pro Xaa Cys Thr Xaa Thr Ser Ala
          325

```

<210> 1362

<211> 316

<212> PRT

<213> Unknown (H38g279 protein)

<220>

<223> Synthetic construct

<400> 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
1      5      10      15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
20      25      30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
35      40      45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
50      55      60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65      70      75      80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
85      90      95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
100     105     110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
130     135     140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
145     150     155     160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
165     170     175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
180     185     190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
195     200     205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
210     215     220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
225     230     235     240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
245     250     255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
260     265     270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
275     280     285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
290     295     300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
305     310     315

```

<210> 1363

<211> 299

<212> PRT

<213> Unknown (H38g280 protein)

<220>

<223> Synthetic construct

<400> 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
1      5      10      15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
20      25      30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
35      40      45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
50      55      60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

65					70					75				80	
Leu	Glu	Cys	Phe	Ala	Gln	Met	Tyr	Ala	Ile	His	Cys	Phe	Val	Ala	Met
				85					90					95	
Glu	Ser	Ser	Thr	Phe	Val	Cys	Met	Ala	Ile	Asp	Arg	Tyr	Val	Ala	Ile
			100					105					110		
Cys	Arg	Pro	Leu	Arg	Tyr	Pro	Ser	Ile	Ile	Thr	Glu	Ser	Phe	Val	Phe
		115					120					125			
Lys	Ala	Asn	Gly	Phe	Met	Ala	Leu	Arg	Asn	Ser	Leu	Cys	Leu	Ile	Ser
	130					135					140				
Val	Pro	Leu	Leu	Ala	Ala	Gln	Arg	His	Tyr	Cys	Ser	Gln	Asn	Gln	Ile
145					150					155					160
Glu	His	Cys	Leu	Cys	Ser	Asn	Leu	Gly	Val	Thr	Ser	Leu	Ser	Cys	Asp
				165					170					175	
Asp	Arg	Arg	Ile	Asn	Ser	Ile	Asn	Gln	Val	Leu	Leu	Ala	Trp	Thr	Leu
			180					185					190		
Met	Gly	Ser	Asp	Leu	Gly	Leu	Ile	Ile	Leu	Ser	Tyr	Ala	Leu	Ile	Leu
		195					200					205			
Tyr	Ser	Val	Leu	Lys	Leu	Asn	Ser	Pro	Glu	Ala	Ala	Ser	Lys	Ala	Leu
		210				215					220				
Ser	Thr	Cys	Thr	Ser	His	Leu	Ile	Leu	Ile	Leu	Phe	Phe	Tyr	Thr	Val
225					230					235					240
Ile	Ile	Val	Ile	Ser	Ile	Thr	Arg	Ser	Thr	Gly	Met	Arg	Val	Pro	Leu
				245					250					255	
Ile	Pro	Val	Leu	Leu	Asn	Val	Leu	His	Asn	Val	Ile	Pro	Pro	Ala	Leu
			260				265					270			
Asn	Pro	Met	Val	Tyr	Ala	Leu	Lys	Asn	Lys	Glu	Leu	Arg	Gln	Gly	Leu
		275					280					285			
Tyr	Lys	Val	Leu	Arg	Leu	Gly	Val	Lys	Gly	Thr					
		290				295									

<210> 1364

<211> 327

<212> PRT

<213> Unknown (H38g281 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1364

Met	Thr	Trp	Ser	Gly	Gly	Thr	Leu	Val	Gly	Glu	Xaa	Gly	Glu	Phe	Val
1				5					10					15	
Leu	Leu	Gly	Phe	Pro	Ala	Pro	Ala	Pro	Leu	Gln	Val	Leu	Ser	Phe	Ala
			20				25						30		
Arg	Xaa	Ser	Ala	Ala	Tyr	Ala	Leu	Val	Leu	Thr	Glu	Asn	Thr	Leu	Ile
		35					40					45			
Ile	Met	Ala	Ser	Arg	Asn	His	Ser	Thr	Leu	His	Lys	Pro	Met	Tyr	Phe
	50					55					60				
Val	Leu	Ala	Asn	Met	Ser	Ser	Leu	Glu	Ile	Trp	Tyr	Val	Thr	Val	Thr
65					70					75					80
Ile	Pro	Lys	Met	Leu	Ala	Gly	Phe	Val	Gly	Ser	Lys	Gln	Asp	His	Gly
			85						90					95	
Gln	Leu	Ile	Ser	Phe	Glu	Gly	Cys	Met	Thr	Gln	Leu	Tyr	Phe	Phe	Leu
			100				105						110		
Gly	Leu	Gly	Cys	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp
		115					120					125			
Arg	Tyr	Met	Ala	Ile	Cys	Tyr	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Ser
		130				135					140				

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
 145 150 155 160
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
 165 170 175
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
 180 185 190
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
 195 200 205
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
 210 215 220
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly
 225 230 235 240
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
 245 250 255
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
 260 265 270
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
 275 280 285
 Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
 290 295 300
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
 305 310 315 320
 Asp Pro Lys Lys Ala Ser Arg
 325

<210> 1365

<211> 333

<212> PRT

<213> Unknown (H38g282 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

	180		185		190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val					
	195		200		205
Gly Thr Phe Ph Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr					
	210		215		220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu					
225		230		235	240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe					
	245		250		255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala					
	260		265		270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr					
	275		280		285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln					
	290		295		300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu					
305		310		315	320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr					
	325		330		

<210> 1366

<211> 280

<212> PRT

<213> Unknown (H38g283 protein)

<220>

<223> Synthetic construct

<400> 1366

Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser					
1	5		10		15
Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met					
	20		25		30
Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu					
	35		40		45
Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser					
	50		55		60
Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val					
65		70		75	80
Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro					
	85		90		95
Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp					
	100		105		110
Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg					
	115		120		125
Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser					
	130		135		140
Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg					
145		150		155	160
Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu					
	165		170		175
Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro					
	180		185		190
Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu					
	195		200		205
Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg					
	210		215		220
Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val					
225		230		235	240
Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg					
	245		250		255

Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
 260 265 270
 Leu Gly Asp Pro Ala Ala Cys Arg
 275 280

<210> 1367
 <211> 313
 <212> PRT
 <213> Unknown (H38g284 protein)

<220>
 <223> Synthetic construct

<400> 1367
 Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20 25 30
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35 40 45
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
 65 70 75 80
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
 85 90 95
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
 100 105 110
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
 130 135 140
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145 150 155 160
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180 185 190
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195 200 205
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210 215 220
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
 225 230 235 240
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245 250 255
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
 260 265 270
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
 290 295 300
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys
 305 310

<210> 1368
 <211> 214
 <212> PRT
 <213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
           20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
           35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
           50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
           65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
           85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
           100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
           115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
           130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
           145          150          155          160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
           165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
           180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
           195          200          205
Gly Lys Ile Ser Cys His
           210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
           20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
           35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
           50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
           65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
           85           90           95

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Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Il S r Phe Ala Gly Cys
 100 105 110
 Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu
 115 120 125
 Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro
 130 135 140
 Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu
 145 150 155 160
 Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr
 165 170 175
 Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His
 180 185 190
 Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala
 195 200 205
 Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe
 210 215 220
 Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala
 225 230 235 240
 Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr
 245 250 255
 Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
 260 265 270
 Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys
 275 280 285
 Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu
 290 295 300
 Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Leu Arg Lys Val
 305 310 315 320
 Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile
 325 330

<210> 1370

<211> 310

<212> PRT

<213> Unknown (H38g287 protein)

<220>

<223> Synthetic construct

<400> 1370

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe
 20 25 30
 Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val
 35 40 45
 Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Val Pro Met Met
 65 70 75 80
 Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His
 85 90 95
 Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly
 100 105 110
 Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr
 115 120 125
 Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser
 130 135 140
 Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe
 145 150 155 160
 Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```
<210> 1371
<211> 305
<212> PRT
<213> Unknown (H38g288 protein)
```

<400> 1371

676

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile
 260 265 270
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu
 290 295 300

Arg
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu
 20 25 30
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile
 35 40 45
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe
 50 55 60
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu
 65 70 75 80
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met
 85 90 95
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile
 100 105 110
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu
 115 120 125
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly
 130 135 140
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser
 145 150 155 160
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe
 165 170 175
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu
 180 185 190
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser
 195 200 205
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu
 210 215 220
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu
 245 250 255
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val
 260 265 270
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu
 275 280 285
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln
 290 295 300
 Arg Leu Lys Gly Leu Cys Lys Ala Gln
 305 310

<210> 1373

<211> 316

<212> PRT

<213> Unkn wn (H38g290 protein)

<220>

<223> Synthetic construct

<400> 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
      20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100           105           110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
      115           120           125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
      130           135           140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145           150           155           160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165           170           175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180           185           190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195           200           205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
      210           215           220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
      225           230           235           240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
      245           250           255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
      260           265           270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
      275           280           285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
      290           295           300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
      305           310           315

```

<210> 1374

<211> 345

<212> PRT

<213> Unknown (H38g291 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(345)

<223> Xaa = Any Amino Acid

<400> 1374

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Met His Leu Pro Asn Ser Ser Glu Ile Ala Il Thr Thr Phe Phe Leu
 1      5      10      15
Il Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
 20      25      30
Ile Cys Leu Met Tyr Leu Val Ala Il L u Gly Asn Cys Thr Ile Leu
 35      40      45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
 50      55      60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
 65      70      75      80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
 85      90      95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
 100      105      110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
 115      120      125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
 130      135      140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
 145      150      155      160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
 165      170      175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
 180      185      190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
 195      200      205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
 210      215      220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
 225      230      235      240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
 245      250      255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
 260      265      270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
 275      280      285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
 290      295      300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
 305      310      315      320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
 325      330      335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
 340      345

```

<210> 1375

<211> 238

<212> PRT

<213> Unknown (H38g292 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(238)

<223> Xaa = Any Amino Acid

<400> 1375

```

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1      5      10      15
Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

	20		25		30											
Gln	Ala	Pro	Xaa	Ser	Arg	Ser	Ile	Ile	Leu	Asn	L	u	Cys	Leu	Ile	Ser
	35		40		45											
Phe	Gly	Ile	Lys	Gly	Met	Trp	Ser	Asn	Val	Asn	Ser	Cys	Phe	Leu	Ser	
	50		55		60											
Ser	Leu	Pro	Arg	Glu	Lys	Glu	Leu	Gly	Leu	Lys	Ser	Glu	Gly	Asn	Tyr	
	65		70		75											
Ser	Ser	Ala	Thr	Gln	Phe	Cys	Leu	Leu	Gly	Phe	Pro	Gly	Phe	Glu	Glu	
			85		90											
Leu	Pro	His	Phe	Leu	Leu	Val	Asn	Phe	Phe	His	Leu	Met	Arg	Leu		
	100		105		110											
Met	Gly	Asn	Ala	Val	Ile	Tyr	Met	Val	Arg	Ile	Asp	Xaa	Ser	Leu	Gln	
	115		120		125											
Ser	Pro	Gly	Asp	Phe	Phe	Leu	Ser	Gln	Leu	Phe	Ile	Phe	Ser	His	Ser	
	130		135		140											
Leu	Leu	Met	Asp	Ile	Ser	Ile	Val	Ile	Ala	Ser	Leu	Ile	Gln	Ile	Asp	
	145		150		155											
Ser	Tyr	Ser	Ser	Ile	Pro	Ser	Ala	Ser	Gly	Gln	Lys	Lys	Ser	Phe	Ser	
			165		170											
Thr	His	Ala	Ser	His	Phe	Thr	Cys	Val	Gly	Ile	Asp	Tyr	Asp	Ser	Cys	
	180		185		190											
Leu	Phe	Leu	Tyr	Val	Lys	Pro	Lys	Gln	Ile	Trp	Ala	Ala	Glu	Xaa	Asn	
	195		200		205											
Lys	Val	Val	Phe	Leu	Phe	Ile	Phe	Leu	Leu	Thr	Pro	Phe	Leu	Asn	Leu	
	210		215		220											
Leu	Thr	Gly	Gln	Ile	Tyr	Xaa	Pro	Lys	Ser	Val	Leu	Gly	Gly			
	225		230		235											

<210> 1376

<211> 311

<212> PRT

<213> Unknown (H38g293 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1376

Pro	Met	Lys	Val	Ala	Asn	Asn	Val	Thr	Glu	Phe	Ile	Phe	Leu	Gly	Leu
1			5				10						15		
Ser	Gln	Asp	Ser	Gly	Met	Gln	Leu	Met	Phe	Phe	Val	Leu	Phe	Leu	Leu
		20					25					30			
Phe	Tyr	Val	Val	Ile	Met	Val	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Met	Val
	35					40						45			
Phe	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn
	50				55					60					
Leu	Ser	Phe	Val	Asp	Ile	Ala	Cys	Ser	Ser	Ala	Thr	Ala	Pro	Lys	Met
	65			70					75					80	
Ile	Glu	Asp	Phe	Val	Ser	Glu	Lys	Lys	Thr	Ile	Ser	Tyr	Trp	Gly	Cys
		85						90						95	
Ile	Thr	Gln	Met	Phe	Thr	Phe	His	Phe	Phe	Gly	Cys	Ala	Glu	Ile	Phe
	100						105						110		
Val	Leu	Thr	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	Gln	Pro
	115					120						125			
Leu	Arg	Tyr	Thr	Val	Ile	Met	Ser	Ala	Asn	Ala	Tyr	Thr	Val	Leu	Ala
	130				135						140				
Ser	Leu	Ser	Trp	Leu	Gly	Ala	Leu	Gly	His	Ser	Phe	Val	Gln	Thr	Leu
	145			150				155						160	

Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr
 165 170 175
 Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr
 180 185 190
 Leu Val Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly
 195 200 205
 Cys Phe Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu
 210 215 220
 Gln Lys Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile
 245 250 255
 Tyr Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe
 260 265 270
 Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Glu Glu Val Lys Asn Ala Met Arg Arg Leu Trp Ser Ser Lys Ile
 290 295 300
 Ser Leu Lys Glu Lys Gln Arg
 305 310

<210> 1377

<211> 323

<212> PRT

<213> Unknown (H38g294 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1377

Met Glu Ile Leu Ser Asn Ser Thr Ser Lys Phe Pro Thr Phe Leu Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Cys Phe Tyr Ala Ile Ala Leu Ser Gly Asn Ser Val Ile Leu
 35 40 45
 Phe Val Ile Ile Thr Gln Gln Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Thr Val Ser Ser Leu
 65 70 75 80
 Ser Thr Thr Leu Gly Ile Leu Trp Phe Glu Ala Arg Glu Ile Ser Leu
 85 90 95
 Tyr Ser Cys Ile Val Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
 100 105 110
 Glu Ser Gly Val Leu Val Ala Thr Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ser Arg Ile Ile
 130 135 140
 Gln Met Gly Leu Leu Met Ile Thr Arg Ala Ile Val Leu Ile Leu Pro
 145 150 155 160
 Leu Leu Leu Leu Lys Pro Leu Tyr Phe Cys Arg Met Asn Ala Leu
 165 170 175
 Ser His Ser Tyr Cys Tyr His Pro Asp Val Ile Gln Leu Ala Cys Ser
 180 185 190
 Asp Ile Arg Ala Asn Ser Ile Cys Gly Leu Ile Asp Leu Ile Leu Thr
 195 200 205
 Thr Gly Ile Asp Thr Pro Cys Ile Val Leu Ser Tyr Ile Leu Ile Ile

210	215	220
Arg Phe Val Leu Arg Ile Ala Ser Pro Glu Glu Trp His Lys Val Phe		
225	230	235
Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His		
	245	250
Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg		
	260	265
Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val		
	275	280
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala		
	290	295
Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp		
305	310	315
Thr Asn Leu		320

<210> 1378

<211> 321

<212> PRT

<213> Unknown (H38g295 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1378

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu		
1	5	10
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser		
	20	25
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser		
	35	40
Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe		
	50	55
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr		
65	70	75
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser		
	85	90
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys		
	100	105
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala		
	115	120
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys		
	130	135
Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu		
145	150	155
His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile		
	165	170
Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser		
	180	185
Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe		
	195	200
Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile		
	210	215
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe		
225	230	235
Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr		
	245	250
		255

Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pr Pro Arg Asn
 260 265 270
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
 275 280 285
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp
 290 295 300
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe
 305 310 315 320
 Ser

<210> 1379

<211> 325

<212> PRT

<213> Unknown (H38g296 protein)

<220>

<223> Synthetic construct

<400> 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu
 1 5 10 15
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe
 35 40 45
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu
 65 70 75 80
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe
 85 90 95
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu
 100 105 110
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu
 130 135 140
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro
 145 150 155 160
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu
 165 170 175
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser
 180 185 190
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu
 195 200 205
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu
 210 215 220
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro
 245 250 255
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg
 260 265 270
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala
 290 295 300
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg
 305 310 315 320
 Gly Leu Arg Gly Arg

325

<210> 1380
 <211> 315
 <212> PRT
 <213> Unknown (H38g297 protein)

<220>
 <223> Synthetic construct

<400> 1380

Met	Glu	Thr	Trp	Val	Asn	Gln	Ser	Tyr	Thr	Asp	Gly	Phe	Phe	Leu	Leu
1				5					10					15	
Gly	Ile	Phe	Ser	His	Ser	Thr	Ala	Asp	Leu	Val	Leu	Phe	Ser	Val	Val
			20					25					30		
Met	Ala	Val	Phe	Thr	Val	Ala	Leu	Cys	Gly	Asn	Val	Leu	Leu	Ile	Phe
		35					40					45			
Leu	Ile	Tyr	Met	Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Gln	Leu	Ser	Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Thr	Asn	Val	Pro
65					70					75					80
Lys	Met	Ala	Ala	Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val
				85					90					95	
Gly	Cys	Gly	Ile	Gln	Ile	Gly	Leu	Phe	Val	Cys	Leu	Val	Gly	Ser	Glu
			100					105					110		
Gly	Leu	Leu	Leu	Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Ser
		115					120					125			
His	Pro	Leu	His	Tyr	Pro	Ile	Leu	Met	Asn	Gln	Arg	Val	Cys	Leu	Gln
		130				135					140				
Ile	Thr	Gly	Ser	Ser	Trp	Ala	Phe	Gly	Ile	Ile	Asp	Gly	Leu	Ile	Gln
145					150					155					160
Met	Val	Val	Val	Met	Asn	Phe	Pro	Tyr	Cys	Gly	Leu	Arg	Lys	Val	Asn
				165					170					175	
His	Phe	Phe	Cys	Glu	Met	Leu	Ser	Leu	Leu	Lys	Leu	Ala	Cys	Val	Asp
			180					185					190		
Thr	Ser	Leu	Phe	Glu	Lys	Val	Ile	Phe	Ala	Cys	Cys	Val	Phe	Met	Leu
		195					200					205			
Leu	Phe	Pro	Phe	Ser	Ile	Ile	Val	Ala	Ser	Tyr	Ala	Arg	Ile	Leu	Gly
	210					215					220				
Thr	Val	Leu	Gln	Met	His	Ser	Ala	Gln	Ala	Trp	Lys	Lys	Ala	Leu	Ala
225					230					235					240
Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Ala	Ala
				245					250					255	
Met	Phe	Ile	Tyr	Leu	Arg	Pro	Arg	His	Tyr	Arg	Ala	Pro	Ser	His	Asp
			260					265					270		
Lys	Val	Ala	Ser	Ile	Phe	Tyr	Thr	Val	Leu	Thr	Pro	Met	Leu	Asn	Pro
		275					280					285			
Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Glu	Val	Met	Gly	Ala	Leu	Arg	Lys
	290					295					300				
Gly	Leu	Asp	Arg	Cys	Arg	Ile	Gly	Ser	Gln	His					
305					310					315					

<210> 1381
 <211> 323
 <212> PRT
 <213> Unknown (H38g298 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1381

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Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
1          5          10          15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
20          25          30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
35          40          45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
50          55          60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
65          70          75          80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
85          90          95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
100          105          110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
115          120          125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
130          135          140
Ser Lys Ile Ala Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
145          150          155          160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
165          170          175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
180          185          190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
195          200          205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
210          215          220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
225          230          235          240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
245          250          255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
260          265          270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Leu Pro Pro
275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
290          295          300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
305          310          315          320
Leu Leu Phe

```

<210> 1382

<211> 312

<212> PRT

<213> Unknown (H38g299 protein)

<220>

<223> Synthetic construct

<400> 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
1          5          10          15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
20          25          30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

```

      35      40      45
Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala
  50      55      60
Met Leu Ala Val Ser Asp Met Gly Leu Ser Leu Ser Ser Leu Pro Thr
  65      70      75      80
Met Leu Arg Val Phe Leu Phe Asn Ala Met Gly Ile Ser Pro Asn Ala
      85      90      95
Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser
      100      105      110
Ser Val Leu Leu Ile Met Ser Leu Asp Arg Phe Leu Ala Ile His Asn
      115      120      125
Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met
      130      135      140
Gly Leu Ile Leu Ala Ile Arg Ser Ile Leu Leu Val Ile Pro Phe Pro
  145      150      155      160
Phe Thr Leu Arg Arg Leu Lys Tyr Cys Gln Lys Asn Leu Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Gln Asp Thr Met Lys Leu Ala Cys Ser Asp Asn
      180      185      190
Lys Thr Asn Val Ile Tyr Gly Phe Phe Ile Ala Leu Cys Thr Met Leu
      195      200      205
Asp Leu Ala Leu Ile Val Leu Ser Tyr Val Leu Ile Leu Lys Thr Ile
  210      215      220
Leu Ser Ile Ala Ser Leu Ala Glu Arg Leu Lys Ala Leu Asn Thr Cys
  225      230      235      240
Val Ser His Ile Cys Ala Val Leu Thr Phe Tyr Val Pro Ile Ile Thr
      245      250      255
Leu Ala Ala Met His His Phe Ala Lys His Lys Ser Pro Leu Val Val
      260      265      270
Ile Leu Ile Ala Asp Met Phe Leu Leu Val Pro Pro Leu Met Asn Pro
      275      280      285
Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Trp Glu Lys Ile Leu Gly
  290      295      300
Lys Leu Leu Asn Val Cys Gly Arg
  305      310

```

<210> 1383

<211> 308

<212> PRT

<213> Unknown (H38g300 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1383

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Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
  1      5      10      15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
      20      25      30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
      35      40      45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
  50      55      60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
  65      70      75      80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
      85      90      95

```

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
 100 105 110
 Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
 115 120 125
 Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
 130 135 140
 Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
 145 150 155 160
 Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
 165 170 175
 Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
 180 185 190
 Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
 195 200 205
 Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
 210 215 220
 Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
 245 250 255
 Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
 260 265 270
 Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
 275 280 285
 Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
 290 295 300
 Trp Lys Asp Ser
 305

<210> 1384

<211> 317

<212> PRT

<213> Unknown (H38g301 protein)

<220>

<223> Synthetic construct

<400> 1384

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu
 20 25 30
 Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp
 115 120 125
 Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

180								185				190			
Ser	Ser	Asn	Glu	Ala	Ala	Ile	Met	Val	Ser	Ser	Il	Val	Leu	Leu	Met
195								200				205			
Thr	Pro	Phe	Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Arg	Ile	Ile	Ser	Thr
210								215				220			
Ile	Leu	Lys	Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr
225								230				235			
Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ala	Leu	Cys	Tyr	Gly	Thr	Thr	Ile
245								250				255			
Phe	Thr	Tyr	Ile	Gln	Pro	His	Ser	Gly	Pro	Ser	Val	Leu	Gln	Glu	Lys
260								265				270			
Leu	Ile	Ser	Val	Phe	Tyr	Ala	Ile	Val	Met	Pro	Leu	Leu	Asn	Pro	Val
275								280				285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	His	Lys	Leu
290								295				300			
Leu	Glu	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Gly	Thr			
305								310				315			

<210> 1385

<211> 306

<212> PRT

<213> Unknown (H38g302 protein)

<220>

<223> Synthetic construct

<400> 1385

Met 1	Glu	Gly	Lys	Asn 5	Gln	Thr	Asn	Ile	Ser 10	Glu	Phe	Leu	Leu	Leu 15	Gly
Phe	Ser	Ser	Trp 20	Gln	Gln	Gln	Gln	Val 25	Leu	Leu	Phe	Ala 30	Leu	Phe	Leu
Cys	Leu	Tyr 35	Leu	Thr	Gly	Leu	Phe 40	Gly	Asn	Leu	Leu	Ile 45	Leu	Leu	Ala
Ile	Gly 50	Ser	Asp	His	Cys	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ala
Asn 65	Leu	Ser	Leu	Val 70	Asp	Leu	Cys	Leu	Pro	Ser 75	Ala	Thr	Val	Pro	Lys 80
Met	Leu	Leu	Asn 85	Ile	Gln	Thr	Gln	Thr 90	Gln	Thr	Ile	Ser	Tyr 95	Pro	Gly
Cys	Leu	Ala 100	Gln	Met	Tyr	Phe	Cys	Met 105	Met	Phe	Ala	Asn	Met 110	Asp	Asn
Phe	Leu	Leu 115	Thr	Val	Met	Ala	Tyr 120	Asp	Arg	Tyr	Val	Ala 125	Ile	Cys	His
Pro	Leu 130	His	Tyr	Ser	Thr	Ile 135	Met	Ala	Leu	Arg	Leu 140	Cys	Ala	Ser	Leu
Val 145	Ala	Ala	Pro	Trp 150	Val	Ile	Ala	Ile	Leu	Asn 155	Pro	Leu	Leu	His	Thr 160
Leu	Met	Met	Ala 165	His	Leu	His	Phe	Cys	Ser 170	Asp	Asn	Val	Ile	His	His 175
Phe	Phe	Cys 180	Asp	Ile	Asn	Ser	Leu	Leu 185	Pro	Leu	Ser	Cys 190	Ser	Asp	Thr
Ser	Leu	Asn 195	Gln	Leu	Ser	Val	Leu 200	Ala	Thr	Val	Gly	Leu 205	Ile	Phe	Val
Val 210	Pro	Ser	Val	Cys	Ile	Leu	Val 215	Ser	Tyr	Ile	Leu 220	Ile	Val	Ser	Ala
Val 225	Met	Lys	Val	Pro 230	Ser	Ala	Gln	Gly	Lys	Leu 235	Lys	Ala	Phe	Ser	Thr 240
Cys	Gly	Ser	His 245	Leu	Ala	Leu	Val	Ile	Leu 250	Phe	Tyr	Gly	Ala 255	Asn	Thr
Gly	Val	Tyr 260	Met	Ser	Pro	Leu	Ser	Asn 265	His	Ser	Thr	Glu	Lys 270	Asp	Ser

Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 290 295 300
 Leu Ser
 305

<210> 1386

<211> 311

<212> PRT

<213> Unknown (H38g303 protein)

<220>

<223> Synthetic construct

<400> 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys
 1 5 10 15
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
 35 40 45
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe
 50 55 60
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser
 100 105 110
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu
 130 135 140
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser
 145 150 155 160
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu
 165 170 175
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala
 195 200 205
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser
 210 215 220
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe
 245 250 255
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Gly Arg Leu Phe Pro Phe
 305 310

<210> 1387

<211> 313

<212> PRT

<213> Unknown (H38g304 protein)

<220>

<223> Synthetic construct

<400> 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
 35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
 65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
 85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
 100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
 130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
 145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
 165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
 180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
 195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
 210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
 225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
 245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
 260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
 290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
305          310

```

<210> 1388

<211> 313

<212> PRT

<213> Unknown (H38g305 protein)

<220>

<223> Synthetic construct

<400> 1388

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Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
 20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
 35           40           45

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Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Phe Cys L u Ala Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Ser Leu Gln Thr Gly S r Lys Ala Ile Ser Tyr Pro Cys
 85 90 95
 Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
 100 105 110
 Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
 130 135 140
 Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145 150 155 160
 Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
 165 170 175
 Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
 180 185 190
 Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
 195 200 205
 Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
 245 250 255
 Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
 260 265 270
 Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
 290 295 300
 Val Asn Arg Lys Ile Thr Ser Ser Ser
 305 310

<210> 1389

<211> 98

<212> PRT

<213> Unknown (H38g306 protein)

<220>

<223> Synthetic construct

<400> 1389

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
 35 40 45
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
 50 55 60
 Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
 65 70 75 80
 Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
 85 90 95
 Ala Gly

<210> 1390

<211> 320

<212> PRT

<213> Unknown (H38g307 protein)

<220>

<223> Synthetic construct

<400> 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1           5           10           15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
      20           25           30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
      35           40           45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
      50           55           60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
      65           70           75           80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
      85           90           95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
      100          105          110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
      115          120          125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
      130          135          140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
      145          150          155          160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
      165          170          175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
      180          185          190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
      195          200          205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
      210          215          220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
      225          230          235          240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
      245          250          255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
      260          265          270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
      275          280          285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
      290          295          300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
      305          310          315          320

```

<210> 1391

<211> 312

<212> PRT

<213> Unknown (H38g308 protein)

<220>

<223> Synthetic construct

<400> 1391

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
      20           25           30

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
 35 40 45
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
 130 135 140
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
 165 170 175
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180 185 190
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
 195 200 205
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
 210 215 220
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
 245 250 255
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
 260 265 270
 Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val
 290 295 300
 Val Gly Arg Val Val Phe Ser Val
 305 310

<210> 1392

<211> 254

<212> PRT

<213> Unknown (H38g309 protein)

<220>

<223> Synthetic construct

<400> 1392

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr
 1 5 10 15
 Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro
 20 25 30
 Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile
 35 40 45
 Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp
 50 55 60
 Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser
 65 70 75 80
 Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile
 85 90 95
 Ile Thr Ala Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg
 100 105 110
 Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

115	120	125
Arg Leu Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr		
130	135	140
Ala Thr Ile Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser		
145	150	155
Tyr Ile Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser		
165	170	175
Arg Arg Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser		
180	185	190
Leu Phe Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly		
195	200	205
Ser Ser Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile		
210	215	220
Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val		
225	230	235
Arg Arg Ala Leu Arg His Leu Val Lys Arg Gln Arg Pro Ser		
245	250	

<210> 1393

<211> 333

<212> PRT

<213> Unknown (H38g310 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1393

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly		
1	5	10
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser		
20	25	30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser		
35	40	45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val		
50	55	60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys		
65	70	75
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly		
85	90	95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met		
100	105	110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys		
115	120	125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe		
130	135	140
Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu		
145	150	155
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser		
165	170	175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr		
180	185	190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val		
195	200	205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr		
210	215	220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu		
225	230	235
		240

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
 305 310 315 320
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
 325 330

<210> 1394

<211> 311

<212> PRT

<213> Unknown (H38g311 protein)

<220>

<223> Synthetic construct

<400> 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu
 1 5 10 15
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile
 20 25 30
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile
 35 40 45
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His
 50 55 60
 Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys
 85 90 95
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe
 100 105 110
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile
 130 135 140
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro
 145 150 155 160
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe
 165 170 175
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala
 180 185 190
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile
 195 200 205
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val
 210 215 220
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
 245 250 255
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val
 260 265 270
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu
 290 295 300
 Gly Arg Phe Lys Gly Pro Gln

305

310

<210> 1395
 <211> 295
 <212> PRT
 <213> Unknown (H38g312 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(295)
 <223> Xaa = Any Amino Acid

<400> 1395
 Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
 1 5 10 15
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
 20 25 30
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
 35 40 45
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
 50 55 60
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
 65 70 75 80
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
 85 90 95
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 100 105 110
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
 115 120 125
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
 130 135 140
 Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
 145 150 155 160
 Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro
 165 170 175
 Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
 180 185 190
 Arg Val Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
 195 200 205
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly
 210 215 220
 Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
 225 230 235 240
 Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 245 250 255
 Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg
 260 265 270
 Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val
 275 280 285
 Xaa Val Arg Lys Gly Ser Lys
 290 295

<210> 1396
 <211> 314
 <212> PRT
 <213> Unknown (H38g313 protein)

<220>
 <223> Synthetic construct

<400> 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Val Ser Ala Thr
 1           5           10           15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
          20           25           30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
          35           40           45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
          50           55           60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
65           70           75           80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
          85           90           95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
          100          105          110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
          115          120          125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
          130          135          140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
145          150          155          160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
          165          170          175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
          180          185          190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
          195          200          205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
          210          215          220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
225          230          235          240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
          245          250          255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
          260          265          270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
          275          280          285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305          310

```

<210> 1397

<211> 330

<212> PRT

<213> Unknown (H38g314 protein)

<220>

<223> Synthetic construct

<400> 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1           5           10           15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
          20           25           30
Arg Gln Ser Lys His Pro Ala Leu Cys Val Val Ile Phe Val Val
          35           40           45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
          50           55           60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

65					70					75				80	
Ser	Leu	Met	Asp	Met	Ala	Tyr	Ile	Ser	Val	Thr	Val	Pro	Lys	Met	Leu
				85					90				95		
Leu	Asp	Gln	Val	Met	Gly	Val	Asn	Lys	Ile	Ser	Ala	Pro	Glu	Cys	Gly
			100					105					110		
Met	Gln	Met	Phe	Phe	Tyr	Val	Thr	Leu	Ala	Gly	Ser	Glu	Phe	Phe	Leu
			115				120					125			
Leu	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu
			130			135					140				
Arg	Tyr	Pro	Val	Leu	Met	Asn	His	Arg	Val	Cys	Leu	Phe	Leu	Ser	Ser
145					150					155					160
Gly	Cys	Trp	Phe	Leu	Gly	Ser	Val	Asp	Gly	Phe	Thr	Phe	Thr	Pro	Ile
				165				170						175	
Thr	Met	Thr	Phe	Pro	Phe	Arg	Gly	Ser	Arg	Glu	Ile	His	His	Phe	Phe
			180					185					190		
Cys	Glu	Val	Pro	Ala	Val	Leu	Asn	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Leu
			195				200					205			
Tyr	Glu	Ile	Phe	Met	Tyr	Leu	Cys	Cys	Val	Leu	Met	Leu	Leu	Ile	Pro
			210			215					220				
Val	Val	Ile	Ile	Ser	Ser	Ser	Tyr	Leu	Leu	Ile	Leu	Leu	Thr	Ile	His
225					230					235					240
Gly	Met	Asn	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Ala	Phe	Ala	Thr	Cys	Ser
				245				250						255	
Ser	His	Leu	Thr	Val	Val	Ile	Leu	Phe	Tyr	Gly	Ala	Ala	Ile	Tyr	Thr
			260					265					270		
Tyr	Met	Leu	Pro	Ser	Ser	Tyr	His	Thr	Pro	Glu	Lys	Asp	Met	Met	Val
			275				280					285			
Ser	Val	Phe	Tyr	Thr	Ile	Leu	Thr	Pro	Val	Val	Asn	Pro	Leu	Ile	Tyr
			290			295					300				
Ser	Leu	Arg	Asn	Lys	Asp	Val	Met	Gly	Ala	Leu	Lys	Lys	Met	Leu	Thr
305					310					315					320
Val	Glu	Pro	Ala	Phe	Gln	Lys	Ala	Met	Glu						
				325					330						

<210> 1398

<211> 197

<212> PRT

<213> Unknown (H38g315 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(197)

<223> Xaa = Any Amino Acid

<400> 1398

Ala	Ala	Met	Ala	Xaa	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Asn	Pro	Leu	Leu
1				5					10					15	
Tyr	Thr	Val	Ile	Met	Ser	Lys	Lys	Val	Cys	Cys	Gln	Leu	Ala	Ile	Gly
			20					25				30			
Ala	Phe	Leu	Gly	Gly	Thr	Met	Ser	Ile	Ile	His	Thr	Thr	Asn	Thr	
			35			40					45				
Phe	His	Leu	Ser	Phe	Cys	Ser	Arg	Asp	Ile	Asn	His	Phe	Phe	Cys	Asp
			50			55				60					
Ile	Ser	Pro	Leu	Phe	Ser	Leu	Ser	Cys	Thr	Asp	Thr	Tyr	Met	His	Asp
65					70				75					80	
Ile	Ile	Leu	Val	Val	Phe	Ala	Ser	Phe	Val	Glu	Ala	Ile	Cys	Leu	Leu
				85					90					95	
Ser	Val	Leu	Leu	Ser	Tyr	Val	Phe	Ile	Met	Ala	Ala	Ile	Leu	Arg	Thr
			100					105					110		

Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His
 115 120 125
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu
 130 135 140
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val
 145 150 155 160
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 165 170 175
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys
 180 185 190
 Leu Leu Pro Xaa Gly
 195

<210> 1399

<211> 313

<212> PRT

<213> Unknown (H38g316 protein)

<220>

<223> Synthetic construct

<400> 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu
 1 5 10 15
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe
 20 25 30
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu
 35 40 45
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Ser Val Ser Pro
 65 70 75 80
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn
 85 90 95
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu
 100 105 110
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln
 130 135 140
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His
 145 150 155 160
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn
 165 170 175
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Asn Pro Thr Ile
 180 185 190
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala
 195 200 205
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile
 210 215 220
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu
 245 250 255
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys
 290 295 300
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

<210> 1400

<211> 323

<212> PRT

<213> Unknown (H38g317 protein)

<220>

<223> Synthetic construct

<400> 1400

```

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1           5           10           15
Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
 20           25           30
Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
 35           40           45
Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
 50           55           60
Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
 65           70           75           80
Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
 85           90           95
Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
 100          105          110
His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
 115          120          125
Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
 130          135          140
Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
 145          150          155          160
Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
 165          170          175
Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
 180          185          190
Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
 195          200          205
Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
 210          215          220
Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
 225          230          235          240
Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
 245          250          255
Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
 260          265          270
Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
 275          280          285
Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
 290          295          300
Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
 305          310          315          320
Gly Ala Gln

```

<210> 1401

<211> 128

<212> PRT

<213> Unknown (H38g318 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(128)

<223> Xaa = Any Amino Acid

<400> 1401

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Ser Arg Ser Asn Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1          5          10          15
Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
          20          25          30
Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
          35          40          45
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
          50          55          60
Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
65          70          75          80
Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
          85          90          95
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
          100          105          110
Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
          115          120          125

```

<210> 1402

<211> 316

<212> PRT

<213> Unknown (H38g319 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1402

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Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1          5          10          15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
          20          25          30
Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35          40          45
Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
          50          55          60
Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
65          70          75          80
Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
          85          90          95
Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
          130          135          140
Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
145          150          155          160
Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
          165          170          175
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
          180          185          190
Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

```

	195		200		205	
Ser	Asp	Ser	Val	Phe	Ile	Ala
210						215
Thr	Val	Leu	Gly	Ile	Ala	Ser
225						230
Thr	Cys	Val	Ser	His	Ile	Cys
						245
Ile	Thr	Leu	Ala	Thr	Met	Arg
						260
Ala	Met	Ile	Leu	Ile	Ala	Asp
						275
Asn	Pro	Ile	Val	Tyr	Cys	Val
						290
Leu	Glu	Lys	Leu	Ala	Leu	Lys
305						310

<210> 1403

<211> 314

<212> PRT

<213> Unknown (H38g320 protein)

<220>

<223> Synthetic construct

<400> 1403

Met	Met	Ala	Ser	Glu	Arg	Asn	Gln	Ser	Ser	Thr	Pro	Thr	Phe	Ile	Leu
1				5					10					15	
Leu	Gly	Phe	Ser	Glu	Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val
			20					25					30		
Phe	Leu	Phe	Val	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile
			35				40					45			
Ile	Ile	Ile	Arg	Leu	Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe
			50			55					60				
Leu	Ser	His	Leu	Ser	Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr
65					70					75					80
Pro	Lys	Leu	Leu	Glu	Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe
				85					90					95	
Ser	Gly	Cys	Ile	Met	Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr
			100					105					110		
Glu	Thr	Phe	Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val
			115				120						125		
Cys	Lys	Pro	Leu	Leu	Tyr	Thr	Thr	Ile	Met	Ser	Gln	Lys	Leu	Cys	Ala
			130			135					140				
Leu	Leu	Val	Ala	Gly	Ser	Tyr	Thr	Trp	Gly	Ile	Val	Cys	Ser	Leu	Ile
145					150					155					160
Leu	Thr	Tyr	Phe	Leu	Leu	Asp	Leu	Ser	Phe	Cys	Glu	Ser	Thr	Phe	Ile
			165						170					175	
Asn	Asn	Phe	Ile	Cys	Asp	His	Ser	Val	Ile	Val	Ser	Ala	Ser	Tyr	Ser
			180					185					190		
Asp	Pro	Tyr	Ile	Ser	Gln	Arg	Leu	Cys	Phe	Ile	Ile	Ala	Ile	Phe	Asn
			195				200					205			
Glu	Val	Ser	Ser	Leu	Ile	Ile	Ile	Leu	Thr	Ser	Tyr	Met	Leu	Ile	Phe
			210			215					220				
Thr	Thr	Ile	Met	Lys	Met	Arg	Ser	Ala	Ser	Gly	Arg	Gln	Lys	Thr	Phe
225					230					235					240
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Ile	Phe	His	Gly	Thr
				245					250					255	
Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Pro	Lys	Thr	Ser	Ser	Leu	Ile
			260					265					270		
Val	Thr	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val	Ala	Ile	Pro	Met	Leu	Asn
			275				280						285		

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu
 290 295 300
 Lys Leu Val Val Thr Lys Leu Ile Tyr His
 305 310

<210> 1404
 <211> 322
 <212> PRT
 <213> Unknown (H38g321 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(322)
 <223> Xaa = Any Amino Acid

<400> 1404
 His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65 70 75 80
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser
 305 310 315 320
 Phe Ser

<210> 1405
 <211> 330
 <212> PRT
 <213> Unknown (H38g322 protein)

<220>
 <223> Synthetic construct

<400> 1405

```

Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu
 1           5           10           15
Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro
          20           25           30
Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu
          35           40           45
Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu
65           70           75           80
Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu
          85           90           95
Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
          100          105          110
Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala
          130          135          140
Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro
145           150           155           160
Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu
          165          170          175
Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr
          180          185          190
Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr
          195          200          205
Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile
          210          215          220
Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe
225           230           235           240
Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro
          245          250          255
Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro
          260          265          270
Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val
          275          280          285
Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala
          290          295          300
Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu
305           310           315           320
Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu
          325          330

```

<210> 1406
 <211> 314
 <212> PRT
 <213> Unknown (H38g323 protein)

<220>
 <223> Synthetic construct

<400> 1406


```

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1          5          10          15
Leu Gly Ph Thr Asp Tyr Pro Lys Leu Gln Ile Pr Leu Phe Leu Val
 20          25          30
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly M t Ile
 35          40          45
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
 50          55          60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
 65          70          75          80
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
 85          90          95
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
 100          105          110
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
 130          135          140
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
 145          150          155          160
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
 165          170          175
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
 180          185          190
Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn
 195          200          205
Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
 210          215          220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe
 225          230          235          240
Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245          250          255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
 260          265          270
Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
 275          280          285
Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
 290          295          300
Lys Leu Ile His Thr Gln Val Pro Phe His
305          310

```

<210> 1407

<211> 314

<212> PRT

<213> Unknown (H38g324 protein)

<220>

<223> Synthetic construct

<400> 1407

```

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile
 1          5          10          15
Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe
 20          25          30
Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu
 35          40          45
Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu
 50          55          60
Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr
 65          70          75          80
Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

```

```
<210> 1408
<211> 287
<212> PRT
<213> Unknown (H38q325 protein)
```

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<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(287)
<223> Xaa = Any Amino Acid
```

<400> 1408															
Tyr	Ile	Leu	Leu	Asp	Ile	Tyr	Ile	Cys	Leu	Asn	Asn	Thr	His	Val	Xaa
1				5					10					15	
Leu	Cys	Val	Glu	Ser	Gln	Arg	Gln	Phe	Lys	Ile	Ser	Phe	Tyr	Phe	Ser
			20					25					30		
Phe	Phe	Leu	Leu	Ala	Ile	Thr	Xaa	Phe	Xaa	Xaa	Xaa	Ile	Leu	Ile	Ile
		35					40					45			
Met	Lys	Thr	Xaa	Gln	Tyr	Phe	Leu	Lys	His	Lys	His	Leu	Lys	Lys	Lys
	50					55					60				
Phe	Ser	Xaa	Cys	Leu	Val	Tyr	Ile	Leu	Thr	Tyr	Ile	Leu	Ser	Leu	Xaa
65					70					75					80
Ser	Lys	Phe	Phe	Ala	Leu	Cys	Xaa	Ile	Phe	Ala	Asp	Lys	Ala	Phe	Gln
				85					90					95	
Glu	Gln	Val	Ser	Gly	Asn	Xaa	Xaa	Ser	Arg	Ser	Xaa	Glu	Ser	Pro	Val
			100					105					110		
His	Tyr	Thr	Leu	Thr	Met	Ser	Gln	Lys	Phe	Cys	Ser	Ile	His	Pro	Ala
		115					120					125			
Gly	Cys	Tyr	Asp	Gln	Gly	Ile	Xaa	Ser	Ile	Pro	Gly	His	Ser	Phe	Ser
	130					135					140				

```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
145          150          155          160
Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala
          165          170          175
Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
          180          185          190
Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
          195          200          205
Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
          210          215          220
Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
225          230          235          240
Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
          245          250          255
Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
          260          265          270
Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
          275          280          285

```

<210> 1409

<211> 323

<212> PRT

<213> Unknown (H38g326 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1409

```

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu
1      5      10      15
Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu
20     25     30
Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile
35     40     45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
50     55     60
Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65     70     75     80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa
85     90     95
Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile
100    105    110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile
115    120    125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
130    135    140
Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145    150    155    160
His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile
165    170    175
Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser
180    185    190
Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe
195    200    205
Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val
210    215    220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

```

225 230 235 240
 Ser Ile Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr
 245 250 255
 Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pr Gly Asn
 260 265 270
 Gly Val Val Ala Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn
 275 280 285
 Ser Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp
 290 295 300
 Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu
 305 310 315 320
 Phe Leu Cys

<210> 1410

<211> 317

<212> PRT

<213> Unknown (H38g327 protein)

<220>

<223> Synthetic construct

<400> 1410

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1 5 10 15
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
 20 25 30
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
 35 40 45
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
 50 55 60
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
 100 105 110
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
 130 135 140
 Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
 145 150 155 160
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
 165 170 175
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
 195 200 205
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
 210 215 220
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile
 260 265 270
 Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
 290 295 300

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln
 305 310 315

<210> 1411
 <211> 312
 <212> PRT
 <213> Unknown (H38g328 protein)

<220>
 <223> Synthetic construct

<400> 1411

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser
 305 310

<210> 1412
 <211> 223
 <212> PRT
 <213> Unknown (H38g329 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1           5           10           15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
          20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
          35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
          50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
          65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
          85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
          115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
          165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
          180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
          195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
          210          215          220

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<210> 1413

<211> 280

<212> PRT

<213> Unknown (H38g330 protein)

<220>

<223> Synthetic construct

<400> 1413

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Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
 1           5           10           15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
          20           25           30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
          35           40           45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
          50           55           60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
          65           70           75           80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
          85           90           95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
          100          105          110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
          115          120          125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
          130          135          140

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Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val
 145 150 155 160
 Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu
 165 170 175
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile
 180 185 190
 Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 210 215 220
 Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
 225 230 235 240
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg
 260 265 270
 Ser Arg Thr Val Glu Ser His Asp
 275 280

<210> 1414

<211> 308

<212> PRT

<213> Unknown (H38g331 protein)

<220>

<223> Synthetic construct

<400> 1414

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Gln Ser Gln Asp Ala Gln Leu Leu Val Phe Val Leu Val Leu
 20 25 30
 Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg
 65 70 75 80
 Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser
 85 90 95
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met
 100 105 110
 Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu
 130 135 140
 Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val
 145 150 155 160
 Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
 165 170 175
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr
 180 185 190
 Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu
 195 200 205
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
 210 215 220
 Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe
 245 250 255
 Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

260 265 270
 Leu Phe His Thr Val Ile Ph Pro Leu Met Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln
 290 295 300
 His Met Phe Cys
 305

<210> 1415
 <211> 154
 <212> PRT
 <213> Unknown (H38g332 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(154)
 <223> Xaa = Any Amino Acid

<400> 1415
 Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu
 1 5 10 15
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser
 20 25 30
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Ile
 35 40 45
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr
 50 55 60
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn
 65 70 75 80
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu
 85 90 95
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala
 100 105 110
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile
 115 120 125
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu
 130 135 140
 Gly Thr His Gln Val Ser Lys Gln Asn Thr
 145 150

<210> 1416
 <211> 324
 <212> PRT
 <213> Unknown (H38g333 protein)

<220>
 <223> Synthetic construct

<400> 1416
 Met Ser Phe Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr
 1 5 10 15
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys
 20 25 30
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr
 35 40 45
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu
 50 55 60
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu
 65 70 75 80


```

Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Met Leu Val Asn Ile Leu
      85          90          95
Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr
      100        105        110
Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met
      115        120        125
Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His Pro Leu Gln Tyr Pro Ala
      130        135        140
Ile Met Thr Val Arg Phe Cys Gly Lys Leu Val Ser Phe Cys Trp Leu
      145        150        155        160
Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Tyr Ile Ser Gln Leu
      165        170        175
Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp
      180        185        190
Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Cys Ile
      195        200        205
Phe Tyr Thr Gln Ser Ser Leu Val Leu Phe Phe Thr Ser Met Tyr Ile
      210        215        220
Leu Arg Ser Tyr Ile Leu Leu Leu Thr Ala Val Phe Gln Val Pro Ser
      225        230        235        240
Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val
      245        250        255
Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro
      260        265        270
Thr Tyr Gly Ile Pro Thr Leu Leu Gln Lys Ile Leu Thr Leu Val Tyr
      275        280        285
Ser Val Thr Thr Pro Leu Phe Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      290        295        300
Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Phe Gly Met Arg Ile
      305        310        315        320
Arg Gln Asn Ser

```

<210> 1417

<211> 315

<212> PRT

<213> Unknown (H38g334 protein)

<220>

<223> Synthetic construct

<400> 1417

```

Met Ala Asn Ile Thr Arg Met Ala Asn His Thr Gly Lys Leu Asp Phe
  1          5          10          15
Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
      20        25        30
Val Val Ile Phe Val Val Phe Leu Lys Ala Leu Ser Gly Asn Ala Val
      35        40        45
Leu Ile Leu Leu Ile His Cys Asp Ala His Leu His Ser Pro Met Tyr
      50        55        60
Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
      65        70        75        80
Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Val
      85        90        95
Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
      100       105       110
Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
      115       120       125
Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
      130       135       140
Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp Gly

```

145		150		155		160
Phe Met Leu Thr Pro	Ile Thr Met Ser	Phe Pro Phe Cys Arg Ser Trp				
	165	170		175		
Glu Ile His His Phe Phe Cys Glu Val	Pro Ala Val Thr Ile Leu Ser					
	180	185		190		
Cys Ser Asp Thr Ser Leu Tyr Glu Thr	Leu Met Tyr Leu Cys Cys Val					
	195	200		205		
Leu Met Leu Leu Ile Pro Val Thr Ile	Ile Ser Ser Ser Tyr Leu Leu					
	210	215		220		
Ile Leu Leu Thr Val His Arg Met Asn Ser	Ala Glu Gly Arg Lys Lys					
	225	230		235		240
Ala Phe Ala Thr Cys Ser Ser His Leu Thr	Val Val Ile Leu Phe Tyr					
	245	250		255		
Gly Ala Ala Val Tyr Thr Tyr Met Leu	Pro Ser Ser Tyr His Thr Pro					
	260	265		270		
Glu Lys Asp Met Met Val Ser Val Phe Tyr	Thr Ile Leu Thr Pro Val					
	275	280		285		
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn	Lys Asp Val Met Gly Ala					
	290	295		300		
Leu Lys Lys Met Leu Thr Val Arg Phe Val	Leu					
	305	310		315		

<210> 1418

<211> 253

<212> PRT

<213> Unknown (H38g335 protein)

<220> .

<223> Synthetic construct

<221> VARIANT

<222> (1)...(253)

<223> Xaa = Any Amino Acid

<400> 1418

Ser His Leu Ser Val Ile Asp Thr Leu Tyr Ile Ser Thr Ile Val Pro														
1		5		10		15								
Lys Met Leu Val Asp Tyr Leu Met Gly Glu Gly Thr Ile Ser Phe Ile														
	20		25		30									
Ala Cys Thr Ala Gln Cys Phe Leu Tyr Met Gly Phe Met Gly Ala Glu														
	35		40		45									
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys														
	50		55		60									
Asn Pro Leu Arg Tyr Pro Val Leu Ile Ser Trp Arg Val Cys Trp Met														
	65		70		75									
Ile Leu Ala Ser Ser Trp Phe Gly Gly Ala Leu Asp Ser Phe Leu Leu														
	85		90		95									
Thr Pro Ile Thr Met Ser Leu Pro Phe Cys Ala Ser His Gln Ile Asn														
	100		105		110									
His Phe Phe Cys Glu Ala Pro Thr Met Leu Arg Leu Ala Cys Gly Asp														
	115		120		125									
Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys Val Ala Met Leu														
	130		135		140									
Leu Ile Pro Phe Ser Val Val Thr Ala Ser Tyr Thr Arg Ile Leu Ile														
	145		150		155									
Thr Val His Gln Met Thr Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala														
	165		170		175									
Thr Cys Ser Ser His Met Met Val Val Thr Leu Phe Tyr Gly Ala Ala														
	180		185		190									
Leu Tyr Thr Tyr Thr Leu Pro Gln Ser Tyr His Thr Pro Ile Lys Asp														
	195		200		205									

Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Ser L u Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg
 225 230 235 240
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg
 245 250

<210> 1419
 <211> 285
 <212> PRT
 <213> Unknown (H38g336 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(285)
 <223> Xaa = Any Amino Acid

<400> 1419
 Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp
 1 5 10 15
 Leu Thr Pro Val Phe Phe Leu Ser Pro Cys Pro Ser Pro Ile Ala
 20 25 30
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg
 35 40 45
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly
 50 55 60
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala
 65 70 75 80
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys
 85 90 95
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe
 100 105 110
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu
 115 120 125
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys
 130 135 140
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile
 145 150 155 160
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val
 165 170 175
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala
 180 185 190
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala
 195 200 205
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser
 210 215 220
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu
 225 230 235 240
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val
 245 250 255
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg
 260 265 270
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys
 275 280 285

<210> 1420
 <211> 271
 <212> PRT
 <213> Unknown (H38g337 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(271)

<223> Xaa = Any Amino Acid

<400> 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10          15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
 20          25          30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
 35          40          45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
 50          55          60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
 65          70          75          80
Leu Tyr Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
 85          90          95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
100         105         110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
115         120         125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
130         135         140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
145         150         155         160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
165         170         175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
180         185         190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
195         200         205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
210         215         220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
225         230         235         240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
245         250         255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
260         265         270

```

<210> 1421

<211> 310

<212> PRT

<213> Unknown (H38g338 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10          15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
 20          25          30

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile
 35 40 45
 Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe
 50 55 60
 Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr
 65 70 75 80
 Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
 85 90 95
 Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala
 100 105 110
 Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala
 130 135 140
 Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr
 145 150 155 160
 Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile
 165 170 175
 Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser
 180 185 190
 Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn
 195 200 205
 Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe
 210 215 220
 Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile
 260 265 270
 Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn
 275 280 285
 Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu
 290 295 300
 Ser Xaa Xaa Ile Thr Gln
 305 310

<210> 1422

<211> 217

<212> PRT

<213> Unknown (H38g339 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 1422

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met
 1 5 10 15
 Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val
 20 25 30
 Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe
 35 40 45
 Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe
 50 55 60
 Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser
 65 70 75 80
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

	85		90		95
Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu Pro Ile Ser Gly Ile					
	100		105		110
Leu Trp Ser Tyr Tyr Lys Ile Val Pro Tyr Ile Leu Arg Ile Ser Ser					
	115		120		125
Ser Asp Gly Lys Tyr Lys Ala Phe Ala Thr Cys Gly Ser His Leu Ala					
	130		135		140
Val Ala Cys Xaa Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser					
145		150		155	160
Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val Met Tyr					
	165		170		175
Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn					
	180		185		190
Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Pro Arg Thr Val Glu					
	195		200		205
Ser His Asp Leu Phe His Pro Phe Ser					
210		215			

<210> 1423

<211> 311

<212> PRT

<213> Unknown (H38g340 protein)

<220>

<223> Synthetic construct

<400> 1423

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly					
1	5		10		15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu					
	20		25		30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Thr Ala Leu					
	35		40		45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ser					
	50		55		60
His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys					
65		70		75	80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly					
	85		90		95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Gly Val Thr Glu Val					
	100		105		110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn					
	115		120		125
Pro Leu Leu Tyr Met Val Thr Met Ser Gln Lys Leu Arg Val Glu Leu					
	130		135		140
Thr Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Ser					
145		150		155	160
Ser Leu Ala Leu Arg Ile Leu Phe Tyr Arg Ser Asn Val Ile Asn His					
	165		170		175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Ser Leu Ala Cys Ser Asp Val					
	180		185		190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser					
	195		200		205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr					
	210		215		220
Ile Leu Lys Ile His Ser Ala Glu Ser Arg His Lys Ala Phe Ser Thr					
225		230		235	240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Ser His Gly Thr Ile Leu					
	245		250		255
Tyr Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Val Asp Lys					
	260		265		270

Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val
 290 295 300
 Met Gly Ser Lys Ile His Ser
 305 310

<210> 1424

<211> 321

<212> PRT

<213> Unknown (H38g341 protein)

<220>

<223> Synthetic construct

<400> 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu
 1 5 10 15
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val
 20 25 30
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile
 35 40 45
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala
 65 70 75 80
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
 85 90 95
 Ser Gly Cys Leu Val Gln Phe Phe Phe Cys Thr Phe Val Val Thr
 100 105 110
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala
 130 135 140
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr
 145 150 155 160
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile
 165 170 175
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro
 180 185 190
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn
 195 200 205
 Glu Ile Ser Thr Leu Leu Ile Ile Leu Thr Ser Tyr Ala Phe Ile Ile
 210 215 220
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr
 260 265 270
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg
 290 295 300
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr
 305 310 315 320
 Pro

<210> 1425

<211> 101

<212> PRT

<213> Unknown (H38g342 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1425

```

Cys Cys Pro Leu His His His Tyr Leu Pro Arg Gln Ser Leu Asp Gln
 1           5           10           15
Leu Thr Tyr Leu Ile Ala Leu Ile Phe Asn Phe Leu Phe Val Phe Gly
      20           25           30
Leu Gln Ser Ser Phe Ile Phe Leu Lys Ala Xaa Gln Cys Phe Pro Lys
      35           40           45
Asp Ile His Tyr Ile Phe Val Lys Ala Arg Arg Ala Ser Gly Tyr Leu
      50           55           60
Thr Tyr His Ile Ala Gly Asn Arg Ser Xaa Thr Val Phe Phe Leu Val
      65           70           75           80
Cys Asn Cys His Tyr Tyr Gly Asp Asp Ile Gly Xaa Val Xaa Ile Phe
      85           90           95
Tyr Val Asn Ile Leu
      100

```

<210> 1426

<211> 319

<212> PRT

<213> Unknown (H38g343 protein)

<220>

<223> Synthetic construct

<400> 1426

```

Met Pro Val Gly Lys Leu Val Phe Asn Gln Ser Glu Pro Thr Glu Phe
 1           5           10           15
Val Phe Arg Ala Phe Thr Thr Ala Thr Glu Phe Gln Val Leu Leu Phe
      20           25           30
Leu Leu Phe Leu Leu Leu Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala
      35           40           45
Ile Ile Trp Val Val Cys Thr His Ser Thr Leu Arg Thr Pro Met Tyr
      50           55           60
Phe Phe Leu Ser Asn Leu Ser Phe Leu Glu Leu Cys Tyr Thr Thr Val
      65           70           75           80
Val Val Pro Leu Met Leu Ser Asn Ile Leu Gly Ala Gln Lys Pro Ile
      85           90           95
Ser Leu Ala Gly Cys Gly Ala Gln Met Phe Phe Phe Val Thr Leu Gly
      100           105           110
Ser Thr Asp Cys Phe Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Val
      115           120           125
Ala Ile Cys His Pro Leu His Tyr Thr Leu Ile Met Thr Arg Glu Leu
      130           135           140
Cys Thr Gln Met Leu Gly Gly Ala Leu Gly Leu Ala Leu Phe Pro Ser
      145           150           155           160
Leu Gln Leu Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly His His
      165           170           175
Gln Glu Ile Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu
      180           185           190
Ala Cys Ala Asp Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser
      195           200           205

```


Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val
 210 215 220
 Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg
 225 230 235 240
 Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln
 245 250 255
 Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser
 260 265 270
 Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro
 275 280 285
 Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly
 290 295 300
 Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn
 305 310 315

<210> 1427

<211> 208

<212> PRT

<213> Unknown (H38g344 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(208)

<223> Xaa = Any Amino Acid

<400> 1427

Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
 20 25 30
 Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
 35 40 45
 Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
 65 70 75 80
 Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
 130 135 140
 Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
 145 150 155 160
 Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
 165 170 175
 Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr
 180 185 190
 Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile
 195 200 205

<210> 1428

<211> 321

<212> PRT

<213> Unknown (H38g345 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Pro Gly Leu Ser
 20           25           30
Leu Ser Met Tyr Leu Leu Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser Asn Pro Ser Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser
 85           90           95
Cys Leu Thr Gln Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp
 100          105          110
Met Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115          120          125
Ser Pro His Tyr Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe
 130          135          140
Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145          150          155          160
Trp Thr Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180          185          190
Val Ile Asp Ser Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe
 195          200          205
Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser
 210          215          220
Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr
 225          230          235          240
Cys Arg Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245          250          255
Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Gly Asp Gly Val
 260          265          270
Val Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Cys Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290          295          300
Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305          310          315          320
Cys

```

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1429

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1 5 10 15
 Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
 20 25 30
 Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
 35 40 45
 Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
 50 55 60
 Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
 65 70 75 80
 Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
 85 90 95
 Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
 100 105 110
 Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
 115 120 125
 Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
 130 135 140
 Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
 145 150 155 160
 Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
 165 170 175
 Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
 180 185 190
 Thr Ser Gly Asn Ser Lys Ile Ile Val Ile Leu Thr Ala Phe Met
 195 200 205
 Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
 210 215 220
 Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
 225 230 235 240
 Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
 245 250 255
 Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
 260 265 270
 Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
 275 280 285
 Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
 290 295 300
 Ile Gly Asn Phe Trp Val
 305 310

<210> 1430

<211> 336

<212> PRT

<213> Unknown (H38g347 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1430

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg
 1 5 10 15
 Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu

35	40	45			
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu					
50	55	60			
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala					
65	70	75			80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala					
85	90	95			
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu					
100	105	110			
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile					
115	120	125			
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly					
130	135	140			
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala					
145	150	155			160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val					
165	170	175			
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala					
180	185	190			
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala					
195	200	205			
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys					
210	215	220			
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa					
225	230	235			240
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr					
245	250	255			
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro					
260	265	270			
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met					
275	280	285			
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val					
290	295	300			
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile					
305	310	315			320
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys					
325	330	335			

<210> 1431

<211> 325

<212> PRT

<213> Unknown (H38g348 protein)

<220>

<223> Synthetic construct

<400> 1431

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln					
1	5	10	15		
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys					
20	25	30			
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr					
35	40	45			
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu					
50	55	60			
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser					
65	70	75			80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val					
85	90	95			
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr					
100	105	110			

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu
 115 120 125
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro L u Asn
 130 135 140
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile
 145 150 155 160
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
 165 170 175
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys
 180 185 190
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn
 195 200 205
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
 210 215 220
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg
 225 230 235 240
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 245 250 255
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr
 260 265 270
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
 275 280 285
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg
 305 310 315 320
 Lys Ile Ser Ser Leu
 325

<210> 1432

<211> 256

<212> PRT

<213> Unknown (H38g349 protein)

<220>

<223> Synthetic construct

<400> 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser
 1 5 10 15
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg
 20 25 30
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala
 35 40 45
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu
 50 55 60
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro
 65 70 75 80
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu
 85 90 95
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly
 100 105 110
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser
 115 120 125
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile
 130 135 140
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr
 145 150 155 160
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro
 165 170 175
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

	180		185		190
Phe	His	Gly	Val	Ile	Leu
	195		200		205
Ser	Trp	Leu	Val	Lys	Val
	210		215		220
Pro	Met	Leu	Asn	Pro	Leu
	225		230		235
Gly	Thr	Val	Arg	Lys	Leu
		245		250	

<210> 1433
 <211> 318
 <212> PRT
 <213> Unknown (H38g350 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(318)
 <223> Xaa = Any Amino Acid

<400> 1433

Met	Ala	Glu	Ser	Gly	Thr	Thr	Val	Thr	Glu	Phe	Phe	Leu	Arg	Gly	Phe
1				5					10					15	
Arg	Leu	Lys	Ala	Glu	Leu	Gln	Ile	Gly	Leu	Phe	Phe	Val	Phe	Leu	Val
			20					25					30		
Ile	Phe	Leu	Ile	Thr	Met	Gly	Gly	Asn	Leu	Gly	Met	Ile	Val	Leu	Met
		35				40					45				
Leu	Ile	Gln	Thr	Asp	Pro	Arg	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	His	Leu	Ser	Phe	Leu	Asp	Ile	Cys	Tyr	Ser	Ser	Val	Ile	Gly	Pro
	65				70				75						80
Gln	Leu	Leu	Glu	Thr	Leu	Ala	Thr	Asp	Lys	Met	Ile	Ile	Thr	Tyr	Glu
			85					90					95		
Arg	Cys	Ala	Ser	Gln	Phe	Phe	Phe	Phe	Thr	Leu	Cys	Ala	Ser	Ile	Glu
		100						105					110		
Cys	Phe	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys	
	115				120						125				
Asn	Pro	Leu	Leu	Tyr	Ala	Ile	Val	Met	Thr	Pro	Lys	Thr	Arg	Leu	Ala
	130				135						140				
Leu	Leu	Ala	Gly	Ala	Tyr	Ser	Gly	Ala	Ile	Val	Asn	Ser	Val	Ile	Cys
	145			150					155					160	
Thr	Gly	Cys	Thr	Phe	Ser	Ile	Ser	Phe	Ser	Lys	Ser	Asn	His	Val	Asp
			165					170					175		
Phe	Phe	Phe	Cys	Asp	Leu	Pro	Pro	Leu	Lys	Leu	Ala	Cys	Ser	Glu	
		180					185					190			
Thr	Arg	Pro	Arg	Glu	Trp	Val	Ile	Tyr	Leu	Ser	Ala	Phe	Leu	Val	Ile
	195					200					205				
Thr	Thr	Ser	Ile	Ser	Val	Ile	Leu	Thr	Ser	Tyr	Leu	Phe	Ile	Ile	Gln
	210				215					220					
Ser	Val	Leu	Lys	Ile	Arg	Thr	Ala	Gly	Gly	Arg	Ala	Lys	Thr	Phe	Ser
	225			230					235					240	
Thr	Cys	Ala	Ser	His	Met	Thr	Ala	Leu	Thr	Leu	Phe	Phe	Gly	Thr	Leu
			245					250					255		
Ile	Phe	Ile	Tyr	Leu	Lys	Gly	Asn	Met	Gly	Glu	Ser	Leu	Glu	Glu	Asp
		260				265						270			
Lys	Ile	Val	Ser	Ile	Phe	Tyr	Thr	Val	Val	Ile	Pro	Met	Leu	Asn	Pro
	275					280					285				
Met	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	Lys	Glu	Ala	Leu	Lys	Lys
	290				295					300					

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe
 20 25 30
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val
 35 40 45
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro
 65 70 75 80
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu
 100 105 110
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu
 130 135 140
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu
 145 150 155 160
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn
 165 170 175
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp
 180 185 190
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu
 195 200 205
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val
 210 215 220
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile
 245 250 255
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val
 260 265 270
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu
 290 295 300
 Ile Leu Asp Thr Lys Val Phe Ser Tyr
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

<400> 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
1      5      10      15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Ph Leu
20     25     30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
35     40     45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50     55     60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
65     70     75     80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
85     90     95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
100    105    110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
115    120    125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
130    135    140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
145    150    155    160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
165    170    175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
180    185    190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
195    200    205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
210    215    220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
225    230    235    240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
245    250    255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
260    265    270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
275    280    285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
290    295    300
Leu Ser Lys Ser Lys Pro Ala Arg
305    310

```

<210> 1436

<211> 254

<212> PRT

<213> Unknown (H38g353 protein)

<220>

<223> Synthetic construct

<400> 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
1      5      10      15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
20     25     30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
35     40     45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
50     55     60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
65     70     75     80

```


Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu
85 90 95
Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His
100 105 110
Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys
115 120 125
Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala
130 135 140
Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr
145 150 155 160
Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg
165 170 175
Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile
180 185 190
Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys
195 200 205
Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu
210 215 220
Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln
225 230 235 240
Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr
245 250

<210> 1437

<211> 188

<212> PRT

<213> Unknown (H38g354 protein)

<220>

<223> Synthetic construct

<400> 1437

Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
1 5 10 15
Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
20 25 30
Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
35 40 45
Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60
His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
65 70 75 80
Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
85 90 95
Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
100 105 110
Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
115 120 125
Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
130 135 140
Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
145 150 155 160
Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
165 170 175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Ser
180 185

<210> 1438

<211> 326

<212> PRT

<213> Unknown (H38g355 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1438

```

Leu Asn Phe Ile Ile Phe Phe Arg Xaa Thr Ser Tyr Ile Glu Pro Met
 1           5           10           15
Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val Phe
          20           25           30
Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu Ser
          35           40           45
Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu Ile
          50           55           60
Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser His
65           70           75           80
Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln Ile
          85           90           95
Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys Arg
          100          105          110
Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys Tyr
          115          120          125
Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn Pro
          130          135          140
Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe Leu
145          150          155          160
Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr Thr
          165          170          175
Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe Phe
          180          185          190
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met Thr
          195          200          205
Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu Ala
210          215          220
Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala Ile
225          230          235          240
Leu Arg Val Lys Ser Ala Gly Gly Xaa Ala Lys Thr Phe Ser Thr Cys
          245          250          255
Thr Ser His Leu Thr Thr Val Val Leu Phe Phe Gly Thr Leu Ala Phe
          260          265          270
Met Tyr Gln Arg Ser Asn Ser Ala Lys Ser Ser Glu Glu Asp Lys Ile
          275          280          285
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu Ile
          290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Gly Lys Leu Val
305          310          315          320
Gly Lys Phe Gln Phe Pro
          325

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<210> 1439

<211> 328

<212> PRT

<213> Unknown (H38g356 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1439

```

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1           5           10           15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
 20           25           30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
 35           40           45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
 50           55           60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
 65           70           75           80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
 85           90           95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
 100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
 115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
 130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
 145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
 165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
 180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
 195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
 210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
 225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
 245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
 260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
 275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
 290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
 305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
 325

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<210> 1440

<211> 311

<212> PRT

<213> Unknown (H38g357 protein)

<220>

<223> Synthetic construct

<400> 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Ph Leu
 20           25           30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

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```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
      145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
      290      295      300
Met Gly Ser Lys Ile His Ser
305      310

```

<210> 1441

<211> 209

<212> PRT

<213> Unknown (H38g358 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(209)

<223> Xaa = Any Amino Acid

<400> 1441

```

Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
 1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
      50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
      65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr
 100 105 110
 Lys Ala Ph Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
 115 120 125
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser
 130 135 140
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro
 145 150 155 160
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser
 165 170 175
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu
 180 185 190
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val
 195 200 205
 Lys

<210> 1442

<211> 212

<212> PRT

<213> Unknown (H38g359 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe
 1 5 10 15
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp
 20 25 30
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile
 35 40 45
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser
 50 55 60
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu
 65 70 75 80
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu
 85 90 95
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu
 100 105 110
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala
 115 120 125
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro
 130 135 140
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser
 145 150 155 160
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr
 165 170 175
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser
 180 185 190
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys
 195 200 205
 Ala Lys Leu Phe
 210

<210> 1443

<211> 315

<212> PRT

<213> Unknown (H38g360 protein)

<220>

<223> Synthetic construct

<400> 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1          5          10          15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
          20          25          30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
          35          40          45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
          50          55          60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
          65          70          75          80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
          85          90          95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
          100          105          110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
          115          120          125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
          130          135          140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
          145          150          155          160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
          165          170          175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
          180          185          190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
          195          200          205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
          210          215          220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
          225          230          235          240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
          245          250          255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
          260          265          270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
          275          280          285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
          290          295          300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
          305          310          315

```

<210> 1444

<211> 278

<212> PRT

<213> Unknown (H38g361 protein)

<220>

<223> Synthetic construct

<400> 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1          5          10          15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
          20          25          30

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met
 35 40 45
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys
 50 55 60
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala
 65 70 75 80
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro
 85 90 95
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly
 100 105 110
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe
 115 120 125
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser
 130 135 140
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg
 145 150 155 160
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val
 165 170 175
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val
 180 185 190
 Leu Glu Leu Ser Ser Arg Arg Ala Leu Lys Ala Phe Asn Thr Cys
 195 200 205
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly
 210 215 220
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val
 225 230 235 240
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu
 245 250 255
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met
 260 265 270
 Phe Ser Gln Gly Gly Lys
 275

<210> 1445

<211> 319

<212> PRT

<213> Unknown (H38g362 protein)

<220>

<223> Synthetic construct

<400> 1445

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
 1 5 10 15
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20 25 30
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50 55 60
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65 70 75 80
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85 90 95
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
 100 105 110
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
 130 135 140
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

```

145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
245          250          255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
260          265          270
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
275          280          285
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
290          295          300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
305          310          315

```

<210> 1446

<211> 322

<212> PRT

<213> Unknown (H38g363 protein)

<220>

<223> Synthetic construct

<400> 1446

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
20     25     30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
35     40     45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
50     55     60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65     70     75     80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
85     90     95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
100    105    110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115    120    125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
130    135    140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145    150    155    160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
165    170    175
Phe Phe Cys Asp Leu Pro Leu Ala Thr Lys Leu Ala Cys Ile Asp Thr
180    185    190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
195    200    205
Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
210    215    220
Val Arg Asn Arg Ser Ser Val Ser Met Val Lys Ala His Ser Thr Leu
225    230    235    240

```


<210> 1447
<211> 322
<212> PRT
<213> Unknown (H38g364 protein)

<400> 1447															
Met	Leu	Gly	Pro	Ala	Tyr	Asn	His	Thr	Met	Glu	Thr	Pro	Ala	Ser	Phe
1				5					10					15	
Leu	Leu	Val	Gly	Ile	Pro	Gly	Leu	Gln	Ser	Ser	His	Leu	Trp	Leu	Ala
			20					25					30		
Ile	Ser	Leu	Ser	Ala	Met	Tyr	Ile	Ile	Ala	Leu	Leu	Gly	Asn	Thr	Ile
		35					40					45			
Ile	Val	Thr	Ala	Ile	Trp	Met	Asp	Ser	Thr	Arg	His	Glu	Pro	Met	Tyr
	50					55					60				
Cys	Phe	Leu	Cys	Val	Leu	Ala	Ala	Val	Asp	Ile	Val	Met	Ala	Ser	Ser
65					70					75					80
Val	Val	Pro	Lys	Met	Val	Ser	Ile	Phe	Cys	Ser	Gly	Asp	Ser	Ser	Ile
				85					90					95	
Ser	Phe	Ser	Ala	Cys	Phe	Thr	Gln	Met	Phe	Phe	Val	His	Leu	Ala	Thr
			100					105					110		
Ala	Val	Glu	Thr	Gly	Leu	Leu	Leu	Thr	Met	Ala	Phe	Asp	Arg	Tyr	Val
		115					120					125			
Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Lys	Arg	Ile	Leu	Thr	Pro	Gln	Val
	130						135					140			
Met	Leu	Gly	Met	Ser	Met	Ala	Ile	Thr	Ile	Arg	Ala	Ile	Ile	Ala	Ile
145					150					155					160
Thr	Pro	Leu	Ser	Trp	Met	Val	Ser	His	Leu	Pro	Phe	Cys	Gly	Ser	Asn
				165					170					175	
Val	Val	Val	His	Ser	Tyr	Cys	Glu	His	Ile	Ala	Leu	Ala	Arg	Leu	Ala
			180					185					190		
Cys	Ala	Asp	Pro	Val	Pro	Ser	Ser	Leu	Tyr	Ser	Leu	Ile	Gly	Ser	Ser
		195					200					205			
Leu	Met	Val	Gly	Ser	Asp	Val	Ala	Phe	Ile	Ala	Ala	Ser	Tyr	Ile	Leu
	210					215					220				
Ile	Leu	Lys	Ala	Val	Phe	Gly	Leu	Ser	Ser	Lys	Thr	Ala	Gln	Leu	Lys
225					230					235					240
Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Val	Gly	Val	Met	Ala	Leu	Tyr	Tyr
				245					250					255	
Leu	Pro	Gly	Met	Ala	Ser	Ile	Tyr	Ala	Ala	Trp	Leu	Gly	Gln	Asp	Val
			260					265					270		
Val	Pro	Leu	His	Thr	Gln	Val	Leu	Leu	Ala	Asp	Leu	Tyr	Val	Ile	Ile
		275					280					285			
Pro	Ala	Thr	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Met	Arg	Thr	Lys	Gln	Leu
	290					295					300				
Arg	Glu	Arg	Ile	Trp	Ser	Tyr	Leu	Met	His	Val	Leu	Phe	Asp	His	Ser

305
Asn Leu

310

315

320

<210> 1448
<211> 314
<212> PRT
<213> Unknown (H38g365 protein)

<220>
<223> Synthetic construct

<400> 1448

Met	Glu	Gly	Phe	Asn	Tyr	Ser	Arg	Val	Ser	Glu	Phe	Met	Leu	Leu	Gly
1				5					10					15	
Leu	Thr	Asp	Ser	Pro	Glu	Leu	Gln	Ile	Phe	Phe	Ser	Val	Val	Phe	Ser
			20				25						30		
Val	Phe	Tyr	Leu	Met	Thr	Met	Leu	Gly	Asn	Cys	Leu	Ile	Leu	Leu	Thr
		35					40					45			
Val	Leu	Ser	Thr	Ser	His	Leu	His	Ser	Arg	Met	Tyr	Phe	Leu	Leu	Ser
	50					55					60				
Asn	Met	Ser	Ile	Asp	Met	Cys	Leu	Ser	Ser	Phe	Ala	Thr	Pro	Lys	Met
65					70					75				80	
Ile	Met	Asp	Phe	Phe	Ala	Leu	Arg	Lys	Thr	Ile	Ser	Phe	Glu	Gly	Cys
			85						90					95	
Ile	Ser	Gln	Ile	Phe	Phe	Leu	His	Leu	Phe	Asn	Gly	Thr	Glu	Ile	Val
			100					105					110		
Leu	Leu	Ile	Ser	Met	Ser	Phe	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Lys	Pro
		115					120					125			
Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Gln	Arg	Val	Cys	Val	Glu	Leu	Val
	130					135					140				
Ala	Val	Ser	Cys	Trp	Thr	Val	Gly	Phe	Leu	His	Thr	Met	Ser	Gln	Leu
145					150					155					160
Val	Phe	Ala	Leu	Tyr	Leu	Pro	Phe	Cys	Val	Pro	Asn	Val	Val	Asp	Ser
			165						170					175	
Phe	Phe	Cys	Asp	Leu	Pro	Leu	Val	Ile	Gln	Leu	Ala	Cys	Ile	Asp	Ile
			180					185					190		
Tyr	Val	Leu	Gly	Thr	Ser	Met	Ile	Ser	Thr	Ser	Gly	Val	Ile	Ala	Leu
	195					200						205			
Ile	Ser	Phe	Leu	Leu	Leu	Leu	Thr	Ser	Tyr	Ile	Ile	Val	Leu	Asn	Ile
	210					215					220				
Val	Arg	Asp	Tyr	Ser	Ser	Thr	Gly	Ser	Ser	Lys	Ala	Leu	Ser	Thr	Cys
225				230						235				240	
Thr	Ala	His	Phe	Ile	Val	Val	Leu	Met	Phe	Phe	Gly	Pro	Cys	Ile	Phe
			245						250					255	
Ile	Tyr	Val	Trp	Pro	Ser	Thr	Asn	Phe	Leu	Val	Asp	Lys	Ile	Leu	Ser
		260					265						270		
Val	Phe	Tyr	Thr	Ile	Phe	Thr	Pro	Phe	Leu	Asn	Pro	Leu	Ile	Tyr	Thr
	275					280						285			
Leu	Arg	Asn	Gln	Glu	Val	Lys	Thr	Ala	Met	Lys	Lys	Lys	Leu	Asn	Ile
	290					295					300				
Gln	Tyr	Phe	Ser	Leu	Gly	Lys	Thr	Ala	Pro						
305					310										

<210> 1449
<211> 317
<212> PRT
<213> Unknown (H38g366 protein)

<220>
<223> Synthetic construct

<400> 1449

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
1           5           10           15
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
20           25           30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
35           40           45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
50           55           60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
65           70           75           80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
85           90           95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
100          105          110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115          120          125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
130          135          140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
145          150          155          160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
165          170          175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
180          185          190
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu
195          200          205
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile
210          215          220
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr
225          230          235          240
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val
245          250          255
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro
260          265          270
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro
275          280          285
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu
290          295          300
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg
305          310          315

```

<210> 1450

<211> 101

<212> PRT

<213> Unknown (H38g367 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1450

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
1           5           10           15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
20           25           30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```

```

      35              40              45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50              55              60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
  65              70              75              80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
      85              90              95
Cys Cys Leu Ala Glu
      100

```

<210> 1451
 <211> 169
 <212> PRT
 <213> Unknown (H38g368 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(169)
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1              5              10              15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
      20              25              30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
      35              40              45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
      50              55              60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
  65              70              75              80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
      85              90              95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
      100              105              110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
      115              120              125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
      130              135              140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
  145              150              155              160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
      165

```

<210> 1452
 <211> 279
 <212> PRT
 <213> Unknown (H38g369 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(279)
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1              5              10              15

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
 20 25 30
 Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
 35 40 45
 Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
 50 55 60
 Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
 65 70 75 80
 Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
 85 90 95
 Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
 100 105 110
 Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
 115 120 125
 Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
 130 135 140
 Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
 145 150 155 160
 His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
 165 170 175
 Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
 180 185 190
 Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
 195 200 205
 Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
 210 215 220
 Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
 225 230 235 240
 Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
 245 250 255
 Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
 260 265 270
 Ser Ile Ile Leu Thr Leu Val
 275

<210> 1453

<211> 154

<212> PRT

<213> Unknown (H38g370 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 1453

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
 1 5 10 15
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
 20 25 30
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
 35 40 45
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
 50 55 60
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
 65 70 75 80
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
 85 90 95
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

```

          100          105          110
Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
          115          120          125
Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
          130          135          140
Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
145          150

```

<210> 1454
 <211> 186
 <212> PRT
 <213> Unknown (H38g371 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

```

<400> 1454
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
 1          5          10          15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
          20          25          30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Pro Thr Pro Asn Ile Phe
          35          40          45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
          50          55          60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
65          70          75          80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
          85          90          95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
          100          105          110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
          115          120          125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
          130          135          140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145          150          155          160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
          165          170          175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
          180          185

```

<210> 1455
 <211> 142
 <212> PRT
 <213> Unknown (H38g372 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(142)
 <223> Xaa = Any Amino Acid

```

<400> 1455
Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
 1          5          10          15

```

```

Leu Phe Ph  His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Il  Lys Lys
      20      25      30
Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
      35      40      45
Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
      50      55      60
Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
65      70      75      80
Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
      85      90      95
Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
      100      105      110
Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
      115      120      125
Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
      130      135      140

```

<210> 1456
 <211> 82
 <212> PRT
 <213> Unknown (H38g373 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(82)
 <223> Xaa = Any Amino Acid

```

<400> 1456
Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His
 1      5      10      15
Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu
      20      25      30
Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys
      35      40      45
Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile
      50      55      60
Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly
65      70      75      80
Tyr Ser

```

<210> 1457
 <211> 207
 <212> PRT
 <213> Unknown (H38g374 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(207)
 <223> Xaa = Any Amino Acid

```

<400> 1457
Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
 1      5      10      15
Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
      20      25      30
Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

```

```

      35              40              45
Xaa Trp Ala Leu Met Cys Val Leu Glu Asn Lys Thr Tyr Ala Ser Val
  50              55              60
Arg Leu Val Xaa Arg Phe Gly Trp Xaa Lys Leu Ala Asn Xaa Met Ser
  65              70              75              80
Val Leu Tyr Leu Glu Ala Asn Leu Gly Asn Met Asp Asn Ala Leu Leu
      85              90              95
Lys Xaa Leu Lys Arg Asn Tyr Phe Val Phe Val Phe Thr Ser Phe Leu
      100              105              110
Phe Gly Cys Ile Ala Phe Lys Xaa Lys Glu Ile Phe Tyr Pro Tyr Thr
      115              120              125
Ser Ile Cys Ile Tyr His Leu Met Met Glu Arg Lys Val Ser Cys
      130              135              140
Leu Thr Leu Ile Cys Leu Ala Xaa Asp Leu Xaa His Phe Xaa Cys Ser
      145              150              155              160
Leu Val Thr Val Leu Ser Leu Glu Cys Xaa Gln Leu Asp Ile Cys Asn
      165              170              175
Val Val Thr Tyr Phe Asn Thr Met Val Xaa Ser Thr Thr Gly Ser Asn
      180              185              190
Ser Xaa Thr Pro Asn His Ser Val Leu Ile Cys Asn Met Leu Lys
      195              200              205

```

<210> 1458

<211> 313

<212> PRT

<213> Unknown (H38g375 protein)

<220>

<223> Synthetic construct

<400> 1458

```

Met Arg Asn Leu Ser Gly Gly His Val Glu Glu Phe Val Leu Val Gly
  1              5              10              15
Phe Pro Thr Thr Pro Pro Leu Gln Leu Leu Phe Val Leu Phe Phe
      20              25              30
Ala Ile Tyr Leu Leu Thr Leu Leu Glu Asn Ala Leu Ile Val Phe Thr
      35              40              45
Ile Trp Leu Ala Pro Ser Leu His Arg Pro Met Tyr Phe Phe Leu Gly
      50              55              60
His Leu Ser Phe Leu Glu Leu Trp Tyr Ile Asn Val Thr Ile Pro Arg
      65              70              75              80
Leu Leu Ala Ala Phe Leu Thr Gln Asp Gly Arg Val Ser Tyr Val Gly
      85              90              95
Cys Met Thr Gln Leu Tyr Phe Phe Ile Ala Leu Ala Cys Thr Glu Cys
      100              105              110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gly
      115              120              125
Pro Leu Leu Tyr Pro Ser Leu Met Pro Ser Ser Leu Ala Thr Arg Leu
      130              135              140
Ala Ala Ala Ser Trp Gly Ser Gly Phe Phe Ser Ser Met Met Lys Leu
      145              150              155              160
Leu Phe Ile Ser Gln Leu Ser Tyr Cys Gly Pro Asn Ile Ile Asn His
      165              170              175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Asn Leu Thr Cys Ser Asp Lys
      180              185              190
Glu Gln Ala Glu Leu Val Asp Phe Leu Leu Ala Leu Val Met Ile Leu
      195              200              205
Leu Pro Leu Leu Ala Val Val Ser Ser Tyr Thr Ala Ile Ile Ala Ala
      210              215              220
Ile Leu Arg Ile Pro Thr Ser Arg Gly Arg His Lys Ala Phe Ser Thr
      225              230              235              240

```


[illegible]

<210> 1459

<211> 322

<212> PRT

<213> Unknown (H38g376 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (322)

<223> Xaa = Any Amino Acid

<400> 1459

His 1	Thr	Glu	Pro	Leu 5	Asn	Leu	Thr	Gly	Val 10	Xaa	Glu	Phe	Leu 15	Leu	
Gly	Leu	Ser	Glu	Asp 20	Pro	Glu	Leu	Gln 25	Pro	Val	Leu	Ala	Leu 30	Leu	Ser
Leu	Ser	Leu	Ser	Met 35	Tyr	Leu	Val 40	Thr	Val	Leu	Arg	Asn 45	Leu	Leu	Ser
Ile 50	Leu	Ala	Val	Ser	Ser	Asp 55	Ser	His	Leu	His	Thr 60	Pro	Met	Tyr	Phe
Phe 65	Leu	Ser	Asn	Leu	Cys 70	Trp	Ala	Asp	Ile	Gly 75	Tyr	Thr	Ser	Ala	Thr
Val	Pro	Lys	Met 85	Ile	Val	Asp	Thr	Gln	Ser 90	His	Gly	Arg	Val 95	Ile	Ser
His	Ala	Gly	Cys 100	Leu	Thr	Gln	Met	Ser 105	Phe	Leu	Val	Leu	Phe 110	Ala	Cys
Ile	Glu	Asp	Met 115	Leu	Leu	Thr	Val 120	Met	Ala	Tyr	Asp	Cys 125	Phe	Val	Ala
Ile 130	Cys	Cys	Pro	Leu	His	Tyr 135	Pro	Val	Ile	Val	Asn 140	Pro	His	Leu	Cys
Val 145	Phe	Phe	Val	Leu	Val	Ser 150	Phe	Phe	Leu	Ser 155	Leu	Leu	Asp 160	Ser	Gln
Leu	His	Ser	Trp 165	Ile	Val	Leu	Gln	Phe 170	Thr	Ile	Ile	Lys	Asn 175	Val	Glu
Ile	Ser	Asn 180	Phe	Val	Cys	Asp	Pro 185	Ser	Gln	Leu	Leu	Lys 190	Leu	Ala	Cys
Ser	Asp 195	Ser	Val	Ile	Asn	Ser	Ile 200	Phe	Ile	Tyr	Phe 205	Asp	Ser	Thr	Met
Phe 210	Gly	Phe	Leu	Pro	Ile	Ser 215	Gly	Ile	Leu	Leu 220	Ser	Tyr	Ser	Lys	Ile
Val 225	Pro	Ser	Val	Leu	Arg 230	Met	Ser	Ser	Ser	Asp 235	Gly	Lys	Tyr	Lys	Ala
Phe	Ser	Thr	Cys 245	Gly	Ser	His	Leu	Ala 250	Val	Val	Cys	Xaa	Phe 255	Asp	Gly
Thr	Gly	Ile	Gly 260	Met	Tyr	Leu	Thr	Ser 265	Ala	Val	Ala	Pro 270	Pro	Pro	Arg
Asn	Gly 275	Val	Glu	Ser	Gly	Met 280	Tyr	Ala	Val	Val 285	Thr	Pro	Met	Leu	
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	His	Thr	Gln	Ser	Ala	Leu

290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro
 305 310 315 320
 Phe Ser

<210> 1400
 <211> 186
 <212> PRT
 <213> Unknown (H38g377 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

<400> 1460
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu
 1 5 10 15
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser
 20 25 30
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn
 35 40 45
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val
 50 55 60
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr
 65 70 75 80
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp
 85 90 95
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly
 100 105 110
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His
 115 120 125
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr
 130 135 140
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg
 145 150 155 160
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr
 165 170 175
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu
 180 185

<210> 1461
 <211> 336
 <212> PRT
 <213> Unknown (H38g378 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(336)
 <223> Xaa = Any Amino Acid

<400> 1461
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe
 20 25 30

Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys
 115 120 125
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala
 145 150 155 160
 Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 165 170 175
 Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
 180 185 190
 Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala
 195 200 205
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys
 210 215 220
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr
 245 250 255
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Pro
 260 265 270
 Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
 275 280 285
 Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val
 290 295 300
 Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile
 305 310 315 320
 Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys
 325 330 335

<210> 1462

<211> 157

<212> PRT

<213> Unknown (H38g379 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1462

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
 1 5 10 15
 Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
 20 25 30
 Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
 35 40 45
 Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
 50 55 60
 Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu

65					70					75				80	
Cys	Thr	Cys	Leu	Asp	Thr	Phe	Thr	Lys	Ser	Tyr	Ile	Thr	Xaa	Ile	Arg
				85					90					95	
Gly	Leu	Lys	Gly	Phe	Asn	His	Leu	Cys	Phe	Leu	Leu	His	Tyr	Cys	His
			100					105					110		
Cys	Ala	Arg	Ala	Gln	Val	Ser	Xaa	Asn	Ala	Pro	Trp	Ser	Leu	Ala	Gln
		115					120					125			
Arg	Cys	Gln	Pro	Asn	Met	Leu	Ile	Arg	Xaa	Leu	Phe	Cys	Leu	Lys	Leu
	130					135					140				
Val	Val	His	Asp	Arg	Leu	Xaa	His	Val	Leu	Ser	Leu	Leu			
145					150					155					

<210> 1463

<211> 325

<212> PRT

<213> Unknown (H38g380 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1463

Met	Lys	Ile	Asn	Gln	Thr	Ile	Leu	Lys	Glu	Phe	Ile	Leu	Val	Gly	Phe
1				5					10					15	
Ser	Val	Tyr	Pro	His	Val	Gln	Thr	Phe	Leu	Phe	Val	Val	Phe	Phe	Cys
			20					25					30		
Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Leu	Thr	Ile	Met	Gly	Leu	Thr
		35				40					45				
Xaa	Val	Asp	Arg	Ser	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Ala
	50				55					60					
Leu	Ser	Phe	Ser	Glu	Thr	Cys	Tyr	Thr	Leu	Thr	Ile	Val	Pro	Lys	Met
65				70				75						80	
Leu	Glu	Asp	Leu	Leu	Ala	Lys	Asp	Arg	Ser	Ile	Ser	Val	Thr	Gly	Cys
			85					90					95		
Ser	Leu	Gln	Met	Cys	Phe	Phe	Leu	Gly	Leu	Gly	Gly	Thr	Asn	Cys	Ile
		100						105					110		
Ile	Leu	Thr	Leu	Met	Gly	Tyr	Asp	Arg	Phe	Leu	Ala	Ile	Cys	Asn	Pro
	115				120						125				
Leu	Arg	Tyr	Pro	Leu	Leu	Met	Thr	Asn	Ile	Val	Cys	Gly	Gln	Leu	Val
	130				135					140					
Ala	Ser	Ala	Cys	Thr	Ala	Gly	Phe	Phe	Ile	Ser	Leu	Thr	Glu	Thr	Ala
145				150				155						160	
Leu	Ile	Phe	Arg	Asp	Ser	Phe	Cys	Arg	Pro	Asn	Leu	Val	Lys	His	Phe
			165					170					175		
Phe	Cys	His	Met	Leu	Ala	Val	Ile	Arg	Leu	Ser	Cys	Ile	Asp	Ser	Asn
		180						185					190		
His	Thr	Glu	Phe	Ile	Ile	Thr	Leu	Ile	Ser	Val	Ser	Gly	Leu	Leu	Gly
	195					200						205			
Thr	Leu	Leu	Leu	Ile	Ile	Leu	Thr	Asp	Val	Phe	Ile	Ile	Ser	Thr	Val
	210				215						220				
Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Thr	Thr	Cys
225				230						235				240	
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Phe	Gly	Phe	Ala	Ser	Ile
			245					250					255		
Val	Tyr	Leu	Lys	Pro	Glu	Ala	Ser	Gly	Asp	Asp	Thr	Leu	Ile	Ala	Val
	260							265				270			
Pro	Tyr	Thr	Val	Ile	Thr	Pro	Phe	Leu	Ser	Pro	Ile	Ile	Phe	Ser	Leu
	275					280						285			

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
 290 295 300
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
 305 310 315 320
 Gly Leu Asn Val Pro
 325

<210> 1464
 <211> 313
 <212> PRT
 <213> Unknown (H38g381 protein)

<220>
 <223> Synthetic construct

<400> 1464
 Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu
 20 25 30
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ala
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly
 85 90 95
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala
 115 120 125
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu
 130 135 140
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr
 145 150 155 160
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His
 165 170 175
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr
 180 185 190
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu
 195 200 205
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln
 260 265 270
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile
 275 280 285
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala
 290 295 300
 Phe Arg Gly Arg Leu Leu Gly Lys Gly
 305 310

<210> 1465
 <211> 289
 <212> PRT
 <213> Unknown (H38g382 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1465

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Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65           70           75           80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85           90           95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

<210> 1466

<211> 318

<212> PRT

<213> Unknown (H38g383 protein)

<220>

<223> Synthetic construct

<400> 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Il  Ile Thr Val
      35              40              45
Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser
      50              55              60
Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
      65              70              75              80
Met Leu Ser Ser Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys
      85              90              95
Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys
      100             105             110
Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro
      115             120             125
Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr
      130             135             140
Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala
      145             150             155             160
Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile
      165             170             175
Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg
      180             185             190
Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile
      195             200             205
Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala
      210             215             220
Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser
      225             230             235             240
Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val
      245             250             255
Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp
      260             265             270
Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro
      275             280             285
Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys
      290             295             300
His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly
      305             310             315

```

<210> 1467

<211> 129

<212> PRT

<213> Unknown (H38g384 protein)

<220>

<223> Synthetic construct

<400> 1467

```

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile
  1              5              10              15
Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu
      20              25              30
Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr
      35              40              45
Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
      50              55              60
Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu
      65              70              75              80
Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr
      85              90              95
Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
      100             105             110
Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

```

Val 115 120 125

<210> 1468
 <211> 162
 <212> PRT
 <213> Unknown (H38g385 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(162)
 <223> Xaa = Any Amino Acid

<400> 1468
 Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
 1 5 10 15
 Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
 20 25 30
 Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
 35 40 45
 Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
 50 55 60
 Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
 65 70 75 80
 Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
 85 90 95
 Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr
 100 105 110
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu
 115 120 125
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser
 130 135 140
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr
 145 150 155 160
 Val Gln

<210> 1469
 <211> 327
 <212> PRT
 <213> Unknown (H38g386 protein)

<220>
 <223> Synthetic construct

<400> 1469
 Met Leu Thr Pro Asn Asn Ala Cys Ser Val Pro Thr Ser Phe Arg Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Ile Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Leu Gly Asn Ile Thr Ile Leu
 35 40 45
 Ala Val Val Arg Met Glu Tyr Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Val Ile Asp Leu Val Leu Ser Thr Ser Thr Met
 65 70 75 80
 Pro Lys Leu Leu Ala Ile Phe Trp Phe Gly Ala His Asn Ile Gly Val
 85 90 95


```

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val
      100      105      110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile
      115      120      125
Cys Asp Pr Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly
      130      135      140
Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro
      145      150      155      160
Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile
      165      170      175
Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys
      180      185      190
Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe
      195      200      205
Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met
      210      215      220
Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys
      225      230      235      240
Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr
      245      250      255
Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val
      260      265      270
Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile
      275      280      285
Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile
      290      295      300
Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile
      305      310      315      320
Lys Ala Arg Thr Gln Thr Arg
      325

```

<210> 1470

<211> 323

<212> PRT

<213> Unknown (H38g387 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1470

```

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
  1      5      10      15
Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
  20      25      30
Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
  35      40      45
Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
  50      55      60
Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
  65      70      75      80
Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
  85      90      95
His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
  100     105     110
Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
  115     120     125
Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

```

130	135	140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val		
145	150	155
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile		
	165	170
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr		
	180	185
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn		
	195	200
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala		
	210	215
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ile Leu Arg Ile		
225	230	235
Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His		
	245	250
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile		
	260	265
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met		
	275	280
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met		
	290	295
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser		
305	310	315
His Ser Ser		

<210> 1471

<211> 202

<212> PRT

<213> Unknown (H38g388 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1471

Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile	
1	5
Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val	
	20
Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser	
	35
Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe	
	50
Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr	
65	70
Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu	
	85
Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu	
	100
Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser	
	115
Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys	
	130
Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe	
145	150
Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile	
	165
	170
	175

Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg
 180 185 190
 Lys Trp Asp Ala His Ser Ser Val Lys Phe
 195 200

<210> 1472

<211> 311

<212> PRT

<213> Unknown (H38g389 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1472

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
 35 40 45
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
 85 90 95
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
 100 105 110
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
 130 135 140
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
 145 150 155 160
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
 165 170 175
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
 180 185 190
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu
 195 200 205
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser
 210 215 220
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr
 225 230 235 240
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile
 245 250 255
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His
 260 265 270
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro
 275 280 285
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu
 290 295 300
 Ser Tyr Ile Gln Arg Ala Arg
 305 310

<210> 1473

<211> 315

<212> PRT

<213> Unknown (H38g390 protein)

<220>

<223> Synthetic construct

<400> 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20           25           30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
          145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
          305          310          315

```

<210> 1474

<211> 326

<212> PRT

<213> Unknown (H38g391 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1474

```

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
          20           25           30
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
          145          150          155          160
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
          165          170          175
His Phe Phe Cys Glu Val Gln Ala Leu Lys Leu Ala Cys Ala Asp
          180          185          190
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
          210          215          220
Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser
          305          310          315          320
Gly Ala Cys Cys Ala Pro
          325

```

<210> 1475

<211> 314

<212> PRT

<213> Unknown (H38g392 protein)

<220>

<223> Synthetic construct

<400> 1475

```

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1           5           10           15
Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
          20           25           30
Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
          35           40           45
Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100          105          110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115          120          125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130          135          140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
      145          150          155          160
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180          185          190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195          200          205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
      210          215          220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
      225          230          235          240
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245          250          255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260          265          270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
      290          295          300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
305          310

```

<210> 1476

<211> 117

<212> PRT

<213> Unknown (H38g393 protein)

<220>

<223> Synthetic construct

<400> 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1          5          10          15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20          25          30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35          40          45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50          55          60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
      65          70          75          80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85          90          95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100          105          110
Pro Arg Lys Asp Val
      115

```

<210> 1477

<211> 316

<212> PRT

<213> Unknown (H38g394 protein)

<220>

<223> Synthetic construct

<400> 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
          20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
          35           40           45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
          50           55           60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65          70          75          80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
          85          90          95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
          100         105         110
Ser Phe Leu Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115         120         125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
          130         135         140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145         150         155         160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
          165         170         175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
          180         185         190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
          195         200         205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
          210         215         220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225         230         235         240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
          245         250         255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
          260         265         270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
          275         280         285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
          290         295         300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
305         310         315

```

<210> 1478

<211> 330

<212> PRT

<213> Unknown (H38g395 protein)

<220>

<223> Synthetic construct

<400> 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
 1           5           10           15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
          20           25           30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```
<210> 1479
<211> 227
<212> PRT
<213> Unknown (H38g396 protein)
```

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(227)
<223> Xaa = Any Amino Acid
```

<400> 1479															
Gly	Lys	Glu	Arg	Glu	Thr	Arg	Val	Trp	Arg	Pro	Arg	Ala	Gln	Asp	Arg
1				5					10					15	
Gly	Val	Ser	Thr	Arg	His	Ala	Ala	Arg	Val	Thr	Ser	Tyr	Gln	Glu	Cys
			20					25					30		
Gly	Val	Arg	Gly	Gly	Gly	Val	Leu	Cys	Gly	Ala	Val	Arg	Pro	Ser	Pro
		35					40					45			
Leu	Asp	Ala	Gln	Leu	His	Asn	Val	Ile	Ala	Tyr	Arg	Arg	Thr	Cys	Phe
	50					55					60				
Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Val	Trp	Asp	Pro	Ser	Gln	Leu	Pro
65					70					75					80


```

Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
      85                      90                      95
Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
      100                      105                      110
Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly
      115                      120                      125
Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
      130                      135                      140
Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
      145                      150                      155                      160
Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
      165                      170                      175
Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
      180                      185                      190
Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
      195                      200                      205
Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
      210                      215                      220
Lys Val Lys
      225

```

<210> 1480

<211> 332

<212> PRT

<213> Unknown (H38g397 protein)

<220>

<223> Synthetic construct

<400> 1480

```

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
  1      5      10      15
Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val
      20      25      30
Val Leu Phe Thr Val Val Tyr Leu Thr Leu Met Gly Asn Gly Ser
      35      40      45
Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
      50      55      60
Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
      65      70      75      80
Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
      85      90      95
Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
      100      105      110
Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu
      115      120      125
Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
      130      135      140
Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe
      145      150      155      160
Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile
      165      170      175
Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys
      180      185      190
Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu
      195      200      205
Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val
      210      215      220
Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

```

<210> 1482

<211> 311
 <212> PRT
 <213> Unknown (H38g399 protein)

<220>
 <223> Synthetic construct

<400> 1482

```

Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1.          5          10          15
Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe
          20          25          30
Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
          35          40          45
Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
          50          55          60
Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
65          70          75          80
Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
          85          90          95
Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
          100          105          110
Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu
          115          120          125
Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
          130          135          140
Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe
145          150          155          160
Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg
          165          170          175
Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr
          180          185          190
Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro
          195          200          205
Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu
          210          215          220
Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys
225          230          235          240
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr
          245          250          255
Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala
          260          265          270
Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu
          275          280          285
Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala
          290          295          300
Leu Lys Lys Phe Trp Gly Thr
305          310

```

<210> 1483
 <211> 326
 <212> PRT
 <213> Unknown (H38g400 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(326)
 <223> Xaa = Any Amino Acid

<400> 1483

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Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
 1          5          10          15
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
          20          25          30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
          35          40          45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
          50          55          60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
          65          70          75          80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
          85          90          95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
          100          105          110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
          115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
          130          135          140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
          145          150          155          160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
          165          170          175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
          180          185          190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
          195          200          205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
          210          215          220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
          225          230          235          240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
          245          250          255
Phe Gly Ala Leu Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
          260          265          270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
          275          280          285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
          290          295          300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
          305          310          315          320
Glu Thr Lys Gln Thr Ile
          325

```

<210> 1484

<211> 315

<212> PRT

<213> Unknown (H38g401 protein)

<220>

<223> Synthetic construct

<400> 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1          5          10          15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
          20          25          30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
          35          40          45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
          50          55          60

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```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
65          70          75          80
Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly
      85          90          95
Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly
      100        105        110
Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
      115        120        125
Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu
      130        135        140
Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile
145          150          155          160
Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln
      165        170        175
Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
      180        185        190
Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile
      195        200        205
Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile
      210        215        220
Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
225          230          235          240
Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu
      245        250        255
Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala
      260        265        270
Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile
      275        280        285
Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe
      290        295        300
Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly
305          310          315

```

<210> 1485

<211> 307

<212> PRT

<213> Unknown (H38g402 protein)

<220>

<223> Synthetic construct

<400> 1485

```

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg
1          5          10          15
Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu
      20        25        30
Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg
      35        40        45
Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu
      50        55        60
Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile
65          70          75          80
Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe
      85          90          95
Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val
      100        105        110
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro
      115        120        125
Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp
      130        135        140
Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

```

```

145          150          155          160
Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro
          165          170          175
Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu
          180          185          190
Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser
          195          200          205
Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro
          210          215          220
Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
225          230          235          240
Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser
          245          250          255
Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val
          260          265          270
Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val
          290          295          300
Ser Gln Asn
305

```

<210> 1486

<211> 256

<212> PRT

<213> Unknown (H38g403 protein)

<220>

<223> Synthetic construct

<400> 1486

```

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr
1      5      10      15
Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg
          20      25      30
Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser
          35      40      45
Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg
          50      55      60
Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro
65      70      75      80
Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu
          85      90      95
Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly
          100      105      110
Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg
          115      120      125
Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His
          130      135      140
Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile
145      150      155      160
Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln
          165      170      175
Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe
          180      185      190
Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro
          195      200      205
Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro
210      215      220
Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile
225      230      235      240

```

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val
 245 250 255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

Ser	Leu	Gly	Ser	Met	Asn	Asn	Ser	Gln	Ile	Ser	Thr	Val	Thr	Gln	Phe	1	5	10	15
Val	Leu	Leu	Gly	Phe	Pro	Gly	Pro	Trp	Lys	Ile	Gln	Ile	Ile	Phe	Phe	20	25	30	
Ser	Met	Ile	Leu	Leu	Val	Tyr	Ile	Phe	Thr	Leu	Thr	Gly	Asn	Met	Ala	35	40	45	
Ile	Ile	Cys	Ala	Val	Arg	Trp	Asp	His	Arg	Leu	His	Thr	Pro	Met	Tyr	50	55	60	
Val	Leu	Leu	Ala	Asn	Phe	Ser	Phe	Leu	Glu	Ile	Trp	Tyr	Val	Thr	Cys	65	70	75	80
Thr	Val	Pro	Asn	Met	Leu	Val	Asn	Phe	Phe	Ser	Lys	Thr	Lys	Thr	Ile	85	90	95	
Ser	Phe	Ser	Gly	Cys	Phe	Thr	Gln	Phe	His	Phe	Phe	Phe	Ser	Leu	Gly	100	105	110	
Thr	Thr	Glu	Cys	Phe	Phe	Leu	Cys	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Leu	115	120	125	
Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Pro	Ser	Ile	Met	Thr	Gly	Gln	Leu	130	135	140	
Cys	Gly	Ile	Leu	Val	Ser	Leu	Cys	Trp	Leu	Ile	Gly	Phe	Leu	Gly	His	145	150	155	160
Ser	Ile	Ser	Ile	Phe	Phe	Ile	Phe	Gln	Leu	Pro	Phe	Cys	Gly	Pro	Asn	165	170	175	
Ile	Ile	Asp	His	Phe	Leu	Cys	Asp	Val	Asp	Pro	Leu	Met	Ala	Leu	Ser	180	185	190	
Ser	Ala	Pro	Thr	His	Ile	Ile	Gly	His	Val	Phe	His	Ser	Val	Ser	Ser	195	200	205	
Leu	Phe	Ile	Asn	Leu	Thr	Met	Val	Tyr	Ile	Leu	Gly	Ser	Tyr	Thr	Leu	210	215	220	
Val	Leu	Arg	Thr	Val	Leu	Xaa	Val	Pro	Ser	Ser	Ala	Gly	Trp	Gln	Lys	225	230	235	240
Ala	Ile	Ser	Thr	Cys	Gly	Ser	His	Leu	Val	Val	Val	Ser	Leu	Phe	Tyr	245	250	255	
Gly	Ala	Ile	Met	Leu	Met	Tyr	Val	Ser	Pro	Thr	Pro	Gly	Asn	Ser	Val	260	265	270	
Ala	Met	His	Lys	Leu	Ile	Thr	Leu	Ile	Tyr	Ser	Val	Val	Thr	Pro	Val	275	280	285	
Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	Lys	Tyr	Ala	290	295	300	
Leu	His	His	Val	Phe	Cys	Gly	Met	Arg	Ile	Ile	Gln	Arg	Ser	Xaa	Ile	305	310	315	320

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1488

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Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
 1           5           10           15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Phe Phe Ile Pro Met Leu
          20           25           30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
          35           40           45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
          50           55           60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
          65           70           75           80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
          85           90           95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
          100          105          110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
          130          135          140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
          145          150          155          160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
          165          170          175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
          195          200          205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
          210          215          220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
          225          230          235          240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
          245          250          255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
          260          265          270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
          290          295          300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
          305          310          315

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<210> 1489

<211> 317

<212> PRT

<213> Unknown (H38g406 protein)

<220>

<223> Synthetic construct

<400> 1489

```

Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
 1           5           10           15

```


Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe
 20 25 30
 Ile Pr Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile
 35 40 45
 Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr
 50 55 60
 Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr
 65 70 75 80
 Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile
 85 90 95
 Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly
 100 105 110
 Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile
 115 120 125
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu
 130 135 140
 Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val
 145 150 155 160
 Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn
 165 170 175
 Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala
 180 185 190
 Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala
 195 200 205
 Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile
 210 215 220
 Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly
 245 250 255
 Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe
 260 265 270
 Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe
 275 280 285
 Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile
 290 295 300
 Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala
 305 310 315

<210> 1490

<211> 277

<212> PRT

<213> Unknown (H38g407 protein)

<220>

<223> Synthetic construct

<400> 1490

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp
 1 5 10 15
 Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu
 20 25 30
 Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp
 35 40 45
 Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln
 50 55 60
 Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala
 65 70 75 80
 Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr
 85 90 95
 Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

<400> 1491																
Met	Asp	Arg	Val	Asn	Asn	Ser	Ala	Val	Ser	Lys	Phe	Val	Leu	Ile	Gly	
1				5					10					15		
Leu	Ser	Ser	Ser	Trp	Glu	Met	His	Leu	Phe	Leu	Phe	Trp	Phe	Phe	Ser	
			20					25					30			
Val	Phe	Tyr	Met	Gly	Ile	Ile	Leu	Glu	Asn	Leu	Phe	Ile	Val	Phe	Thr	
		35					40					45				
Val	Ile	Ile	Asp	Ser	His	Leu	Asn	Ser	Pro	Val	Tyr	Cys	Leu	Leu	Ala	
	50					55					60					
Asn	Ile	Tyr	Leu	Leu	Asp	Leu	Val	Phe	Ser	Tyr	Ser	Ser	Asp	Phe	Phe	
65					70					75					80	
Thr	Asn	Cys	Ser	Ile	Ile	Ser	Phe	Pro	Arg	Cys	Met	Ile	Gln	Ile	Phe	
				85					90					95		
Phe	Ile	Cys	Val	Met	Arg	Lys	Ile	Glu	Met	Val	Leu	Leu	Ile	Thr	Met	
			100					105					110			
Ala	Xaa	Ser	Arg	Tyr	Thr	Ala	Ile	Cys	Lys	Pro	Pro	His	Tyr	Leu	Thr	
		115					120					125				
Thr	Met	Asn	Pro	Lys	Met	Cys	Val	Ser	Leu	Leu	Glu	Ala	Ser	Trp	Ile	
	130					135					140					
Val	Arg	Ile	Ile	His	Ala	Val	Ser	Gln	Phe	Val	Phe	Ala	Ile	Asn	Leu	
145					150					155					160	
Pro	Phe	Cys	Gly	Pro	Asn	Arg	Val	Gly	Ser	Phe	His	Cys	Asp	Phe	Pro	
				165					170					175		
Tyr	Val	Met	Lys	Leu	Ala	Cys	Val	Asp	Thr	Tyr	Lys	Leu	Glu	Val	Val	
			180					185					190			

Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
 195 200 205
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
 210 215 220
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
 225 230 235 240
 Gly

<210> 1492

<211> 312

<212> PRT

<213> Unknown (H38g409 protein)

<220>

<223> Synthetic construct

<400> 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
 20 25 30
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35 40 45
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130 135 140
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145 150 155 160
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
 290 295 300
 Leu Lys Arg Ile Gly Ile Leu Ala
 305 310

<210> 1493

<211> 212

<212> PRT

<213> Unknown (H38g410 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1493

```

Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu
 1           5           10           15
Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu
      20           25           30
Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile
      35           40           45
Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu
      50           55           60
Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val
      65           70           75           80
Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe
      85           90           95
Thr Gly Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala
      100          105          110
Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val
      130          135          140
Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala
      145          150          155          160
His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile
      165          170          175
Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met
      180          185          190
Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro
      195          200          205
Trp Ala Gly Pro
      210

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<210> 1494

<211> 263

<212> PRT

<213> Unknown (H38g411 protein)

<220>

<223> Synthetic construct

<400> 1494

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu
      20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val
      35           40           45
Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His
      50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met
      65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
      85           90           95

```

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu
 100 105 110
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
 115 120 125
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val
 130 135 140
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val
 145 150 155 160
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His
 165 170 175
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr
 180 185 190
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile
 195 200 205
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr
 210 215 220
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu
 245 250 255
 Phe Leu Tyr Val Lys Pro Lys
 260

<210> 1495

<211> 317

<212> PRT

<213> Unknown (H38g412 protein)

<220>

<223> Synthetic construct

<400> 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu
 20 25 30
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val
 35 40 45
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
 85 90 95
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met
 130 135 140
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val
 145 150 155 160
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His
 165 170 175
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr
 180 185 190
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu
 195 200 205
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala
 210 215 220
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225		230		235		240									
Cys	Ala	Ser	His	Leu	Ala	Val	Val	Leu	Ile	Phe	Phe	Gly	Ser	Ile	Ile
			245						250					255	
Phe	Met	Tyr	Val	Arg	Leu	Lys	Lys	Ser	Tyr	Ser	Leu	Thr	Leu	Asp	Arg
			260						265					270	
Thr	Leu	Ala	Ile	Val	Tyr	Ser	Val	Leu	Thr	Pro	Met	Val	Asn	Pro	Ile
			275						280					285	
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Ile	Ile	Lys	Ala	Ile	Lys	Arg	Thr
			290						295					300	
Ile	Phe	Gln	Lys	Gly	Asp	Lys	Ala	Ser	Leu	Ala	His	Leu			
305					310					315					

<210> 1496

<211> 315

<212> PRT

<213> Unknown (H38g413 protein)

<220>

<223> Synthetic construct

<400> 1496

Met	Gln	Gly	Leu	Asn	His	Thr	Ser	Val	Ser	Glu	Phe	Ile	Leu	Val	Gly
1				5					10					15	
Phe	Ser	Ala	Phe	Pro	His	Leu	Gln	Leu	Met	Leu	Phe	Leu	Leu	Phe	Leu
			20						25					30	
Leu	Met	Tyr	Leu	Phe	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Met	Ala	Thr
			35					40					45		
Val	Trp	Ser	Glu	Arg	Ser	Leu	His	Met	Pro	Met	Tyr	Leu	Phe	Leu	Cys
			50				55				60				
Ala	Leu	Ser	Ile	Thr	Glu	Ile	Leu	Tyr	Thr	Val	Ala	Ile	Ile	Pro	Arg
					70					75				80	
Met	Leu	Ala	Asp	Leu	Leu	Ser	Thr	Gln	Arg	Ser	Ile	Ala	Phe	Leu	Ala
			85						90					95	
Cys	Ala	Ser	Gln	Met	Phe	Phe	Ser	Phe	Ser	Phe	Gly	Phe	Thr	His	Ser
			100						105					110	
Phe	Leu	Leu	Thr	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
			115					120					125		
Pro	Leu	Arg	Tyr	Asn	Val	Leu	Met	Ser	Leu	Arg	Gly	Cys	Thr	Cys	Arg
			130				135					140			
Val	Gly	Cys	Ser	Trp	Ala	Gly	Gly	Leu	Val	Met	Gly	Met	Val	Val	Thr
			145			150				155				160	
Ser	Ala	Ile	Phe	His	Leu	Ala	Phe	Cys	Gly	His	Lys	Glu	Ile	His	His
			165						170					175	
Phe	Phe	Cys	His	Val	Pro	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Gly	Asp	Asp
			180					185						190	
Val	Leu	Val	Val	Ala	Lys	Gly	Val	Gly	Leu	Val	Cys	Ile	Thr	Ala	Leu
			195				200					205			
Leu	Gly	Cys	Phe	Leu	Leu	Ile	Leu	Leu	Ser	Tyr	Ala	Phe	Ile	Val	Ala
			210				215				220				
Ala	Ile	Leu	Lys	Ile	Pro	Ser	Ala	Glu	Gly	Arg	Asn	Lys	Ala	Phe	Ser
					230					235				240	
Thr	Cys	Ala	Ser	His	Leu	Thr	Val	Val	Val	Val	His	Tyr	Gly	Phe	Ala
					245					250				255	
Ser	Val	Ile	Tyr	Leu	Lys	Pro	Lys	Gly	Pro	Gln	Ser	Pro	Glu	Gly	Asp
			260					265						270	
Thr	Leu	Met	Gly	Ile	Thr	Tyr	Thr	Val	Leu	Thr	Pro	Phe	Leu	Ser	Pro
			275				280						285		
Ile	Ile	Phe	Ser	Leu	Arg	Asn	Lys	Glu	Leu	Lys	Val	Ala	Met	Lys	Lys
			290				295					300			
Thr	Cys	Phe	Thr	Lys	Leu	Phe	Pro	Gln	Asn	Cys					
305					310					315					

<210> 1497
 <211> 319
 <212> PRT
 <213> Unknown (H38g414 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1497
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala
 85 90 95
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His
 165 170 175
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315

<210> 1498
 <211> 157
 <212> PRT
 <213> Unknown (H38g415 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1498

Val	Ser	Pro	Leu	Trp	Glu	Cys	Val	Ser	Xaa	Gln	Arg	Ser	Pro	His	Phe
1				5					10					15	
Leu	Cys	Ser	Gly	Asp	Ser	Val	Phe	Cys	Leu	Val	His	Ser	Val	Gly	Cys
			20					25					30		
Cys	Thr	Leu	Leu	Leu	Ser	Gln	Ser	Leu	Arg	Leu	Leu	Ser	Val	Phe	Leu
		35					40					45			
Leu	Ser	Ser	Cys	Ala	Ala	Ser	Trp	Lys	Lys	Val	His	Ser	Met	Asn	Leu
	50					55					60				
Tyr	Thr	Pro	Phe	Cys	Leu	Ser	Lys	Trp	Xaa	Asn	His	Val	Asn	Asn	Ala
65					70					75				80	
Phe	Asn	Leu	Pro	Ser	Trp	Lys	Lys	Ser	Lys	Ser	Val	Val	Thr	Met	Phe
				85					90					95	
Xaa	Gly	Pro	Ala	Met	Ile	Thr	Tyr	Leu	Arg	Ser	Asp	Ser	Xaa	Tyr	Asn
			100					105					110		
Pro	Thr	Val	Gly	Lys	Gln	Leu	Val	Leu	Phe	Tyr	Ser	Ile	Val	Ser	Ala
		115					120					125			
Phe	Ile	Lys	Pro	Ile	Ile	Ser	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly
	130					135					140				
Ala	Ser	Trp	Lys	Val	Leu	Arg	Val	Lys	Gly	Thr	Ala	Gln			
145					150					155					

<210> 1499

<211> 287

<212> PRT

<213> Unknown (H38g416 protein)

<220>

<223> Synthetic construct

<400> 1499

Met	Glu	Asn	Tyr	Asn	Gln	Thr	Ser	Thr	Asp	Phe	Ile	Leu	Leu	Gly	Leu
1				5					10					15	
Phe	Pro	Pro	Ser	Arg	Ile	Asp	Leu	Phe	Phe	Phe	Ile	Leu	Phe	Val	Leu
			20					25					30		
Ile	Phe	Leu	Met	Ala	Leu	Ile	Gly	Asn	Leu	Ser	Met	Ile	Leu	Leu	Ile
		35					40					45			
Phe	Leu	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ser	Gln
	50				55					60					
Leu	Ser	Leu	Ile	Asp	Leu	Asn	Tyr	Ile	Ser	Thr	Ile	Val	Pro	Lys	Met
65					70					75				80	
Ala	Ser	Asp	Phe	Leu	Tyr	Gly	Asn	Lys	Ser	Ile	Ser	Phe	Ile	Gly	Cys
			85						90					95	
Gly	Ile	Gln	Ser	Phe	Phe	Phe	Met	Thr	Phe	Ala	Gly	Ala	Glu	Ala	Leu
		100						105					110		
Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro
		115					120					125			
Leu	His	Tyr	Pro	Ile	Arg	Met	Ser	Lys	Arg	Met	Tyr	Val	Leu	Met	Ile
	130					135					140				
Thr	Gly	Ser	Trp	Met	Ile	Gly	Ser	Ile	Asn	Ser	Cys	Ala	His	Thr	Val
145					150					155					160
Tyr	Ala	Phe	Arg	Ile	Pro	Tyr	Cys	Lys	Ser	Arg	Ala	Ile	Asn	His	Phe
				165					170					175	
Phe	Cys	Asp	Val	Pro	Ala	Met	Leu	Thr	Leu	Ala	Cys	Thr	Asp	Thr	Trp
			180						185					190	

Val Tyr Glu Tyr Thr Val Phe Leu Ser Ser Thr Ile Phe Leu Val Phe
 195 200 205
 Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Trp Val Leu Leu Ala Val
 210 215 220
 Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys
 225 230 235 240
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Leu Arg Tyr
 245 250 255
 Thr Tyr Leu Cys Pro Arg Ser Leu Phe Ile Ser Thr Glu Asp Lys Val
 260 265 270
 Gly Gly Gly Gly Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile
 275 280 285

<210> 1500

<211> 310

<212> PRT

<213> Unknown (H38g417 protein)

<220>

<223> Synthetic construct

<400> 1500

Met Asp Lys Glu Asn Ser Ser Met Val Thr Glu Phe Ile Phe Met Gly
 1 5 10 15
 Ile Thr Gln Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu
 20 25 30
 Ile Val Tyr Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu
 35 40 45
 Ile Thr Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg
 65 70 75 80
 Met Leu Ala Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser
 85 90 95
 Cys Ala Thr Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys
 100 105 110
 Tyr Val Leu Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu
 130 135 140
 Met Leu Gly Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr
 145 150 155 160
 Thr Leu Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Ile Ser Glu Ile Leu Leu Phe Ser Leu Cys Gly Phe Ile Glu Phe
 195 200 205
 Ser Thr Ile Leu Ile Ile Phe Ile Ser Tyr Thr Phe Ile Leu Val Ala
 210 215 220
 Ile Ile Arg Met Arg Ser Ala Glu Gly Arg Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Gly Ile Thr Leu Phe Tyr Gly Thr Val Met
 245 250 255
 Phe Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Leu Asp Gln Asp Lys
 260 265 270
 Trp Ala Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Lys Lys Leu
 290 295 300
 Ile Gly Lys Lys Ser Gln

305

310

<210> 1501

<211> 335

<212> PRT

<213> Unknown (H38g418 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1501

```

Ser Thr Asp Pro Gln Asn Leu Ile Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Arg Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Thr Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Ser Ala Val Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Val Leu Leu Thr Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
          165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Pro Leu Pro His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
          290          295          300
Arg Trp Leu His Gly Ser Ser Val Xaa Ser Gln His Leu Leu Ile Cys
305          310          315          320
Cys Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Arg Val Lys
          325          330          335

```

<210> 1502

<211> 303

<212> PRT

<213> Unknown (H38g419 protein)

<220>

<223> Synthetic construct

<400> 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1           5           10           15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
          20           25           30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
          35           40           45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
          50           55           60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
65           70           75           80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
          85           90           95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
          100          105          110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
          115          120          125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
          130          135          140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
145          150          155          160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
          165          170          175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
          180          185          190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
          195          200          205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
210          215          220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
          245          250          255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
          260          265          270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
290          295          300

```

<210> 1503

<211> 336

<212> PRT

<213> Unknown (H38g420 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1503

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Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1           5           10           15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```

20						25						30					
Leu	Thr	Leu	Cys	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Val	Ile	Ile	Val	Thr		
35						40						45					
Ile	Ile	Ser	Ile	Asp	Arg	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Val		
50						55			60								
Ser	Met	Leu	Ser	Thr	Ser	Glu	Thr	Val	Tyr	Thr	Leu	Val	Ile	Val	Pro		
65				70			75						80				
Arg	Met	Leu	Ser	Ser	Leu	Leu	Ser	Leu	Ser	Gln	Pro	Ile	Ser	Leu	Gly		
			85			90						95					
Gly	Cys	Ala	Thr	Gln	Met	Phe	Phe	Phe	Ile	Thr	Leu	Ala	Ile	Asn	Asn		
			100			105						110					
Cys	Phe	Leu	Thr	Ala	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys			
			115			120			125								
Asn	Pro	Leu	Arg	Tyr	Met	Ile	Ile	Met	Asn	Lys	Lys	Val	Cys	Val	Gln		
130			135			140											
Leu	Val	Cys	Gly	Ser	Cys	Ser	Val	Gly	Leu	Leu	Val	Ala	Ile	Val	Gln		
145				150			155						160				
Ile	Ser	Ser	Val	Phe	Arg	Leu	Pro	Phe	Cys	Asp	Lys	Gln	Val	Ala	His		
			165			170						175					
Tyr	Phe	Cys	Asp	Ile	His	Pro	Val	Met	Lys	Leu	Ser	Cys	Val	Asp	Thr		
			180			185						190					
Thr	Leu	His	Asp	Leu	Ile	Asn	Phe	Val	Val	Ser	Ser	Leu	Val	Ile	Val		
195			200			205											
Val	Pro	Leu	Gly	Leu	Val	Phe	Ile	Ser	Tyr	Ile	Leu	Ile	Ile	Ser	Thr		
210			215			220											
Ile	Leu	Lys	Val	Thr	Ser	Pro	Glu	Gly	Arg	Lys	Lys	Ala	Phe	Ala	Thr		
225				230			235						240				
Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Tyr	Gly	Cys	Ala	Ser		
			245			250						255					
Ile	Ala	Tyr	Leu	Lys	Pro	Lys	Ser	Glu	Asn	Thr	Arg	Asp	Gln	Asp	Gln		
			260			265						270					
Leu	Ile	Ser	Val	Thr	Tyr	Thr	Val	Phe	Thr	Pro	Leu	Leu	Asn	Pro	Val		
275			280			285											
Val	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Asn	Ala	Leu	His	Arg	Ala		
290			295			300											
Ile	Gly	Lys	Lys	Pro	Phe	Ala	Xaa	Asn	Leu	His	Gln	Phe	Asp	Ile	Xaa		
305				310			315						320				
Ser	Val	Met	Ser	Leu	Gly	Ile	Phe	Leu	Ser	Ser	Arg	Lys	Leu	Asn	Pro		
			325			330						335					

<210> 1504

<211> 315

<212> PRT

<213> Unknown (H38g421 protein)

<220>

<223> Synthetic construct

<400> 1504

Met 1	Ser	Ile	Thr	Lys 5	Ala	Trp	Asn	Ser	Ser 10	Ser	Val	Thr	Met	Phe 15	Ile
Leu	Leu	Gly	Phe 20	Thr	Asp	His	Pro	Glu 25	Leu	Gln	Ala	Leu	Leu 30	Phe	Val
Thr	Phe	Leu 35	Gly	Ile	Tyr	Leu	Thr 40	Thr	Leu	Ala	Trp	Asn 45	Leu	Ala	Leu
Ile	Phe 50	Leu	Ile	Arg	Gly	Asp 55	Thr	His	Leu	His	Thr 60	Pro	Met	Tyr	Phe
Phe 65	Leu	Ser	Asn	Leu	Ser 70	Phe	Ile	Asp	Ile	Cys 75	Tyr	Ser	Ser	Ala 80	Val
Ala	Pro	Asn	Met	Leu 85	Thr	Asp	Phe	Phe 90	Trp	Glu	Gln	Lys	Thr 95	Ile	Ser

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu
 100 105 110
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala
 115 120 125
 Ile Ser Ser Pro Leu Leu Tyr Pr Thr Ile Met Thr Gln Gly Leu Cys
 130 135 140
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu
 145 150 155 160
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile
 165 170 175
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys
 180 185 190
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr
 195 200 205
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile
 210 215 220
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala
 225 230 235 240
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly
 245 250 255
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly
 260 265 270
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu
 290 295 300
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser
 305 310 315

<210> 1505

<211> 317

<212> PRT

<213> Unknown (H38g422 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu
 1 5 10 15
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu
 20 25 30
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile
 35 40 45
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr
 65 70 75 80
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile
 85 90 95
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly
 100 105 110
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys
 130 135 140
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

```

145          150          155          160
Val Ile Asn Val Leu Thr L u Ser Leu Pro Tyr Cys Gly Pr Asn Ile
          165          170          175
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile
          195          200          205
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile
          210          215          220
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala
225          230          235          240
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly
          245          250          255
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala
          260          265          270
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg
          290          295          300
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu
305          310          315

```

<210> 1506

<211> 340

<212> PRT

<213> Unknown (H38g423 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400> 1506

```

Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly
1          5          10          15
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe
          20          25          30
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr
          35          40          45
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro
65          70          75          80
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln
          85          90          95
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn
          100          105          110
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln
          130          135          140
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln
145          150          155          160
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser
          165          170          175
His Phe Phe Cys Asp Val Arg His Leu Leu Lys Leu Ala Cys Thr Asp
          180          185          190
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu
          195          200          205

```

Val Leu Pro Met Gly Leu Val Phe Il Ser Tyr Val Leu Ile Ile Ser
 210 215 220
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala
 245 250 255
 Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp
 260 265 270
 Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val
 275 280 285
 Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala
 290 295 300
 Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala
 305 310 315 320
 Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile
 325 330 335
 Met Pro Leu Cys
 340

<210> 1507

<211> 313

<212> PRT

<213> Unknown (H38g424 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1507

Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser
 1 5 10 15
 Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp
 20 25 30
 Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Ile Thr
 35 40 45
 Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly
 50 55 60
 Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys
 65 70 75 80
 Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu
 85 90 95
 Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser
 100 105 110
 Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr
 115 120 125
 Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala
 130 135 140
 Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro
 145 150 155 160
 Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln
 165 170 175
 Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr
 180 185 190
 Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly
 195 200 205
 Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser
 210 215 220
 Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

225 230 235 240
 Cys Ser Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Ala Ile Ile
 245 250 255
 Val Val Ser Val Thr Asn Leu Ala Gly Arg Arg Ala Pro Arg Ile Pro
 260 265 270
 Val Leu Leu Asn Val Leu His Ile Val Ile Pro Ser Ala Leu Asn Pro
 275 280 285
 Ile Val Tyr Ala Leu Arg Thr Xaa Glu Leu Arg Ala Gly Phe Gln Lys
 290 295 300
 Leu Leu Gly Leu Gly Glu Tyr Val Ser
 305 310

<210> 1508

<211> 315

<212> PRT

<213> Unknown (H38g425 protein)

<220>

<223> Synthetic construct

<400> 1508

Met Phe Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu
 20 25 30
 Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu
 35 40 45
 Ile Arg Thr Asn Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn
 65 70 75 80
 Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly
 85 90 95
 Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe
 100 105 110
 Tyr Ile Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Val Cys Leu
 130 135 140
 Val Thr Ile Pro Tyr Met Tyr Gly Phe Leu Ser Gly Phe Ser Gln Ser
 145 150 155 160
 Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His
 165 170 175
 Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Asn Leu Ser
 195 200 205
 Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala
 210 215 220
 Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe
 245 250 255
 Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Glu Ser Lys
 260 265 270
 Ile Thr Ala Val Phe Tyr Thr Phe Leu Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Thr Asp Val Ile Leu Ala Met Gln Gln Met
 290 295 300
 Ile Arg Gly Lys Ser Phe His Lys Ile Ala Val
 305 310 315

<210> 1509
 <211> 257
 <212> PRT
 <213> Unknown (H38g426 protein)

<220>
 <223> Synthetic construct

<400> 1509
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala
 1 5 10 15
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg
 20 25 30
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala
 35 40 45
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg
 50 55 60
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys
 65 70 75 80
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Lys Ala Val Ala
 85 90 95
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln
 100 105 110
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu
 115 120 125
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu
 130 135 140
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr
 145 150 155 160
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His
 165 170 175
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala
 180 185 190
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His
 195 200 205
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu
 210 215 220
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys
 225 230 235 240
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro
 245 250 255
 Leu

<210> 1510
 <211> 358
 <212> PRT
 <213> Unknown (H38g427 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(358)
 <223> Xaa = Any Amino Acid

<400> 1510
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro
 1 5 10 15
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

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<210> 1511
<211> 313
<212> PRT
<213> Unknown (H38g428 protein)
```

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid
```

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<400> 1511
Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu
 1             5             10            15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro
          20             25            30

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Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Il
 35 40 45
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu
 50 55 60
 Ala Gly Thr Asp Ile L u Leu Ser Thr Thr Thr Val Pro Lys Ala Leu
 65 70 75 80
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile
 85 90 95
 Thr Gln Met Phe Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile
 100 105 110
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu
 115 120 125
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu
 130 135 140
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu
 145 150 155 160
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr
 165 170 175
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val
 180 185 190
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp
 195 200 205
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe
 210 215 220
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly
 225 230 235 240
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr
 245 250 255
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile
 260 265 270
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met
 290 295 300
 Leu Ser Val Val Gly Lys Ser Xaa Asp
 305 310

<210> 1512

<211> 314

<212> PRT

<213> Unknown (H38g429 protein)

<220>

<223> Synthetic construct

<400> 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu
 1 5 10 15
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu
 20 25 30
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe
 35 40 45
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met
 50 55 60
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr
 65 70 75 80
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr
 85 90 95
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu
 100 105 110
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

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      115      120      125
Met Ala Ile Cys Asn Pro Leu His Tyr Ser Ser Lys Met Ser Arg Ala
  130      135      140
Val Cys Ile Cys Leu Val Thr Phe Pro Tyr Phe Trp Gly Ser Met Val
  145      150      155      160
Gly Thr Met Gln Val Ile Leu Thr Ser Arg Leu Ser Phe Phe Gly Pro
      165      170      175
Asn Thr Ile Asn His Phe Tyr Cys Thr Asp Pro Pro Leu Leu Met Leu
      180      185      190
Thr Ser Ser Asp Thr Tyr Ile Lys Gln Thr Ala Leu Phe Val Ser Ala
      195      200      205
Gly Ile Asn Leu Thr Val Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile
      210      215      220
Phe Ile Phe Ile Thr Ile Met Arg Ile Arg Ser Ser Glu Gly Gln Leu
  225      230      235      240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Thr Met Phe
      245      250      255
Tyr Gly Ser Leu Phe Cys Met Tyr Leu Arg Pro Thr Asn Glu Leu Ser
      260      265      270
Val Glu Gln Gly Lys Met Gly Val Val Phe Cys Ile Phe Val Ser Pro
      275      280      285
Met Leu Asn Pro Phe Ile Tyr Arg Leu Arg Asn Lys Asp Val Lys Gln
      290      295      300
Ala Leu Lys Arg Val Phe Met Arg Asn Leu
  305      310

```

<210> 1513

<211> 320

<212> PRT

<213> Unknown (H38g430 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1513

```

Met Ser Leu Leu Phe Xaa Asp Xaa Asp Met Arg Asn Phe Thr Pro Leu
  1      5      10      15
Ser Gly Phe Ile Ile Leu Gly Phe Thr Asp His Pro Glu Leu Gln Cys
      20      25      30
Leu Leu Phe Val Leu Phe Leu Leu Ile Tyr Met Phe Thr Val Val Gly
      35      40      45
Asn Leu Gly Met Ile Leu Leu Ile Lys Ile Asp Ser His Leu His Thr
      50      55      60
Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Leu Val Asp Phe Cys Tyr
      65      70      75      80
Ser Ser Val Ile Ala Pro Asn Met Leu Ile Asn Phe Trp Val Glu Asn
      85      90      95
Pro Val Ile Ser Phe Asn Glu Cys Ala Thr Gln Phe Phe Phe Phe Gly
      100      105      110
Ser Phe Ala Gly Ile Glu Gly Phe Leu Leu Ala Val Met Ala Tyr Asp
      115      120      125
Cys Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Val Leu Met Ser
      130      135      140
Pro His Leu Ser Ala Leu Leu Val Leu Ala Thr Tyr Leu Leu Gly Phe
  145      150      155      160
Val Asn Ala Ala Ile His Thr Gly Phe Thr Phe Gln Leu Ser Phe Cys
      165      170      175

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His Ser Asn Ile Ile Asn Tyr Phe Phe Cys Asp Ile Pro Pro Leu Leu
 180 185 190
 Lys Leu Cys Ser Asp Thr His Ile Asn Glu Val Val Ile Phe Ala Phe
 195 200 205
 Ala Ser Phe Asn Glu Leu Ser Cys Leu Leu Leu Ile Leu Val Ser Cys
 210 215 220
 Leu Tyr Ile Leu Ala Ala Ile Leu Lys Ile His Ser Ala Glu Gly Arg
 225 230 235 240
 His Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile
 245 250 255
 Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Leu Arg Pro Ser Ser Ser
 260 265 270
 Tyr Ser Met Asp Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Val
 275 280 285
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val
 290 295 300
 Lys Ala Ser Leu Ser Lys Met Phe Lys Thr Val Ser Tyr Ile Ser Thr
 305 310 315 320

<210> 1514

<211> 299

<212> PRT

<213> Unknown (H38g431 protein)

<220>

<223> Synthetic construct

<400> 1514

Met Gly Leu Pro Gly Ile His Glu Trp Gln His Trp Leu Ser Leu Pro
 1 5 10 15
 Leu Thr Leu Leu Tyr Leu Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile
 20 25 30
 Ile Thr Ile Gln His Glu Thr Val Leu His Glu Pro Met Tyr His Leu
 35 40 45
 Leu Gly Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met
 50 55 60
 Pro Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu
 65 70 75 80
 Pro Met Cys Phe Ala Gln Ile Tyr Ala Ile His Cys Phe Phe Cys Ile
 85 90 95
 Glu Ser Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Ile Ala Ile
 100 105 110
 Cys Arg Pro Leu Gln Tyr Pro Ser Ile Val Thr Lys Ala Phe Val Phe
 115 120 125
 Lys Ala Thr Gly Phe Ile Met Leu Arg Asn Gly Leu Leu Thr Ile Pro
 130 135 140
 Val Pro Ile Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile
 145 150 155 160
 Glu His Cys Leu Cys Ser Asn Leu Gly Val Ile Ser Leu Ala Cys Asp
 165 170 175
 Asp Ile Thr Val Asn Lys Phe Tyr Gln Leu Met Leu Ala Trp Val Leu
 180 185 190
 Val Gly Ser Asp Met Ala Leu Val Phe Ser Ser Tyr Ala Val Ile Leu
 195 200 205
 His Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Met Ser Lys Ala Leu
 210 215 220
 Ser Thr Cys Ser Ser His Leu Ile Leu Ile Leu Phe His Thr Gly Ile
 225 230 235 240
 Ile Val Leu Ser Val Thr His Leu Ala Glu Lys Lys Ile Pro Leu Ile
 245 250 255
 Pro Val Phe Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu Asn

260 265 270
 Pro Leu Ala Cys Ala Leu Arg Met His Lys Leu Arg Leu Gly Phe Gln
 275 280 285
 Arg Leu Leu Gly Leu Gly Gln Asp Val Ser Lys
 290 295

<210> 1515
 <211> 317
 <212> PRT
 <213> Unknown (H38g432 protein)

<220>
 <223> Synthetic construct

<400> 1515
 Met Met Arg Leu Met Lys Glu Val Arg Gly Arg Asn Gln Thr Glu Val
 1 5 10 15
 Thr Glu Phe Leu Leu Leu Gly Leu Ser Asp Asn Pro Asp Leu Gln Gly
 20 25 30
 Val Leu Phe Ala Leu Phe Leu Leu Ile Tyr Met Ala Asn Met Val Gly
 35 40 45
 Asn Leu Gly Met Ile Val Leu Ile Lys Ile Asp Leu Cys Leu His Thr
 50 55 60
 Pro Met Tyr Phe Phe Leu Ser Ser Leu Ser Phe Val Asp Ala Ser Tyr
 65 70 75 80
 Ser Ser Ser Val Thr Pro Lys Met Leu Val Asn Leu Met Ala Glu Asn
 85 90 95
 Lys Ala Ile Ser Phe His Gly Cys Ala Ala Gln Phe Tyr Phe Phe Gly
 100 105 110
 Ser Phe Leu Gly Thr Glu Cys Phe Leu Leu Ala Met Met Ala Tyr Asp
 115 120 125
 Arg Tyr Ala Ala Ile Trp Asn Pro Leu Leu Tyr Pro Val Leu Val Ser
 130 135 140
 Gly Arg Ile Cys Phe Leu Leu Ile Ala Thr Ser Phe Leu Ala Gly Cys
 145 150 155 160
 Gly Asn Ala Ala Ile His Thr Gly Met Thr Phe Arg Leu Ser Phe Cys
 165 170 175
 Gly Ser Asn Arg Ile Asn His Phe Tyr Cys Asp Thr Pro Pro Leu Leu
 180 185 190
 Lys Leu Ser Cys Ser Asp Thr His Phe Asn Gly Ile Val Ile Met Ala
 195 200 205
 Phe Ser Ser Phe Ile Val Ile Ser Cys Val Met Ile Val Leu Ile Ser
 210 215 220
 Tyr Leu Cys Ile Phe Ile Ala Val Leu Lys Met Pro Ser Leu Glu Gly
 225 230 235 240
 Arg His Lys Ala Phe Ser Thr Cys Ala Ser Tyr Leu Met Ala Val Thr
 245 250 255
 Ile Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Arg Pro Thr Ser Ser
 260 265 270
 Tyr Ser Met Glu Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Ile
 275 280 285
 Ile Pro Val Leu Asn Pro Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val
 290 295 300
 Lys Lys Ala Leu Lys Lys Ile Leu Trp Lys His Ile Leu
 305 310 315

<210> 1516
 <211> 317
 <212> PRT
 <213> Unknown (H38g433 protein)

<220>

<223> Synthetic construct

<400> 1516

```

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu
1           5           10           15
Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro
20           25           30
Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile
35           40           45
Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe
50           55           60
Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val
65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe
85           90           95
Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly
100          105          110
Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
115          120          125
Cys Ala Pro Leu Arg Tyr Thr Val Leu Thr Trp Pro Val Val Gly
130          135          140
Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro
145          150          155          160
Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val
165          170          175
Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala
180          185          190
Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met
195          200          205
Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu
210          215          220
Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu
225          230          235          240
Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro
245          250          255
Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln
260          265          270
His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met
275          280          285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly
290          295          300
Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys
305          310          315

```

<210> 1517

<211> 305

<212> PRT

<213> Unknown (H38g434 protein)

<220>

<223> Synthetic construct

<400> 1517

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
35           40           45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

```

50	55	60
Leu Ser Phe Leu Asp	Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile	
65	70	75
Leu Val Thr Cys Ile	Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys	80
	85	90
Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr		95
	100	105
Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro		110
	115	120
Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val		125
	130	135
Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys		140
145	150	155
Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe		160
	165	170
Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly		175
	180	185
Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys		190
	195	200
Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val		205
	210	215
Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys		220
225	230	235
Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr		240
	245	250
Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile		255
	260	265
Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile		270
	275	280
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu		285
290	295	300
Pro		
305		

<210> 1518

<211> 314

<212> PRT

<213> Unknown (H38g435 protein)

<220>

<223> Synthetic construct

<400> 1518

Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu	
1	5
Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro	10
	15
	20
Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu	25
	30
	35
Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe	40
	45
	50
Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu	55
65	60
	65
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe	70
	75
	80
	85
Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met	90
	95
	100
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile	105
	110
	115
Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr	120
	125
	130
	135
	140

Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
 180 185 190
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser
 195 200 205
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
 210 215 220
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
 225 230 235 240
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
 245 250 255
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
 260 265 270
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
 275 280 285
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr
 290 295 300
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met
 305 310

<210> 1519

<211> 312

<212> PRT

<213> Unknown (H38g436 protein)

<220>

<223> Synthetic construct

<400> 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu
 20 25 30
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu
 35 40 45
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly
 85 90 95
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr
 100 105 110
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu
 130 135 140
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr
 145 150 155 160
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His
 165 170 175
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr
 180 185 190
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile
 195 200 205
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala
 210 215 220
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

225					230					235					240
Cys	Gly	Ser	His	Val	Thr	Ala	Val	Thr	Val	Phe	Tyr	Gly	Thr	Leu	Phe
				245					250					255	
Cys	Met	Tyr	Leu	Arg	Pr	Pro	Ser	Glu	Thr	Ser	Ile	Gln	Gln	Gly	Lys
			260					265				270			
Ile	Val	Ala	Val	Phe	Tyr	Ile	Phe	Val	Ser	Pro	Met	Leu	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Arg	Ser	Ile	Arg	Lys	Val
	290					295					300				
Ile	Gln	Lys	Lys	Leu	Phe	Ala	Lys								
305					310										

<210> 1520

<211> 314

<212> PRT

<213> Unknown (H38g437 protein)

<220>

<223> Synthetic construct

<400> 1520

Met	Ser	Ala	Ser	Asn	Ile	Thr	Leu	Thr	His	Pro	Thr	Ala	Phe	Leu	Leu
1				5					10					15	
Val	Gly	Ile	Pro	Gly	Leu	Glu	His	Leu	His	Ile	Trp	Ile	Ser	Ile	Pro
			20					25					30		
Phe	Cys	Leu	Ala	Tyr	Thr	Leu	Ala	Leu	Leu	Gly	Asn	Cys	Thr	Leu	Leu
		35					40					45			
Leu	Ile	Ile	Gln	Ala	Asp	Ala	Ala	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe
	50					55					60				
Leu	Ala	Met	Leu	Ala	Ala	Ile	Asp	Leu	Val	Leu	Ser	Ser	Ser	Ala	Leu
65					70					75					80
Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Asp	Arg	Glu	Ile	Asn	Phe
				85					90					95	
Phe	Ala	Cys	Leu	Ala	Gln	Met	Phe	Phe	Leu	His	Ser	Phe	Ser	Ile	Met
			100						105					110	
Glu	Ser	Ala	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
			115				120						125		
Cys	Lys	Pro	Leu	His	Tyr	Thr	Lys	Val	Leu	Thr	Gly	Ser	Leu	Ile	Thr
	130					135					140				
Lys	Ile	Gly	Met	Ala	Ala	Val	Ala	Arg	Ala	Val	Thr	Leu	Met	Thr	Pro
145					150					155					160
Leu	Pro	Phe	Leu	Leu	Arg	Cys	Phe	His	Tyr	Cys	Arg	Gly	Pro	Val	Ile
				165					170					175	
Ala	His	Cys	Tyr	Cys	Glu	His	Met	Ala	Val	Val	Arg	Leu	Ala	Cys	Gly
			180					185					190		
Asp	Thr	Ser	Phe	Asn	Asn	Ile	Tyr	Gly	Ile	Ala	Val	Ala	Met	Phe	Ile
		195					200						205		
Val	Val	Leu	Asp	Leu	Leu	Leu	Val	Ile	Leu	Ser	Tyr	Ile	Phe	Ile	Leu
	210					215					220				
Gln	Ala	Val	Leu	Leu	Leu	Ala	Ser	Gln	Glu	Ala	Arg	Tyr	Lys	Ala	Phe
225					230					235					240
Gly	Thr	Cys	Val	Ser	His	Ile	Gly	Ala	Ile	Leu	Ala	Phe	Tyr	Thr	Thr
				245					250					255	
Val	Val	Ile	Ser	Ser	Val	Met	His	Arg	Val	Ala	Arg	His	Ala	Ala	Pro
			260					265					270		
His	Val	His	Ile	Leu	Leu	Ala	Asn	Phe	Tyr	Leu	Leu	Phe	Pro	Pro	Met
		275					280					285			
Val	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys	Gln	Ile	Arg	Glu	Ser
	290					295					300				
Ile	Leu	Gly	Val	Phe	Pro	Arg	Lys	Asp	Met						
305					310										

<210> 1521
 <211> 313
 <212> PRT
 <213> Unknown (H38g438 protein)

<220>
 <223> Synthetic construct

<400> 1521
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
 35 40 45
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu
 50 55 60
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro
 65 70 75 80
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe
 85 90 95
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu
 100 105 110
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys
 130 135 140
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu
 145 150 155 160
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala
 165 170 175
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn
 180 185 190
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly
 195 200 205
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln
 210 215 220
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser
 245 250 255
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His
 260 265 270
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val
 290 295 300
 Leu Gly Val Phe Pro Arg Lys Asp Val
 305 310

<210> 1522
 <211> 318
 <212> PRT
 <213> Unknown (H38g439 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1522

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1          5          10          15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20          25          30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35          40          45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50          55          60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65          70          75          80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85          90          95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
 145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
 165          170          175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
 180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
 195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
 210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
 225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
 245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
 260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
 275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
 290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
 305          310          315

```

<210> 1523

<211> 313

<212> PRT

<213> Unknown (H38g440 protein)

<220>

<223> Synthetic construct

<400> 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20          25          30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35          40          45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60

```

Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
 85 90 95
 Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
 100 105 110
 Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
 130 135 140
 Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
 145 150 155 160
 Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
 165 170 175
 Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
 180 185 190
 Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
 195 200 205
 Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
 210 215 220
 Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
 245 250 255
 Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
 260 265 270
 Met Val Ser Leu Phe Tyr Gly Ile Ala Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
 290 295 300
 Val Ala Arg Val Phe Leu Ile Lys Lys
 305 310

<210> 1524

<211> 333

<212> PRT

<213> Unknown (H38g441 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1524

Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe
 20 25 30
 Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val
 35 40 45
 Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly
 85 90 95
 Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys
 100 105 110
 Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

      115      120      125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130      135      140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145      150      155      160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180      185      190
Arg Ala Val Glu Met Leu Ala Phe Ala Val Leu Ile Val Leu
      195      200      205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
      210      215      220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305      310      315      320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325      330

```

<210> 1525

<211> 317

<212> PRT

<213> Unknown (H38g442 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1      5      10      15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20      25      30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35      40      45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50      55      60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
      65      70      75      80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85      90      95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100      105      110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115      120      125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130      135      140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
  145      150      155      160

```

Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val
 165 170 175
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val
 180 185 190
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser
 195 200 205
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys
 210 215 220
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro
 225 230 235 240
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr
 245 250 255
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 260 265 270
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu
 275 280 285
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu
 290 295 300
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu
 305 310 315

<210> 1526

<211> 239

<212> PRT

<213> Unknown (H38g443 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(239)

<223> Xaa = Any Amino Acid

<400> 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
 1 5 10 15
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
 20 25 30
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr
 35 40 45
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr
 50 55 60
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu
 65 70 75 80
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His
 85 90 95
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu
 100 105 110
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu
 115 120 125
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met
 130 135 140
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His
 145 150 155 160
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile
 165 170 175
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln
 180 185 190
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys
 195 200 205
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

210	215	220
Arg Ile Leu Arg Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn		
225	230	235

<210> 1527
 <211> 255
 <212> PRT
 <213> Unknown (H38g444 protein)

<220>
 <223> Synthetic construct

<400> 1527

Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile		
1	5	10
Ser Thr Ile Val Pro Lys Met Ala Ser Asp Phe Leu His Gly Asn Lys		
20	25	30
Ser Ile Ser Phe Thr Gly Cys Gly Ile His Ser Phe Phe Phe Thr Thr		
35	40	45
Leu Ala Val Val Glu Ala Leu Leu Leu Ile Ser Met Ala Tyr Val Arg		
50	55	60
Cys Ile Ala Ile Cys Phe Pro Leu His Tyr Leu Met Arg Met Ser Lys		
65	70	75
Arg Val Cys Val Leu Met Ile Thr Gly Ser Trp Ile Ile Gly Ser Ile		
85	90	95
Asn Ala Cys Ala His Thr Val Tyr Ile Leu His Ile Pro Tyr Cys Pro		
100	105	110
Ser Arg Val Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Val Thr		
115	120	125
Leu Ala Cys Met Asp Thr Trp Val Tyr Glu Gly Thr Val Leu Leu Ser		
130	135	140
Ala Thr Ile Phe Leu Val Phe Pro Phe Ile Ala Ile Ser Cys Ser Tyr		
145	150	155
Gly Arg Val Leu Leu Ala Val Tyr His Met Lys Ser Ala Glu Gly Lys		
165	170	175
Lys Lys Ala Tyr Leu Thr Cys Ser Thr His Leu Thr Val Val Thr Phe		
180	185	190
Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg		
195	200	205
Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr		
210	215	220
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Met		
225	230	235
Gly Ala Leu Thr Arg Val Ile Gln Lys Ile Phe Ser Val Lys Ile		
245	250	255

<210> 1528
 <211> 320
 <212> PRT
 <213> Unknown (H38g445 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1528

Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly
1
5
10
15


```

Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu
      20      25      30
Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Ile Leu Ile
      35      40      45
Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln
      65      70      75      80
Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly
      85      90      95
Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys
      100      105      110
Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu
      130      135      140
Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val
      145      150      155      160
Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr
      180      185      190
Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu
      195      200      205
Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala
      210      215      220
Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met
      225      230      235      240
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu
      290      295      300
Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe
      305      310      315      320

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<210> 1529

<211> 126

<212> PRT

<213> Unknown (H38g446 protein)

<220>

<223> Synthetic construct

<400> 1529

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu
      1      5      10      15
Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe
      20      25      30
Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
      35      40      45
Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
      50      55      60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
      65      70      75      80
Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly
      85      90      95
Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

```

100 105 110
 Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125

<210> 1530
 <211> 326
 <212> PRT
 <213> Unknown (H38g447 protein)

<220>
 <223> Synthetic construct

<400> 1530
 Met Glu Arg Ala Asn Asp Ser Thr Phe Ser Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn Arg Pro Gln Leu Glu Thr Ala Leu Phe Val Val Ile Leu
 20 25 30
 Ile Ile Tyr Phe Leu Ser Phe Leu Gly Asn Gly Thr Ile Ile Leu Leu
 35 40 45
 Ser Ile Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Met Asp Leu Cys Leu Thr Thr Cys Thr Val Pro Gln
 65 70 75 80
 Thr Leu Val Asn Phe Lys Gly Lys Asp Lys Thr Ile Thr Tyr Gly Gly
 85 90 95
 Cys Val Thr Gln Leu Phe Ile Ala Leu Gly Leu Gly Gly Ser Glu Cys
 100 105 110
 Val Leu Leu Ser Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg
 115 120 125
 Pro Leu His Tyr Met Val Ser Met His Pro Gln Leu Cys Leu Gln Leu
 130 135 140
 Val Val Thr Thr Trp Leu Thr Gly Phe Gly Asn Ser Val Ile Gln Thr
 145 150 155 160
 Ala Leu Thr Met Thr Leu Pro Leu Cys Asp Lys Asn Gln Val Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Val Met Leu Lys Leu Ser Cys Thr Asn Thr
 180 185 190
 Ser Ile Asn Glu Ala Glu Ile Phe Ala Val Ser Val Phe Phe Leu Val
 195 200 205
 Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly His Ile Thr His Ala
 210 215 220
 Val Leu Lys Ile Lys Ser Ala Gln Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Leu Val Val Ile Ile Phe Phe Gly Thr Leu Ile
 245 250 255
 Ser Met Tyr Leu Gln Pro Pro Ser Ser Tyr Ser Gln Asp Val Asn Lys
 260 265 270
 Ser Ile Ala Leu Phe Tyr Thr Leu Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Thr Lys Lys Thr
 290 295 300
 Ser Gly Glu Asp His Arg Cys Met Arg Lys Leu Thr Gln Gly Leu Gln
 305 310 315 320
 Phe Gln Thr Phe Val His
 325

<210> 1531
 <211> 312
 <212> PRT
 <213> Unknown (H38g448 protein)

<220>

<223> Synthetic construct

<400> 1531

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1           5           10           15
Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe
          20           25           30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
          35           40           45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50           55           60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
65           70           75           80
Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys
          85           90           95
Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu
          100          105          110
Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro
          115          120          125
Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile
          130          135          140
Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val
145          150          155          160
Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe
          165          170          175
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
          180          185          190
Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe
          195          200          205
Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val
          210          215          220
Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys
225          230          235          240
Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
          245          250          255
Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val
          260          265          270
Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser
          290          295          300
Gln Arg Ile Cys Ser Val Lys Met
305          310

```

<210> 1532

<211> 312

<212> PRT

<213> Unknown (H38g449 protein)

<220>

<223> Synthetic construct

<400> 1532

```

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1           5           10           15
Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
          20           25           30
Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
          35           40           45
Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```

50	55	60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys		
65	70	75
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val		
	85	90
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe		
	100	105
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu		
	115	120
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu		
	130	135
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser		
145	150	155
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe		
	165	170
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser		
	180	185
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Cys		
	195	200
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu		
	210	215
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile		
225	230	235
Pro His Ile Leu Val Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val		
	245	250
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu		
	260	265
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr		
	275	280
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys		
	290	295
Arg Ile Phe Tyr Ser Glu Asn Val		300
305	310	

<210> 1533

<211> 311

<212> PRT

<213> Unknown (H38g450 protein)

<220>

<223> Synthetic construct

<400> 1533

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile	
1	5
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile	
	20
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val	
	35
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe	
	50
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile	
65	70
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser	
	85
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly	
	100
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala	
	115
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys	
	130
	135
	140

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala
 145 150 155 160
 His Ile Ser Tyr Met Pr His Ile Pro Val Cys Ser Ala Arg Ala Cys
 165 170 175
 Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr
 180 185 190
 Glu Cys Thr Val Phe Lev Ser Thr Leu Phe Leu Met Phe Thr Phe
 195 200 205
 Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His
 210 215 220
 Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr
 225 230 235 240
 His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr
 245 250 255
 Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg
 290 295 300
 Ile Phe Pro Val Lys Met Lys
 305 310

<210> 1534

<211> 192

<212> PRT

<213> Unknown (H38g451 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(192)

<223> Xaa = Any Amino Acid

<400> 1534

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu
 20 25 30
 Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn
 35 40 45
 Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr
 65 70 75 80
 Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg
 85 90 95
 Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu
 100 105 110
 Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly
 115 120 125
 Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro
 130 135 140
 His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu
 145 150 155 160
 Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys
 165 170 175
 Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn
 180 185 190

<210> 1535
 <211> 317
 <212> PRT
 <213> Unknown (H38g452 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1535

```

Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly
 1           5           10           15
Phe Ser Glu His Gln Glu Gln Gln Ala Leu Leu Phe Gly Leu Phe Leu
           20           25           30
Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala
           35           40           45
Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
           50           55           60
Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys
65           70           75           80
Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu
           85           90           95
Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn
           100          105          110
Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser
           115          120          125
His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu
           130          135          140
Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His
145          150          155          160
Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro
           165          170          175
His Phe Phe Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser
           180          185          190
Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu
           195          200          205
Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu
           210          215          220
Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser
225          230          235          240
Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala
           245          250          255
Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp
           260          265          270
Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
           275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys
           290          295          300
Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg
305          310          315

```

<210> 1536
 <211> 252
 <212> PRT
 <213> Unknown (H38g453 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(252)

<223> Xaa = Any Amino Acid

<400> 1536

```

His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
          20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
          35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
 50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
 65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
          85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
          100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
          115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
          130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
          145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
          165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Thr Tyr Trp Asp Ser Phe
          180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
          195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
          210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
          225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
          245          250

```

<210> 1537

<211> 313

<212> PRT

<213> Unknown (H38g454 protein)

<220>

<223> Synthetic construct

<400> 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Phe Leu Phe Val Val Phe Phe
          20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
          35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
          50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
          65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
          85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

```
<210> 1538
<211> 309
<212> PRT
<213> Unknown (H38g455 protein)
```

<220>
<223> Synthetic construct

808

Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu Ala Pro Ile Val Leu
 195 200 205
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr
 210 215 220
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile
 245 250 255
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His
 260 265 270
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu
 290 295 300
 Met Ser Lys Arg Ser
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser
 1 5 10 15
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile
 20 25 30
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr
 35 40 45
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu
 50 55 60
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile
 65 70 75 80
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala
 85 90 95
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile
 100 105 110
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu
 115 120 125
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser
 130 135 140
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly
 145 150 155 160
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe
 165 170 175
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met
 180 185 190
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys
 195 200 205
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu
 210 215 220
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe
 225 230 235 240
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val
 245 250 255
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu
 260 265 270
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

275 280 285
 Ser Leu Arg Asn Asn Asp Met Lys Cys Ala Leu Ile Arg Leu Leu Gln
 290 295 300
 Lys Thr Tyr Gly Gln Glu Ala Tyr Phe
 305 310

<210> 1540
 <211> 324
 <212> PRT
 <213> Unknown (H38g457 protein)

<220>
 <223> Synthetic construct

<400> 1540
 Met Ala Val Gly Arg Asn Asn Thr Ile Val Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Ser Asp His Pro Gln Met Lys Ile Phe Leu Phe Met Leu Phe
 20 25 30
 Leu Gly Leu Tyr Leu Leu Thr Leu Ala Trp Asn Leu Ser Leu Ile Ala
 35 40 45
 Leu Ile Lys Met Asp Ser His Leu His Met Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Ser Thr Ala Pro
 65 70 75 80
 Lys Met Leu Ser Asp Ile Ile Thr Glu Gln Lys Thr Ile Ser Phe Val
 85 90 95
 Gly Cys Ala Thr Gln Tyr Phe Val Phe Cys Gly Met Gly Leu Thr Glu
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Leu Ile Ser His Thr Leu Cys Leu Lys
 130 135 140
 Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Phe Ile Glu
 145 150 155 160
 Thr Tyr Ser Val Tyr Gln His Asp Phe Cys Gly Pro Tyr Met Ile Asn
 165 170 175
 His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp
 180 185 190
 Thr Phe Thr Ser Glu Val Val Thr Phe Ile Val Ser Val Val Val Gly
 195 200 205
 Ile Val Ser Val Leu Val Val Leu Ile Ser Tyr Gly Tyr Ile Val Ala
 210 215 220
 Ala Val Val Lys Ile Ser Ser Ala Thr Gly Arg Thr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ser Gly
 245 250 255
 Phe Phe Met Tyr Met Arg Pro Ser Ser Ser Tyr Ser Leu Asn Arg Asp
 260 265 270
 Lys Val Val Ser Ile Phe Tyr Ala Leu Val Ile Pro Val Val Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Asn Ala Met Arg Lys
 290 295 300
 Ala Met Glu Arg Asp Pro Gly Ile Ser His Gly Gly Pro Phe Ile Phe
 305 310 315 320
 Met Thr Leu Gly

<210> 1541
 <211> 314
 <212> PRT

<213> Unknown (H38g458 pr tein)

<220>

<223> Synthetic construct

<400> 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
 1           5           10           15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
          20           25           30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
          35           40           45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
          50           55           60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
          65           70           75           80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
          85           90           95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
          100          105          110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
          115          120          125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
          130          135          140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
          145          150          155          160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
          165          170          175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
          180          185          190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
          195          200          205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
          210          215          220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
          225          230          235          240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
          245          250          255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
          260          265          270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
          275          280          285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
          290          295          300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
          305          310

```

<210> 1542

<211> 307

<212> PRT

<213> Unknown (H38g459 protein)

<220>

<223> Synthetic construct

<400> 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1           5           10           15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
          20           25           30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

```

```

      35      40      45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
  50      55      60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
  65      70      75      80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
      85      90      95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
      100      105      110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      115      120      125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
      130      135      140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
      145      150      155      160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
      165      170      175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
      180      185      190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
      195      200      205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
      210      215      220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
      225      230      235      240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
      245      250      255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
      260      265      270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
      275      280      285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
      290      295      300
Leu Lys His
305

```

<210> 1543

<211> 270

<212> PRT

<213> Unknown (H38g460 protein)

<220>

<223> Synthetic construct

<400> 1543

```

Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
  1      5      10      15
Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
      20      25      30
Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
      65      70      75      80
Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
      85      90      95
Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
      100      105      110
Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
      115      120      125

```

Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
 130 135 140
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
 145 150 155 160
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pr Asn Ile Ile Gln
 165 170 175
 His The Phe Cys Asn Thr Leu Gln Ile Ser Leu Ser Cys Ser Asn
 180 185 190
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
 195 200 205
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
 210 215 220
 Ser Ile Leu Lys Ile Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
 245 250 255
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
 260 265 270

<210> 1544

<211> 329

<212> PRT

<213> Unknown (H38g461 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1544

Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys
 1 5 10 15
 Cys Gly Xaa His Asn Lys Ile Thr Phe Leu Phe Ile Leu Leu Glu
 20 25 30
 Phe Thr Glu Asp Leu Gly Leu Gln Val Leu Phe Phe Ile Phe Leu
 35 40 45
 Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu
 50 55 60
 Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly
 65 70 75 80
 Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp
 85 90 95
 Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly
 100 105 110
 Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr
 115 120 125
 Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro
 130 135 140
 Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val
 145 150 155 160
 Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser
 165 170 175
 Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe
 180 185 190
 Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu
 195 200 205
 Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro
 210 215 220
 Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

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225          230          235          240
Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly
          245          250          255
Ser Pro Leu Thr Ala L u Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile
          260          265          270
Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly
          275          280          285
Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
          290          295          300
Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp
305          310          315          320
Arg Leu Gln Phe Leu Lys Glu Lys Tyr
          325

```

<210> 1545

<211> 349

<212> PRT

<213> Unknown (H38g462 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(349)

<223> Xaa = Any Amino Acid

<400> 1545

```

Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
1          5          10          15
Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu
          20          25          30
Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile
          35          40          45
His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50          55          60
Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys
          85          90          95
Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe
          100          105          110
Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val
          130          135          140
Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro
145          150          155          160
Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe
          165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
          180          185          190
Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile
          195          200          205
Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val
210          215          220
Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys
225          230          235          240
Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
          245          250          255
Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala
          260          265          270

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Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
      275                280                285
Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val
      290                295                300
Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala
      305                310                315                320
Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala
      325                330                335
Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro
      340                345

```

<210> 1546

<211> 319

<212> PRT

<213> Unknown (H38g463 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1546

```

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly
  1          5          10          15
Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala
      20          25          30
Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala
      35          40          45
Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala
      50          55          60
Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys
      65          70          75          80
Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg
      85          90          95
Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys
      100         105         110
Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser
      115         120         125
Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val
      130         135         140
Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu His Val
      145         150         155         160
Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln
      165         170         175
Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met
      180         185         190
His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile
      195         200         205
Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr
      210         215         220
Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr
      225         230         235         240
Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr
      245         250         255
Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala
      260         265         270
Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val
      275         280         285
Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

```

290 295 300
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr
 305 310 315

<210> 1547
 <211> 280
 <212> PRT
 <213> Unknown (H38g464 protein)

<220>
 <223> Synthetic construct

<400> 1547
 Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu Ile
 1 5 10 15
 Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 20 25 30
 Leu Ala Leu Thr Tyr Phe Ser Phe Ser Ser Val Thr Val Pro Lys Met
 35 40 45
 Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys
 50 55 60
 Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe
 65 70 75 80
 Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 85 90 95
 Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val
 100 105 110
 Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu
 115 120 125
 Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val
 130 135 140
 Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe
 145 150 155 160
 Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu
 165 170 175
 Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile
 180 185 190
 Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly
 210 215 220
 Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile
 225 230 235 240
 Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Ile Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe
 260 265 270
 Ser Arg Ala Thr Phe Phe Ser Trp
 275 280

<210> 1548
 <211> 303
 <212> PRT
 <213> Unknown (H38g465 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(303)
 <223> Xaa = Any Amino Acid

<400> 1548

```

Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn
 1          5          10          15
Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro
 20          25          30
Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu
 35          40          45
Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala
 50          55          60
Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu
 65          70          75          80
Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu
 85          90          95
Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu
100          105          110
Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val
115          120          125
Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr
130          135          140
Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys
145          150          155          160
Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln
165          170          175
Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val
180          185          190
Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala
195          200          205
Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile
210          215          220
Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg
225          230          235          240
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu
245          250          255
Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu
260          265          270
Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe
275          280          285
Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu
290          295          300

```

<210> 1549

<211> 309

<212> PRT

<213> Unknown (H38g466 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1549

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1          5          10          15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20          25          30
Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35          40          45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

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      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

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<210> 1550

<211> 312

<212> PRT

<213> Unknown (H38g467 protein)

<220>

<223> Synthetic construct

<400> 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
      65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```

Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
 145 150 155 160
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
 165 170 175
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
 180 185 190
 Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
 195 200 205
 Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
 210 215 220
 Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
 225 230 235 240
 Cys Leu Ser His Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
 245 250 255
 Tyr Gly Tyr Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
 260 265 270
 Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
 290 295 300
 Leu Gly Lys Gly Arg Glu Val Gly
 305 310

<210> 1551

<211> 82

<212> PRT

<213> Unknown (H38g468 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(82)

<223> Xaa = Any Amino Acid

<400> 1551

Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala
 1 5 10 15
 Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg
 20 25 30
 Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val
 35 40 45
 Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile
 50 55 60
 Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg
 65 70 75 80
 Lys Thr

<210> 1552

<211> 312

<212> PRT

<213> Unknown (H38g469 protein)

<220>

<223> Synthetic construct

<400> 1552

Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu

	20		25		30										
Met	Leu	Tyr	Leu	Ile	Thr	Leu	Ser	Gly	Asn	Met	Thr	Leu	Val	Ile	Leu
	35		40		45										
Ile	Arg	Thr	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Ile	Gly
	50		55		60										
Asn	Leu	Ser	Phe	Leu	Asp	Phe	Trp	Tyr	Thr	Ser	Val	Tyr	Thr	Pro	Lys
65			70		75										80
Ile	Leu	Ala	Ser	Cys	Val	Ser	Glu	Asp	Lys	Arg	Ile	Ser	Leu	Ala	Gly
			85		90										95
Cys	Gly	Ala	Gln	Leu	Phe	Phe	Ser	Cys	Val	Val	Ala	Tyr	Thr	Glu	Cys
	100		105		110										
Tyr	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	His	Ala	Ala	Ile	Cys	Asn
	115		120		125										
Pro	Leu	Leu	Tyr	Ser	Gly	Thr	Met	Ser	Thr	Ala	Leu	Cys	Thr	Gly	Leu
	130		135		140										
Val	Ala	Gly	Ser	Tyr	Ile	Gly	Gly	Phe	Leu	Asn	Ala	Ile	Ala	His	Thr
145			150		155										160
Ala	Asn	Thr	Phe	Arg	Leu	His	Phe	Cys	Gly	Lys	Asn	Ile	Ile	Asp	His
			165		170										175
Phe	Phe	Cys	Asp	Ala	Pro	Pro	Leu	Val	Lys	Met	Ser	Cys	Thr	Asn	Thr
	180		185		190										
Arg	Val	Tyr	Glu	Lys	Val	Leu	Leu	Gly	Val	Val	Gly	Phe	Thr	Val	Leu
	195		200		205										
Ser	Ser	Ile	Leu	Ala	Ile	Leu	Ile	Ser	Tyr	Val	Asn	Ile	Leu	Leu	Ala
	210		215		220										
Ile	Leu	Arg	Ile	His	Ser	Ala	Ser	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr
225			230		235										240
Cys	Ala	Ser	His	Leu	Ile	Ser	Val	Met	Leu	Phe	Tyr	Gly	Ser	Leu	Leu
			245		250										255
Phe	Met	Tyr	Ser	Arg	Pro	Ser	Ser	Thr	Tyr	Ser	Leu	Glu	Arg	Asp	Lys
	260		265		270										
Val	Ala	Ala	Leu	Phe	Tyr	Thr	Val	Ile	Asn	Pro	Leu	Leu	Asn	Pro	Leu
	275		280		285										
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Ile	Lys	Glu	Ala	Phe	Arg	Lys	Ala
	290		295		300										
Thr	Gln	Thr	Ile	Gln	Pro	Gln	Thr								
305			310												

<210> 1553

<211> 318

<212> PRT

<213> Unknown (H38g470 protein)

<220>

<223> Synthetic construct

<400> 1553

Met	Pro	Thr	Val	Asn	His	Ser	Gly	Thr	Ser	His	Thr	Val	Phe	His	Leu
1			5				10						15		
Leu	Gly	Ile	Pro	Gly	Leu	Gln	Asp	Gln	His	Met	Trp	Ile	Ser	Ile	Pro
			20				25						30		
Phe	Phe	Ile	Ser	Tyr	Val	Thr	Ala	Leu	Leu	Gly	Asn	Ser	Leu	Leu	Ile
	35		40				45								
Phe	Ile	Ile	Leu	Thr	Lys	Arg	Ser	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe
	50		55		60										
Leu	Cys	Met	Leu	Ala	Gly	Ala	Asp	Ile	Val	Leu	Ser	Thr	Cys	Thr	Ile
65			70		75										80
Pro	Gln	Ala	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Ala	Gly	Asp	Ile	Ser	Leu
			85		90										95
Asp	Arg	Cys	Ile	Thr	Gln	Leu	Phe	Phe	Ile	His	Ser	Thr	Phe	Ile	Ser
			100		105										110

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
 130 135 140
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
 145 150 155 160
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
 165 170 175
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
 180 185 190
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
 195 200 205
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
 210 215 220
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
 225 230 235 240
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
 245 250 255
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
 260 265 270
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
 275 280 285
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
 290 295 300
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val
 305 310 315

<210> 1554

<211> 314

<212> PRT

<213> Unknown (H38g471 protein)

<220>

<223> Synthetic construct

<400> 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu
 1 5 10 15
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe
 20 25 30
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala
 35 40 45
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu
 50 55 60
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro
 65 70 75 80
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp
 100 105 110
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg
 115 120 125
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala
 130 135 140
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr
 145 150 155 160
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro
 165 170 175
 His Phe Phe Cys Asp His Gln Pro Leu Arg Leu Ser Cys Ser Asp
 180 185 190
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

```

      195              200              205
Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala
  210              215              220
Ala Val Leu Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val
      245              250              255
Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly
      260              265              270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala
      290              295              300
Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser
  305              310

```

<210> 1555

<211> 316

<212> PRT

<213> Unknown (H38g472 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1555

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
      20              25              30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
      35              40              45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
      50              55              60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
      65              70              75              80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
      85              90              95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
      100              105              110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
      115              120              125
Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
      130              135              140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
      145              150              155              160
Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
      165              170              175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
      180              185              190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
      195              200              205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
      210              215              220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
      225              230              235              240
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
      245              250              255

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Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp
      260      265      270
Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro
      275      280      285
Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg
      290      295      300
Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile
305      310      315

```

<210> 1556

<211> 320

<212> PRT

<213> Unknown (H38g473 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1556

```

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
      20      25      30
Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
      65      70      75      80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
      100      105      110
Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
      115      120      125
Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe
      130      135      140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145      150      155      160
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
      165      170      175
Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
      180      185      190
Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly
      195      200      205
Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
      210      215      220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
      225      230      235      240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245      250      255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly
      260      265      270
Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
      290      295      300
Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

```

305

310

315

320

<210> 1557

<211> 329

<212> PRT

<213> Unknown (H38g474 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1557

```

Met Lys Leu Ile Asn His Thr Asp Gln Asn Pro Thr Ser Phe Leu Leu
 1           5           10           15
Met Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro
          20           25           30
Phe Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu
          35           40           45
Leu Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe
          50           55           60
Leu Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val
          65           70           75           80
Pro Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe
          85           90           95
Gly Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val
          100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile
          115          120          125
Cys Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly
          130          135          140
Lys Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro
          145          150          155          160
Leu Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala
          165          170          175
His Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly
          180          185          190
Thr Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val
          195          200          205
Gly Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg
          210          215          220
Ala Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly
          225          230          235          240
Thr Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly
          245          250          255
Leu Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His
          260          265          270
Ile His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu
          275          280          285
Asn Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala
          290          295          300
Leu Arg Leu Leu Lys Trp Gly Pro Ala Gln Ser Xaa Ser Leu Gln Pro
          305          310          315          320
His Pro Glu Thr Phe Ile Phe Phe Ala
          325

```

<210> 1558

<211> 330

<212> PRT

<213> Unknown (H38g475 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1558

His	Thr	Glu	Pro	Arg	His	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Val
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Gly	Gly	Val	Ser
			20					25					30		
Leu	Ser	Met	Tyr	Gly	Val	Thr	Val	Ile	Arg	Asn	Val	Leu	Ile	Ile	Leu
		35					40					45			
Gly	Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Val	Trp	Trp	Ala	Asp	Ile	Ser	Phe	Thr	Ser	Ala	Gly	Val	Pro
65					70					75					80
Lys	Met	Thr	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Tyr	Tyr	Ala
				85					90					95	
Gly	Cys	Met	Thr	Arg	Met	Ser	Phe	Phe	Val	Leu	Leu	Ala	Cys	Ile	Glu
			100					105					110		
Asp	Met	Leu	Val	Cys	Val	Met	Ala	Xaa	Glu	Cys	Phe	Val	Ala	Met	Cys
	115						120					125			
Arg	Pro	Val	Gln	Tyr	Thr	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135						140			
Arg	Val	Gly	Val	Ser	Phe	Leu	Gln	Ser	Val	Leu	Tyr	Ser	Gln	Val	His
145					150					155					160
Arg	Xaa	Ser	Val	Ser	Gln	Phe	Thr	Phe	Phe	Lys	Asn	Val	Glu	Ile	Ser
				165					170					175	
His	Phe	Val	Cys	Glu	Pro	Ser	Gln	Phe	Leu	His	Phe	Ala	Cys	Cys	Asp
		180						185					190		
Ser	Phe	Ile	Lys	Ser	Ile	Phe	Met	Tyr	Phe	Asp	Ser	Asn	Met	Phe	Gly
	195						200					205			
Phe	Leu	Pro	Ile	Thr	Gly	Ile	Phe	Leu	Ser	Xaa	Tyr	Lys	Ser	Val	Pro
	210					215					220				
Ser	Ile	Ile	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
225					230					235					240
Thr	Cys	Gly	Ser	His	Val	Ala	Val	Val	Cys	Leu	Leu	Tyr	Gly	Thr	Gly
				245					250					255	
Ile	Gly	Val	Tyr	Met	Thr	Ser	Gly	Val	Ala	Pro	Pro	Pro	Ser	Asn	Gly
		260						265					270		
Val	Val	Ala	Ser	Val	Lys	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Thr	Pro
		275					280					285			
Phe	Ile	Tyr	Ser	Val	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Pro	Leu	Trp	Ser
	290					295					300				
Val	Cys	Ser	Ser	Thr	Val	Lys	Ser	Phe	Asp	Val	Ser	His	Leu	Phe	Cys
305					310					315					320
Val	Trp	Val	Arg	Lys	Gly	Thr	His	Ile	Lys						
				325					330						

<210> 1559

<211> 170

<212> PRT

<213> Unknown (H38g476 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(170)

<223> Xaa = Any Amino Acid

<400> 1559

```

His Thr Gln Pro Arg Gly Leu Thr Arg Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Gln Asp Pro Gln Leu Gln Pro Val Leu Ser Gly Leu Ser
 20           25           30
Leu Cys Met Cys Leu Gly Thr Gln Leu Gly Asn Leu Leu Ile Ile Leu
 35           40           45
Gly Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Ser Phe Leu
 50           55           60
Ser Asn Leu Ser Gly Ala Asp Ile Ser Phe Thr Ser Thr Thr Gly Pro
 65           70           75           80
Lys Leu Ile Val Asp Ile His Ser Tyr Thr Arg Asp Ile Ser Tyr Ala
 85           90           95
Arg Cys Leu Thr His Thr Pro Leu Phe Ala Ile Phe Gly Gly Val Glu
 100          105          110
Arg Asp Met Leu Leu Arg Val Met Gly Tyr Asp Arg Val Val Asp Ile
 115          120          125
Cys Asp Pro Leu Tyr His Ser His Ala Met Asn Pro Cys Val Cys Gly
 130          135          140
Ser Leu Asp Leu Trp Ser Leu Phe Phe Leu Thr Leu Leu Tyr Thr His
 145          150          155          160
Leu His Asn Ser Ile Ala Leu His Met Thr
 165          170

```

<210> 1560

<211> 322

<212> PRT

<213> Unknown (H38g477 protein)

<220>

<223> Synthetic construct

<400> 1560

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
 20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
 65           70           75           80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
 85           90           95
Arg Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
 130          135          140
Phe Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr
 180          185          190

```

Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
 195 200 205
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
 210 215 220
 Val Arg Asn Ser Ser Ser Val Ser Met Val Lys Ala Cys Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
 290 295 300
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
 305 310 315 320
 Leu Glu

<210> 1561

<211> 314

<212> PRT

<213> Unknown (H38g478 protein)

<220>

<223> Synthetic construct

<400> 1561

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Phe Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Arg Thr Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
 65 70 75 80
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
 85 90 95
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu Arg Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Thr Ala Leu
 195 200 205
 Thr Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Thr
 210 215 220
 Ile Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Il Leu Ser

	260		265		270											
Val	Phe	Tyr	Thr	Ile	Phe	Thr	Pro	Phe	L	u	Asn	Pro	Leu	Ile	Tyr	Thr
	275		280		285											
Leu	Arg	Asn	Gln	Glu	Val	Lys	Thr	Ala	Met	Lys	Lys	Lys	Lys	Leu	Asn	Ile
	290		295		300											
Gln	Tyr	Phe	Ser	Leu	Gly	Lys	Thr	Ala	Pro							
305					310											

<210> 1562

<211> 198

<212> PRT

<213> Unknown (H38g479 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(198)

<223> Xaa = Any Amino Acid

<400> 1562

Met	Asn	Pro	Cys	Leu	Cys	Gly	Phe	Arg	Val	Val	Val	Ser	Phe	Phe	Phe
1				5					10					15	
His	Ser	Leu	Leu	Gly	Ala	Gln	Val	His	Asn	Leu	Ser	Ala	Ser	Gln	Met
		20						25					30		
Thr	Cys	Phe	Glu	Tyr	Val	Glu	Ile	His	Asn	Phe	Leu	Trp	Ala	Leu	Ser
		35					40					45			
Gln	Leu	Pro	His	Arg	Ala	Trp	Cys	Asp	Thr	Phe	Pro	Asn	Asn	Ile	Ile
	50					55					60				
Val	Tyr	Phe	Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ala	Gly	Thr
65				70					75					80	
Leu	Phe	Ser	Xaa	Tyr	Glu	Ser	Val	Ser	Ser	Ile	Glu	Arg	Val	Ser	Ser
				85					90					95	
Xaa	Gly	Gly	Glu	Tyr	Lys	Ala	Phe	Pro	Thr	Cys	Gly	Ser	His	Leu	Ser
			100					105					110		
Val	Val	Cys	Xaa	Leu	Tyr	Gly	Thr	Gly	Val	Gly	Gly	His	Leu	Ser	Ser
		115				120						125			
Asp	Val	Ser	Ser	Ser	Pro	Arg	Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr
	130					135					140				
Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Met	Arg	Asn
145					150					155					160
Arg	Asp	Thr	Lys	Ser	Val	Leu	Arg	Arg	Pro	His	Gly	Ser	Thr	Val	Xaa
				165					170					175	
Phe	Xaa	Tyr	Leu	Leu	Ile	Cys	Pro	Ile	Pro	Phe	Val	Val	Trp	Val	Lys
			180					185					190		
Lys	Gly	Arg	Lys	Val	Lys										
			195												

<210> 1563

<211> 314

<212> PRT

<213> Unknown (H38g480 protein)

<220>

<223> Synthetic construct

<400> 1563

Met	Leu	Gly	Leu	Asn	Gly	Thr	Pro	Phe	Gln	Pro	Ala	Thr	Leu	Gln	Leu
1				5					10					15	
Thr	Gly	Ile	Pro	Gly	Ile	Gln	Thr	Gly	Leu	Thr	Trp	Val	Ala	Leu	Ile
			20					25					30		

Phe Cys Ile Leu Tyr Met Ile Ser Ile Val Gly Asn Leu Ser Ile Leu
 35 40 45
 Thr Leu Val Phe Trp Glu Pro Ala Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Leu Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Ile Ser Thr Phe Cys Phe Asn Tyr Asn His Val Ala Phe
 85 90 95
 Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Ser Phe Met
 100 105 110
 Glu Ser Gly Ile Leu Leu Ala Met Ser Leu Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Val Thr Val Leu Thr His Asn Arg Ile Leu
 130 135 140
 Ala Met Gly Leu Gly Ile Leu Thr Lys Ser Phe Thr Thr Leu Phe Pro
 145 150 155 160
 Phe Pro Phe Val Val Lys Arg Leu Pro Phe Cys Lys Gly Asn Val Leu
 165 170 175
 His His Ser Tyr Cys Leu His Pro Asp Leu Met Lys Val Ala Cys Gly
 180 185 190
 Asp Ile His Val Asn Asn Ile Tyr Gly Leu Leu Val Ile Ile Phe Thr
 195 200 205
 Tyr Gly Met Asp Ser Thr Phe Ile Leu Leu Ser Tyr Ala Leu Ile Leu
 210 215 220
 Arg Ala Met Leu Val Ile Ile Ser Gln Glu Gln Arg Leu Lys Ala Leu
 225 230 235 240
 Asn Thr Cys Met Ser His Ile Cys Ala Val Leu Ala Phe Tyr Val Pro
 245 250 255
 Ile Ile Ala Val Ser Met Ile His Arg Phe Trp Lys Ser Ala Pro Pro
 260 265 270
 Val Val His Val Met Met Ser Asn Val Tyr Leu Phe Val Pro Pro Met
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Glu Ile Arg Lys Gly
 290 295 300
 Ile Leu Lys Phe Phe His Lys Ser Gln Ala
 305 310

<210> 1564

<211> 312

<212> PRT

<213> Unknown (H38g481 protein)

<220>

<223> Synthetic construct

<400> 1564

Met Gly Leu Phe Asn Val Thr His Pro Ala Phe Phe Leu Leu Thr Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Ser Ser His Ser Trp Leu Ser Gly Pro Leu Cys
 20 25 30
 Val Met Tyr Ala Val Ala Leu Gly Gly Asn Thr Val Ile Leu Gln Ala
 35 40 45
 Val Arg Val Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Met Leu Ser Phe Ser Asp Val Ala Ile Ser Met Ala Thr Leu Pro Thr
 65 70 75 80
 Val Leu Arg Thr Phe Cys Leu Asn Ala Arg Asn Ile Thr Phe Asp Ala
 85 90 95
 Cys Leu Ile Gln Met Phe Leu Ile His Phe Phe Ser Met Met Glu Ser
 100 105 110
 Gly Ile Leu Leu Ala Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Asp

```

      115      120      125
Pro Leu Arg Tyr Ala Thr Val Leu Thr Thr Glu Val Ile Ala Ala Met
  130      135      140
Gly L u Gly Ala Ala Ala Arg Ser Phe Ile Thr Leu Phe Pro Leu Pro
  145      150      155      160
Phe Leu Ile Lys Arg Leu Pro Ile Cys Arg Ser Asn Val Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Pro Asp Met Met Arg Leu Ala Cys Ala Asp Ile
      180      185      190
Ser Ile Asn Ser Ile Tyr Gly Leu Phe Val Leu Val Ser Thr Phe Gly
      195      200      205
Met Asp Leu Phe Phe Ile Phe Leu Ser Tyr Val Leu Ile Leu Arg Ser
      210      215      220
Val Met Ala Thr Ala Ser Arg Glu Glu Arg Leu Lys Ala Leu Asn Thr
  225      230      235      240
Cys Val Ser His Ile Leu Ala Val Leu Ala Phe Tyr Val Pro Met Ile
      245      250      255
Gly Val Ser Thr Val His Arg Phe Gly Lys His Val Pro Cys Tyr Ile
      260      265      270
His Val Leu Met Ser Asn Val Tyr Leu Phe Val Pro Pro Val Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Ala Lys Thr Lys Glu Ile Arg Arg Ala Ile Phe
      290      295      300
Arg Met Phe His His Ile Lys Ile
  305      310

```

<210> 1565
 <211> 156
 <212> PRT
 <213> Unknown (H38g482 protein)

<220>
 <223> Synthetic construct

```

<400> 1565
Met Glu Ser Asn Gln Thr Trp Ile Thr Glu Val Ile Leu Leu Gly Phe
  1      5      10      15
Gln Val Asp Pro Ala Leu Glu Leu Phe Leu Phe Gly Phe Phe Leu Leu
      20      25      30
Phe Tyr Ser Leu Thr Leu Met Gly Asn Gly Ile Ile Leu Gly Leu Ile
      35      40      45
Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe Leu Ser His
      50      55      60
Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val Pro Lys Met
      65      70      75      80
Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe Ala Pro Cys
      85      90      95
Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr Glu Cys Leu
      100      105      110
Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Ala Tyr Thr Pro Ile Ile Met Asn Trp Arg Val Cys Thr Val Leu
      130      135      140
Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala
  145      150      155

```

<210> 1566
 <211> 329
 <212> PRT
 <213> Unknown (H38g483 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1566

```

Met Glu Cys Asn Gln Thr Trp Ile Thr Asp Ile Thr Leu Leu Gly Phe
 1          5          10          15
Gln Val Gly Pro Ala Leu Ala Ile Leu Ile Tyr Glu Leu Phe Ser Val
 20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
 35          40          45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65          70          75          80
Leu Ala Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys
 85          90          95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu
100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
115          120          125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val
130          135          140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile
145          150          155          160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
165          170          175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
180          185          190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
195          200          205
Pro Leu Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile
210          215          220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
245          250          255
Val Tyr Met Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
260          265          270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Met Leu Asn Pro Leu Ile
275          280          285
Tyr Ser Leu Arg Asn Ala Gln Leu Lys Gly Ala Leu His Arg Ala Leu
290          295          300
Gln Arg Lys Arg Ser Met Arg Thr Val Tyr Gly Leu Cys Leu Xaa Asn
305          310          315          320
Met Trp Phe Ala Glu Ala Arg Ile Leu
325

```

<210> 1567

<211> 313

<212> PRT

<213> Unknown (H38g484 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1567

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Met Gly Val Asn Gln Ser Trp Ser Pro Glu Phe Ile Leu Val Glu Ser
 1           5           10           15
Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Xaa Ile Phe Ser Leu
 20           25           30
Leu Tyr Ile Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35           40           45
Cys Leu Asp His Ile Leu Pro Thr Pro Met Tyr Phe Phe Leu Ser His
 50           55           60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65           70           75           80
Leu Ala Asn Leu Met Asn Lys Lys Arg Thr Ile Ser Phe Leu Pro Cys
 85           90           95
Ile Met Gln Thr Tyr Leu Tyr Phe Ser Phe Ala Ala Thr Glu Cys Leu
 100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 115          120          125
Leu Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala
 130          135          140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Ala Ile
 145          150          155          160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
 165          170          175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ser Asp Thr Trp
 180          185          190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
 195          200          205
Pro Leu Cys Leu Met Leu Val Ser Tyr Met His Ile Leu Leu Ala Ile
 210          215          220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
 225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
 245          250          255
Val Tyr Ile Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
 260          265          270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Ile Leu Asn Pro Leu Ile
 275          280          285
Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu His Arg Ala Leu
 290          295          300
Gln Arg Thr Leu Ser Met Xaa Gly Val
 305          310

```

<210> 1568

<211> 334

<212> PRT

<213> Unknown (H38g485 protein)

<220>

<223> Synthetic construct

<400> 1568

```

Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
 1           5           10           15
His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
 20           25           30
Ile Leu Leu Gly Phe Ser Asp Tyr Pro Gln Leu Gln Lys Val Leu Phe
 35           40           45
Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
 50           55           60

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Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
65          70          75          80
Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
      85          90          95
Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
      100         105         110
Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
      115         120         125
Ser Thr Glu Cys Val Leu Pro Ala Val Met Ser Cys Asp Arg Tyr Val
      130         135         140
Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
145         150         155         160
Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
      165         170         175
Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
      180         185         190
Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
      195         200         205
Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
      210         215         220
Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
225         230         235         240
Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Arg Arg Gln Lys
      245         250         255
Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
      260         265         270
Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
      275         280         285
Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
      290         295         300
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
305         310         315         320
Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
      325         330

```

<210> 1569

<211> 170

<212> PRT

<213> Unknown (H38g486 protein)

<220>

<223> Synthetic construct

<400> 1569

```

Met Glu Gly Asn Lys Thr Trp Ile Thr Asp Ile Thr Leu Pro Arg Phe
1          5          10          15
Gln Val Gly Pro Ala Leu Glu Ile Leu Leu Cys Gly Leu Phe Ser Ala
      20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
      35          40          45
Cys Leu Asp Cys Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
      50          55          60
Leu Ala Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met
65          70          75          80
Leu Thr Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys
      85          90          95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu
      100         105         110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro
      115         120         125
Leu Arg Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala

```

130	135	140
Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Phe Ser		
145	150	155
Ser Gln Ser Leu Arg Cys Met Asn Val Leu		160
165	170	

<210> 1570

<211> 308

<212> PRT

<213> Unknown (H38g487 protein)

<220>

<223> Synthetic construct

<400> 1570

Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly	
1 5 10 15	
Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu	
20 25 30	
Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu	
35 40 45	
Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50 55 60	
Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys	
65 70 75 80	
Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser	
85 90 95	
Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr	
100 105 110	
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr	
115 120 125	
Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu	
130 135 140	
Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr	
145 150 155 160	
Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His	
165 170 175	
Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr	
180 185 190	
Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Val Ile Leu	
195 200 205	
Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr	
210 215 220	
Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr	
225 230 235 240	
Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val	
245 250 255	
Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys	
260 265 270	
Ala Val His Val Leu Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe	
275 280 285	
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys	
290 295 300	
Trp Lys Gly Lys	
305	

<210> 1571

<211> 223

<212> PRT

<213> Unknown (H38g488 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1571

```

Lys Glu Met Gly Cys His Gln Ser Met Val Thr Glu Phe Ile Leu Val
 1          5          10          15
Gly Phe Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Trp Ser Phe
 20          25          30
Ser Leu Gly Ile Ala Leu Glu Leu Ile Cys Leu Asp His Ser Leu His
 35          40          45
Thr Pro Tyr Phe Phe Leu Ser His Leu Ala Val Ile Asp Met Ala Tyr
 50          55          60
Ala Ser Asn Asn Val Pro Lys Met Leu Val Asp Leu Ala Asn Xaa Lys
 65          70          75          80
Ser Thr Met Cys Phe Phe Pro Cys Ile Met Gln Thr Phe Leu Tyr Leu
 85          90          95
Ala Phe Ala His Ile Glu Cys Leu Ile Leu Val Val Leu Ser Tyr Asp
100          105          110
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Asn Val Leu Met Ser
115          120          125
Trp Arg Glu Cys Thr Val Leu Ala Val Ala Ser Trp Val Phe Ser Phe
130          135          140
Leu Leu Ala Leu Val His Leu Val Leu Ile Leu Arg Leu Pro Phe Ser
145          150          155          160
Gly Pro His Glu Ile Asn His Tyr Cys Glu Ile Leu Ser Val Leu Lys
165          170          175
Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile Phe Ala Ser
180          185          190
Cys Met Phe Ile Leu Val Gly Xaa Leu Cys Leu Val Leu Val Ser Tyr
195          200          205
Leu Gly Ile Trp Arg His Leu Arg Ser Val Ala Lys Pro Lys Arg
210          215          220

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<210> 1572

<211> 309

<212> PRT

<213> Unknown (H38g489 protein)

<220>

<223> Synthetic construct

<400> 1572

```

Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu
 20          25          30
Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile Ile
 35          40          45
Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln
 65          70          75          80
Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly
 85          90          95
Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys
100          105          110
Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys

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115	120	125
Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu		
130	135	140
Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala		
145	150	155
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His		
	165	170
Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr		
	180	185
Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val		
	195	200
Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala		
	210	215
Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr		
225	230	235
Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile		
	245	250
Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys		
	260	265
Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile		
	275	280
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu		
	290	295
Leu Ser Gly Lys Leu		300
305		

<210> 1573

<211> 337

<212> PRT

<213> Unknown (H38g490 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 1573

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Val Phe Leu Leu Leu		
1	5	10
Gly Thr Thr Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe		
	20	25
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu		
	35	40
Ala Ile Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu		
	50	55
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro		
65	70	75
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala		
	85	90
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu		
	100	105
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile		
	115	120
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly		
	130	135
Phe Leu Val Leu Leu Ser Phe Phe Ser Val Leu Ser Leu Leu Asp Ser		
145	150	155
Gln Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val		
	165	170
		175

Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
 180 185 190
 Cys Cys Asp Thr Phe Thr Asn Lys Ile Ile Met Tyr Phe Pro Ala Ala
 195 200 205
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys
 210 215 220
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Gly Gly Lys Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr
 245 250 255
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Asp Val Ser Ser Ser
 260 265 270
 Pro Arg Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 275 280 285
 Met Pro Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser
 290 295 300
 Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu
 305 310 315 320
 Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val
 325 330 335
 Lys

<210> 1574

<211> 293

<212> PRT

<213> Unknown (H38g491 protein)

<220>

<223> Synthetic construct

<400> 1574

Met Gly Phe Ser Asn Ser Trp Asp Ile Gln Ile Val His Ala Ala Leu
 1 5 10 15
 Phe Phe Leu Val Tyr Leu Ala Ala Val Ile Gly Asn Leu Leu Ile Ile
 20 25 30
 Ile Leu Thr Thr Leu Asp Val His Leu Gln Thr Pro Met Tyr Phe Phe
 35 40 45
 Leu Arg Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ile Ser Val Thr Ile
 50 55 60
 Pro Lys Ser Ile Val Ser Ser Leu Thr His Asp Thr Ser Ile Ser Phe
 65 70 75 80
 Phe Gly Cys Ala Leu Gln Ala Phe Phe Phe Met Asp Leu Ala Thr Thr
 85 90 95
 Glu Val Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Met Ala Ile
 100 105 110
 Cys Arg Pro Leu His Tyr Glu Val Ile Ile Asn Gln Gly Val Cys Leu
 115 120 125
 Arg Met Met Ala Met Ser Trp Leu Ser Gly Val Ile Cys Gly Phe Met
 130 135 140
 His Val Ile Ala Thr Phe Ser Leu Pro Phe Cys Gly Arg Asn Arg Ile
 145 150 155 160
 Arg Gln Phe Phe Cys Asn Ile Pro Gln Leu Leu Ser Leu Leu Asp Pro
 165 170 175
 Lys Val Ile Thr Ile Glu Ile Gly Val Met Val Phe Gly Thr Ser Leu
 180 185 190
 Val Ile Ile Ser Phe Val Val Ile Thr Leu Ser Tyr Met Tyr Ile Phe
 195 200 205
 Ser Val Ile Met Arg Ile Pro Ser Lys Glu Gly Arg Ser Lys Thr Phe
 210 215 220
 Ser Thr Cys Ile Pro His Leu Val Val Val Thr Leu Phe Met Ile Ser

225 230 235 240
 Gly Ser Ile Ala Tyr Val Lys Pro Ile Ser Asn Ser Pro Pro Val Leu
 245 250 255
 Asp Val Phe Leu Ser Ala Phe Tyr Thr Val Val Pro Pro Thr Leu Asn
 260 265 270
 Pro Val Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg
 275 280 285
 Arg Gln Cys Gly Pro
 290

<210> 1575

<211> 341

<212> PRT

<213> Unknown (H38g492 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400> 1575

Met Met Gly His Gln Asn His Thr Phe Ser Ser Asp Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Phe Ser Ser Ser Pro Thr Ser Val Val Phe Phe Leu Asp Asn
 20 25 30
 Leu Phe Ile Phe Ile Met Ser Val Thr Glu Asn Thr Leu Met Ile Leu
 35 40 45
 Leu Ile Arg Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
 50 55 60
 Ser His Leu Ser Leu Met Asp Ile Leu His Val Ser Asn Ile Val Pro
 65 70 75 80
 Lys Met Val Thr Asn Phe Leu Ser Gly Ser Arg Thr Ile Ser Phe Ala
 85 90 95
 Gly Cys Gly Phe Gln Val Phe Leu Ser Leu Thr Leu Leu Gly Gly Glu
 100 105 110
 Cys Leu Leu Leu Ala Ala Met Ser Cys Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 His Pro Leu Arg Tyr Pro Ile Leu Met Lys Glu Tyr Ala Ser Ala Leu
 130 135 140
 Met Ala Gly Gly Ser Trp Leu Ile Gly Val Phe Asn Ser Thr Val His
 145 150 155 160
 Thr Ala Tyr Ala Leu Gln Phe Pro Phe Cys Gly Ser Arg Ala Ile Asp
 165 170 175
 His Phe Phe Cys Glu Val Pro Ala Met Leu Lys Leu Ser Cys Ala Asp
 180 185 190
 Thr Thr Arg Tyr Glu Arg Gly Val Cys Val Ser Ala Val Ile Phe Leu
 195 200 205
 Leu Ile Pro Phe Ser Leu Ile Ser Ala Ser Tyr Gly Gln Ile Ile Leu
 210 215 220
 Thr Val Leu Gln Met Lys Ser Ser Glu Ala Arg Lys Lys Ser Phe Ser
 225 230 235 240
 Thr Cys Ser Phe His Met Ile Val Val Thr Met Tyr Tyr Gly Pro Phe
 245 250 255
 Ile Phe Thr Tyr Met Arg Pro Lys Ser Tyr His Thr Pro Gly Gln Asp
 260 265 270
 Lys Phe Leu Ala Ile Phe Tyr Thr Ile Leu Thr Pro Thr Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Phe Arg Asn Lys Asp Val Leu Ala Val Met Thr Lys
 290 295 300

Tyr Ala Gln Lys Xaa Leu Ser Ala Gln Lys Asn Glu Xaa Glu Asn Ser
 305 310 315 320
 Xaa Met Cys Val Leu Ser Ile Ser Met Leu Asn Ala Xaa Arg Ile Leu
 325 330 335
 Met Arg Trp Phe Pro
 340

<210> 1576
 <211> 311
 <212> PRT
 <213> Unknown (H38g493 protein)

<220>
 <223> Synthetic construct

<400> 1576
 Met Lys Trp Ala Asn Gln Thr Ala Val Thr Glu Tyr Val Leu Met Gly
 1 5 10 15
 Leu His Glu His Cys Asn Leu Glu Val Val Leu Phe Val Phe Cys Leu
 20 25 30
 Gly Ile Tyr Ser Val Asn Val Leu Gly Asn Ala Leu Leu Ile Gly Leu
 35 40 45
 Asn Val Leu His Pro Arg Leu His Asn Pro Met Tyr Phe Phe Ser Asn
 50 55 60
 Leu Ser Leu Met Asp Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Met
 65 70 75 80
 Leu Asp Asn Phe Leu Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys
 85 90 95
 Ala Leu Gln Met Tyr Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu
 100 105 110
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro
 115 120 125
 Leu Arg Tyr Pro Glu Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala
 130 135 140
 Ala Leu Ser Trp Gly Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile
 145 150 155 160
 Leu Val Trp His Leu Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr
 165 170 175
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn
 180 185 190
 Ala Leu Ala Leu Met Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu
 195 200 205
 Leu Leu Ile Cys Leu Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg
 210 215 220
 Val Pro Ser Ala Ala Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala
 225 230 235 240
 His Arg Thr Val Val Val Val Phe Tyr Gly Thr Ile Ser Phe Met Tyr
 245 250 255
 Phe Lys Pro Lys Ala Lys Asp Pro Asn Val Asp Lys Thr Val Ala Leu
 260 265 270
 Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Ile Ile Tyr Ser Leu
 275 280 285
 Arg Asn Ala Glu Val Lys Ala Ala Val Leu Thr Leu Leu Arg Gly Gly
 290 295 300
 Leu Leu Ser Arg Lys Ala Ser
 305 310

<210> 1577
 <211> 319
 <212> PRT
 <213> Unknown (H38g494 protein)

<220>

<223> Synthetic construct

<400> 1577

```

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1           5           10           15
Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
      20           25           30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Leu
      35           40           45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
      65           70           75           80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
      85           90           95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
      100          105          110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
      115          120          125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
      130          135          140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
      145          150          155          160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
      165          170          175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
      180          185          190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
      195          200          205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
      210          215          220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
      225          230          235          240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
      245          250          255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
      260          265          270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
      275          280          285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
      290          295          300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
      305          310          315

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<210> 1578

<211> 264

<212> PRT

<213> Unknown (H38g495 protein)

<220>

<223> Synthetic construct

<400> 1578

```

Met Met Val Leu Ser Ile Val Leu Thr Ser Leu Phe Gly Asn Ser Leu
 1           5           10           15
Met Ile Leu Leu Ile His Trp Asp His Arg Phe His Thr Pro Met Tyr
      20           25           30
Phe Leu Leu Ser Gln Leu Ser Leu Met Asp Val Met Leu Val Ser Thr
      35           40           45

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Thr Val Pro Lys Met Ala Ala Asp Tyr Leu Thr Gly Ser Lys Ala Il
 50 55 60
 Ser Arg Ala Gly Cys Gly Ala Gln Ile Phe Phe Leu Pro Thr Leu Gly
 65 70 75 80
 Gly Gly Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala
 85 90 95
 Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu
 100 105 110
 Cys Leu Arg Met Asn Leu Ser Cys Trp Leu Leu Gly Ala Ala Asp Gly
 115 120 125
 Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His
 130 135 140
 Glu Ile Asp His Phe Phe Cys Glu Thr Pro Val Leu Val Arg Leu Ala
 145 150 155 160
 Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val
 165 170 175
 Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu
 180 185 190
 Ile Leu Ala Ala Val Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys
 195 200 205
 Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe Tyr
 210 215 220
 Gly Ala Ala Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr
 225 230 235 240
 Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro Leu
 245 250 255
 Leu Asn Pro Leu Ile Tyr Ser Val
 260

<210> 1579

<211> 220

<212> PRT

<213> Unknown (H38g496 protein)

<220>

<223> Synthetic construct

<400> 1579

Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 1 5 10 15
 Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
 20 25 30
 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
 35 40 45
 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
 50 55 60
 Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
 65 70 75 80
 Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
 85 90 95
 Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
 100 105 110
 Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
 115 120 125
 Met Leu Val Glu Ala Ile Thr Phe Ala Leu Gly Val Ala Leu Leu Leu
 130 135 140
 Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr Gly Val Ile Ala Ala Ala
 145 150 155 160
 Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
 165 170 175
 Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile

	180		185		190
Tyr Val Tyr	Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp	Gln Gly Lys			
	195		200		205
Phe Leu Thr	Leu Phe Tyr Thr Ile Val Ile Pro Ser				
	210		215		220

<210> 1580
 <211> 312
 <212> PRT
 <213> Unknown (H38g497 protein)

<220>
 <223> Synthetic construct

<400> 1580

Met Glu Pro	Leu Asn Arg Thr Glu Val	Ser Glu Phe Phe Leu Lys Gly
1	5	10 15
Phe Ser Gly	Tyr Pro Ala Leu Glu His Leu Leu Phe Pro Leu Cys Ser	
	20	25 30
Ala Met Tyr	Leu Val Thr Leu Leu Gly Asn Thr Ala Ile Met Ala Val	
	35	40 45
Ser Val Leu	Asp Ile His Leu His Thr Pro Val Tyr Phe Phe Leu Gly	
	50	55 60
Asn Leu Ser	Thr Leu Asp Ile Cys Tyr Thr Pro Thr Phe Val Pro Leu	
65	70	75 80
Met Leu Val	His Leu Leu Ser Ser Arg Lys Thr Ile Ser Phe Ala Val	
	85	90 95
Cys Ala Ile	Gln Met Cys Leu Ser Leu Ser Thr Gly Ser Thr Glu Cys	
	100	105 110
Leu Leu Leu	Ala Ile Thr Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln	
	115	120 125
Pro Leu Arg	Tyr His Val Leu Met Ser His Arg Leu Cys Val Leu Leu	
	130	135 140
Met Gly Ala	Ala Trp Val Leu Cys Leu Leu Lys Ser Val Thr Glu Met	
145	150	155 160
Val Ile Ser	Met Arg Leu Pro Phe Cys Gly His His Val Val Ser His	
	165	170 175
Phe Thr Cys	Lys Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asn Thr	
	180	185 190
Ser Val Ser	Glu Asp Phe Leu Leu Ala Gly Ser Ile Leu Leu Leu Pro	
	195	200 205
Val Pro Leu	Ala Phe Ile Cys Leu Ser Tyr Leu Leu Ile Leu Ala Thr	
	210	215 220
Ile Leu Arg	Val Pro Ser Ala Ala Arg Cys Cys Lys Ala Phe Ser Thr	
225	230	235 240
Cys Leu Ala	His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Ile	
	245	250 255
Phe Met Tyr	Leu Lys Pro Lys Ser Lys Glu Ala His Ile Ser Asp Glu	
	260	265 270
Val Phe Thr	Val Leu Tyr Ala Met Val Thr Thr Met Leu Asn Pro Thr	
	275	280 285
Ile Tyr Ser	Leu Arg Asn Lys Glu Val Lys Glu Ala Ala Arg Lys Val	
	290	295 300
Trp Gly Arg	Ser Arg Ala Ser Arg	
305	310	

<210> 1581
 <211> 314
 <212> PRT
 <213> Unknown (H38g498 protein)

<220>

<223> Synthetic construct

<400> 1581

```

Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly
1           5           10           15
Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr
20           25           30
Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu
35           40           45
Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys
65           70           75           80
Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu
85           90           95
Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe
100          105          110
Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser
115          120          125
Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu
130          135          140
Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr
145          150          155          160
Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His
165          170          175
Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile
180          185          190
Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu
195          200          205
Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr
210          215          220
Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr
225          230          235          240
Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile
245          250          255
Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys
260          265          270
Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe
275          280          285
Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala
290          295          300
Val Gly Arg Arg Thr Glu Leu Ala Gln Arg
305          310

```

<210> 1582

<211> 309

<212> PRT

<213> Unknown (H38g499 protein)

<220>

<223> Synthetic construct

<400> 1582

```

Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser
1           5           10           15
Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile
20           25           30
Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr
35           40           45
Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

```

50 55 60
 Ser Phe Leu Asp L u Cys Leu Ile Ser Val Thr Ala Pro Lys Ser Ile
 65 70 75 80
 Ala Asn Ser Leu Ile His Asn Asn Ser Ile Ser Phe Leu Gly Cys Val
 85 90 95
 Ser Gln Val Phe Leu Leu Ser Ser Ala Ser Ala Glu Leu Leu Leu
 100 105 110
 Leu Thr Val Met Ser Phe Asp Arg Tyr Thr Ala Ile Cys His Pro Leu
 115 120 125
 His Tyr Asp Val Ile Met Asp Arg Ser Thr Cys Val Gln Arg Ala Thr
 130 135 140
 Val Ser Trp Leu Tyr Gly Gly Leu Ile Ala Val Met His Thr Ala Gly
 145 150 155 160
 Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe
 165 170 175
 Cys Asp Ile Pro Gln Leu Leu Ala Ile Ser Cys Ser Glu Asn Leu Ile
 180 185 190
 Arg Glu Ile Ala Leu Ile Leu Ile Asn Val Val Leu Asp Phe Cys Cys
 195 200 205
 Phe Ile Val Ile Ile Ile Thr Tyr Val His Val Phe Ser Thr Val Lys
 210 215 220
 Lys Ile Pro Ser Thr Glu Gly Gln Ser Lys Ala Tyr Ser Ile Cys Leu
 225 230 235 240
 Pro His Leu Leu Val Val Leu Phe Leu Ser Thr Gly Phe Ile Ala Tyr
 245 250 255
 Leu Lys Pro Ala Ser Glu Ser Pro Ser Ile Leu Asp Ala Val Ile Ser
 260 265 270
 Val Phe Tyr Thr Met Leu Pro Pro Thr Phe Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Lys Ala Ile Lys Val Ala Leu Gly Met Leu Ile Lys Gly
 290 295 300
 Lys Leu Thr Lys Lys
 305

<210> 1583

<211> 314

<212> PRT

<213> Unknown (H38g500 protein)

<220>

<223> Synthetic construct

<400> 1583

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1 5 10 15
 Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
 20 25 30
 Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
 35 40 45
 Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys
 65 70 75 80
 Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
 85 90 95
 Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
 100 105 110
 Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
 115 120 125
 Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
 130 135 140

Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
 145 150 155 160
 Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
 165 170 175
 Phe Phe Cys Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
 180 185 190
 Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
 195 200 205
 Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
 210 215 220
 Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
 225 230 235 240
 Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
 245 250 255
 Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
 260 265 270
 Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
 290 295 300
 Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
 305 310

<210> 1584

<211> 312

<212> PRT

<213> Unknown (H38g501 protein)

<220>

<223> Synthetic construct

<400> 1584

Met Asp Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser
 20 25 30
 Leu Ile Tyr Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr
 35 40 45
 Val Thr Cys Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys
 65 70 75 80
 Met Ile Ile Asp Leu Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly
 85 90 95
 Cys Val Thr Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met
 100 105 110
 Thr Leu Leu Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe
 130 135 140
 Ala Ile Leu Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile
 145 150 155 160
 Val Leu Thr Met Asn Leu Pro Phe Cys Gly His Asn Val Ile Asn Asn
 165 170 175
 Ile Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Ile Glu Thr
 180 185 190
 Tyr Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe
 195 200 205
 Thr Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser
 210 215 220
 Val Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu

225 230 235 240
 Ser Ala His Ile Ile Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Leu Ala Ser Asn Lys Thr Leu Ala
 260 265 270
 Val Phe Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Ser Ile Tyr Thr
 275 280 285
 Leu Arg Asn Lys Lys Met Gln Glu Ala Ile Arg Lys Leu Arg Phe Gln
 290 295 300
 Tyr Val Ser Ser Ala Gln Asn Phe
 305 310

<210> 1585

<211> 325

<212> PRT

<213> Unknown (H38g502 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1585

Met Pro Thr Asp Lys Gln Met Glu Lys Gln Asn Gln Ser Met Val Pro
 1 5 10 15
 Glu Phe Ile Leu Tyr Gly Ile Gln Lys Ser His Glu Leu Gln Ile Phe
 20 25 30
 Phe Ile Leu Phe Phe His Ser Leu His Ile Ala Xaa Leu Ser Asn Leu
 35 40 45
 Ile Ile Ile Phe Val Val Lys Leu Asp Pro Gln Leu His Ser Pro Met
 50 55 60
 Tyr Phe Leu Leu Ala Asn Leu Ser Ser Thr Asp Met Pro Leu Ala Ser
 65 70 75 80
 Phe Ala Thr Pro Lys Lys Ile Asp Asn Val Ile Ser Glu Tyr Arg Thr
 85 90 95
 Ile Ser Tyr Glu Gly Cys Met Thr Xaa Arg Phe Phe Leu His Phe Leu
 100 105 110
 Ser Gly Ser Glu Met Val Leu Leu Leu Ala Met Ala Ile Asp Arg Xaa
 115 120 125
 Phe Ala Ile Cys Lys Pro Leu His Tyr Lys Ser Ile Ala Ser Asp Leu
 130 135 140
 Leu Leu Ala Ser Trp Thr Met Asp Phe Met His Thr Met Ser Gln Ile
 145 150 155 160
 Val Leu Thr Val Thr Leu Pro Phe Cys Gly Leu Ser Val Val Asp Ile
 165 170 175
 Phe Val Cys Asp Val Ile Cys Leu Val Ile Lys Leu Ala Cys Thr Asp
 180 185 190
 Thr Tyr Ile Leu Glu Leu Xaa Val Ile Ala Asp Ser Gly Leu Leu Ser
 195 200 205
 Leu Leu Cys Phe Met Phe Leu Leu Ile Ser Tyr Ser Thr Val Leu Ile
 210 215 220
 Ile Ile Xaa His His Ser Ser Arg Gly Ser Ser Lys Thr Leu Ser Thr
 225 230 235 240
 Leu Ser Ala His Ile Met Val Val Val Leu Phe Phe Gly Ala Cys Ile
 245 250 255
 Phe Thr Cys Glu Arg Pro Phe Ser Thr Val Ser Ile Asp Ser Val Phe
 260 265 270
 Xaa Thr Ile Phe Ala Pro Leu Leu Asn Pro Ile Ile Tyr Thr Phe Arg
 275 280 285

Asn Asn Asp Met Lys Lys Ala Leu Arg Lys Met Lys Ile Asn Phe Val
 290 295 300
 Ser Ser Arg Ser Thr Xaa Xaa Leu Lys Tyr Tyr Asn His Xaa Lys His
 305 310 315 320
 His His Tyr Cys Cys
 325

<210> 1586
 <211> 312
 <212> PRT
 <213> Unknown (H38g503 protein)

<220>
 <223> Synthetic construct

<400> 1586
 Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Ser
 20 25 30
 Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr
 35 40 45
 Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe
 130 135 140
 Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu
 145 150 155 160
 Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr
 180 185 190
 Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
 195 200 205
 Ala Ser Phe Leu Ile Leu Ile Ser Tyr Ile Phe Ile Leu Val Thr
 210 215 220
 Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu
 225 230 235 240
 Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe
 245 250 255
 Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln
 290 295 300
 Phe Val Asn Tyr Ser Lys Ile Phe
 305 310

<210> 1587
 <211> 322
 <212> PRT
 <213> Unknown (H38g504 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1587

```

Met Asn Arg Asp Asn Gln Ser Val Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Asn Ser Trp Glu Ile Lys Ile Phe Leu Phe Cys Phe Ser Cys
          20           25           30
Leu Phe Tyr Val Ser Gly Val Met Ala Asn Leu Ile Val Val Val Ile
          35           40           45
Val Thr Ser Asp Pro Tyr Leu His Ser Ser Leu Tyr Ile Leu Leu Ala
          50           55           60
Asn Leu Ser Val Ile Asp Leu Thr Phe Cys Ser Ile Ala Ala Arg Lys
          65           70           75           80
Met Ile Cys Asp Ile Phe Arg Lys Gln Lys Val Ile Ser Phe Trp Gly
          85           90           95
Cys Val Ala Gln Ile Phe Phe Ser His Ala Val Gly Gly Thr Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu Ile
          130          135          140
Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln Leu
          145          150          155          160
Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn Thr
          180          185          190
Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
          195          200          205
Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala Thr
          210          215          220
Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr Leu
          225          230          235          240
Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
          245          250          255
Phe Tyr Val Trp Pro Ser Pro Pro Thr His Leu Asn Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Ile Phe Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
          275          280          285
Phe Arg Asn Arg Glu Met Lys Ile Ala Ile Arg Arg Val Phe Gly Gln
          290          295          300
Phe Met Gly Phe Arg Lys Thr Thr Xaa Val Ala Leu Leu Lys His Arg
          305          310          315          320
Ile Ser

```

<210> 1588

<211> 291

<212> PRT

<213> Unknown (H38g505 protein)

<220>

<223> Synthetic construct

<400> 1588

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
 35 40 45
 Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe
 130 135 140
 Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu
 145 150 155 160
 Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser
 180 185 190
 Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
 195 200 205
 Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr
 210 215 220
 Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
 245 250 255
 Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
 275 280 285
 Phe Arg Asn
 290

<210> 1589

<211> 312

<212> PRT

<213> Unknown (H38g506 protein)

<220>

<223> Synthetic construct

<400> 1589

Met Asn Gly Met Asn His Ser Val Val Ser Glu Phe Val Phe Met Gly
 1 5 10 15
 Leu Thr Asn Ser Arg Glu Ile Gln Leu Leu Phe Val Phe Ser Leu
 20 25 30
 Leu Phe Tyr Phe Ala Ser Met Met Gly Asn Leu Val Ile Val Phe Thr
 35 40 45
 Val Thr Met Asp Ala His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Ile Ile Asp Met Ala Phe Cys Ser Ile Thr Ala Pro Lys
 65 70 75 80
 Met Ile Cys Asp Ile Phe Lys Lys His Lys Ala Ile Ser Phe Arg Gly
 85 90 95
 Cys Ile Thr Gln Ile Phe Phe Ser His Ala Leu Gly Gly Thr Glu Met

```

      100      105      110
Val Leu L u Ile Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Tyr Phe
      130      135      140
Leu Ala Thr Ser Ser Ile Ile Gly Leu Ile His Ser Leu Val Gln Leu
145      150      155      160
Val Phe Val Val Asp Leu Pro Phe Cys Gly Pro Asn Ile Phe Asp Ser
      165      170      175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asn Thr
      180      185      190
Gln Glu Leu Glu Phe Met Val Thr Val Asn Ser Gly Leu Ile Ser Val
      195      200      205
Gly Ser Phe Val Leu Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
      210      215      220
Val Trp Lys His Ser Ser Gly Gly Leu Ala Lys Ala Leu Ser Thr Leu
225      230      235      240
Ser Ala His Val Thr Val Val Ile Leu Phe Phe Gly Pro Leu Met Phe
      245      250      255
Phe Tyr Thr Trp Pro Ser Pro Thr Ser His Leu Asp Lys Tyr Leu Ala
      260      265      270
Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
      275      280      285
Phe Arg Asn Lys Asp Met Lys Val Ala Met Arg Arg Leu Cys Ser Arg
      290      295      300
Leu Ala His Phe Thr Lys Ile Leu
305      310

```

<210> 1590

<211> 327

<212> PRT

<213> Unknown (H38g507 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1590

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
 1      5      10      15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
      20      25      30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
      35      40      45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
      50      55      60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
65      70      75      80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile
      85      90      95
Thr Gln Ile Phe Ile Gly His Leu Phe Gly Gly Ala Glu Ile Leu Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Gly Tyr Val Thr Ile Cys Lys Pro Leu
      115      120      125
His Tyr Leu Thr Ile Met Asn Gln Arg Val Cys Ile Leu Leu Leu Leu
      130      135      140
Leu Ala Trp Ala Gly Gly Phe Leu His Ala Val Val Gln Leu Leu Phe
145      150      155      160

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Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
      165                      170                      175
Cys Asp Met Tyr Pr  Leu Leu Lys Leu Ala Cys Thr Asp Thr Tyr Val
      180                      185                      190
Thr Gly Leu Thr Val Val Ala Asn Asp Gly Ala Ile Cys Val Val Ile
      195                      200                      205
Phe Met Leu Leu Leu Phe Ser Tyr Gly Val Ile Leu His Ser Leu Lys
      210                      215                      220
Asn Leu Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Gly Ser
      225                      230                      235                      240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245                      250                      255
Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr Val Phe
      260                      265                      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275                      280                      285
Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg Lys Arg
      290                      295                      300
Lys Xaa Gly Gly Asp Lys Cys Ile Ile Tyr Phe Gln Xaa Arg Val Ala
      305                      310                      315                      320
Pro Ser Arg Lys Ala Ile Cys
      325

```

<210> 1591

<211> 306

<212> PRT

<213> Unknown (H38g508 protein)

<220>

<223> Synthetic construct

<400> 1591

```

Met Asn Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly
  1          5          10          15
Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser
      20          25          30
Leu Ile Tyr Gly Ala Thr Val Val Gly Asn Ile Leu Ile Met Val Thr
      35          40          45
Val Thr Cys Ser Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly
      50          55          60
Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys
      65          70          75          80
Met Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr Gln Lys Phe
      85          90          95
Phe Met His Phe Phe Gly Ser Ala Glu Met Thr Leu Leu Ile Ile Met
      100         105         110
Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His Tyr Arg Thr
      115         120         125
Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu Ser Trp Ile
      130         135         140
Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr Met Asn Leu
      145         150         155         160
Pro Phe Cys Gly His Asn Val Ile Asn Asn Ile Phe Cys Asp Leu Pro
      165         170         175
Leu Val Ile Lys Leu Ala Cys Ile Glu Thr Tyr Thr Leu Glu Leu Phe
      180         185         190
Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr Cys Phe Ile Leu Leu
      195         200         205
Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val Pro Lys Lys Ser Ser
      210         215         220
His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ile Ile Val

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225 230 235 240
 Val Thr Leu Phe Phe Gly Pro Cys Ile Phe Ile Tyr Val Trp Pro Phe
 245 250 255
 Ser Ser Leu Ala Ser Asn Lys Thr Leu Ala Val Phe Tyr Thr Val Ile
 260 265 270
 Thr Pro Leu Leu Asn Pro Ser Ile Tyr Thr Leu Arg Asn Lys Lys Met
 275 280 285
 Gln Glu Ala Ile Arg Lys Leu Arg Phe Gln Tyr Val Ser Ser Ala Gln
 290 295 300
 Asn Phe
 305

<210> 1592

<211> 336

<212> PRT

<213> Unknown (H38g509 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1592

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Gly Thr Ser Glu Asp Pro Glu Xaa Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Ile Phe Phe
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Phe Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Leu Ser Leu Leu Asp Val
 145 150 155 160
 Gln Leu Arg Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 165 170 175
 Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
 180 185 190
 Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Leu Tyr Phe Pro Ala Ala
 195 200 205
 Ile Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Tyr Tyr Lys
 210 215 220
 Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Val Ser His Leu Ser Val Val Cys Xaa Phe Tyr
 245 250 255
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro
 260 265 270
 Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met
 275 280 285

Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
 290 295 300
 Leu Arg Arg Pro His Ser Ser Thr Val Xaa Ser Xaa Tyr L u Leu Ile
 305 310 315 320
 Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1593

<211> 319

<212> PRT

<213> Unknown (H38g510 protein)

<220>

<223> Synthetic construct

<400> 1593

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1 5 10 15
 Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
 20 25 30
 Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
 35 40 45
 Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
 65 70 75 80
 Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
 85 90 95
 Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
 100 105 110
 Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
 130 135 140
 Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
 145 150 155 160
 Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
 165 170 175
 His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
 195 200 205
 Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
 210 215 220
 Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
 245 250 255
 Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
 260 265 270
 Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
 290 295 300
 Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
 305 310 315

<210> 1594

<211> 304

<212> PRT

<213> Unknown (H38g511 protein)

<220>

<223> Synthetic construct

<400> 1594

```

Met Glu Arg Ala Asn His Ser Val Val Ser Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Lys Ser Gln Asn Leu Gln Ile Leu Phe Phe Leu Gly Phe Ser
          20           25           30
Val Val Phe Val Gly Ile Val Leu Gly Asn Leu Leu Ile Leu Val Thr
          35           40           45
Val Thr Phe Asp Ser Leu Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Asn Leu Ser Cys Ile Asp Met Ile Leu Ala Ser Phe Ala Thr Pro Lys
65           70           75           80
Met Ile Val Asp Phe Leu Arg Glu Arg Lys Thr Ile Ser Trp Trp Gly
          85           90           95
Cys Tyr Ser Gln Met Phe Phe Met His Leu Leu Gly Gly Ser Glu Met
          100          105          110
Met Leu Leu Val Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu His Tyr Met Thr Ile Met Ser Pro Arg Val Leu Thr Gly Leu
          130          135          140
Leu Leu Ser Ser Tyr Ala Val Gly Phe Val His Ser Ser Ser Gln Met
145           150           155           160
Ala Phe Met Leu Thr Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Lys Asp Thr
          180          185          190
Tyr Ile Leu Gln Leu Leu Val Ile Ala Asp Ser Gly Leu Leu Ser Leu
          195          200          205
Val Cys Phe Leu Leu Leu Leu Val Ser Tyr Gly Val Ile Ile Phe Ser
          210          215          220
Val Arg Tyr Arg Ala Ala Ser Arg Ser Ser Lys Ala Phe Ser Thr Leu
225           230           235           240
Ser Ala His Ile Thr Val Val Thr Leu Phe Phe Ala Pro Cys Val Phe
          245          250          255
Ile Tyr Val Trp Pro Phe Ser Arg Tyr Ser Val Asp Lys Ile Leu Ser
          260          265          270
Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr Thr
          275          280          285
Leu Arg Asn Gln Glu Val Lys Ala Ala Ile Lys Lys Arg Leu Cys Ile
          290          295          300

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<210> 1595

<211> 321

<212> PRT

<213> Unknown (H38g512 protein)

<220>

<223> Synthetic construct

<400> 1595

```

Met Val Asn Leu Thr Ser Met Ser Gly Phe Leu Leu Met Gly Phe Ser
 1           5           10           15
Asp Glu Arg Lys Leu Gln Ile Leu His Ala Leu Val Phe Leu Val Thr
          20           25           30
Tyr Leu Leu Ala Leu Thr Gly Asn Leu Leu Ile Ile Thr Ile Ile Thr
          35           40           45
Val Asp Arg Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys His Leu
          50           55           60

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Ser Leu Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln Ser Ile
65          70          75          80
Ala Asn Ser Leu Met Gly Asn Gly Tyr Ile Ser Leu Val Gln Cys Ile
          85          90          95
Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val Ala Ile
          100          105          110
Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
          115          120          125
His Tyr Glu Thr Ile Met Asp Pro Arg Ala Cys Arg His Ala Val Ile
          130          135          140
Ala Val Trp Ile Ala Gly Gly Leu Ser Gly Leu Met His Ala Ala Ile
145          150          155          160
Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Val Ile His Gln Phe Phe
          165          170          175
Cys Asp Val Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu Phe Ile
          180          185          190
Asn Glu Ile Ala Leu Ala Ala Phe Thr Thr Ser Ala Ala Phe Ile Cys
          195          200          205
Leu Ile Ser Ile Val Leu Ser Tyr Ile Arg Ile Phe Ser Thr Val Leu
210          215          220
Arg Ile Pro Ser Ala Glu Gly Arg Thr Lys Val Phe Ser Thr Cys Leu
225          230          235          240
Pro His Leu Phe Val Ala Thr Phe Phe Leu Ser Ala Ala Gly Phe Glu
          245          250          255
Phe Leu Arg Leu Pro Ser Asp Ser Ser Ser Thr Val Asp Leu Val Phe
          260          265          270
Ser Val Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Val Ile Tyr
          275          280          285
Ser Leu Arg Asn Asp Ser Met Lys Ala Ala Leu Arg Lys Met Leu Ser
          290          295          300
Lys Glu Glu Leu Pro Gln Arg Lys Met Cys Leu Lys Ala Met Phe Lys
305          310          315          320
Leu

```

<210> 1596

<211> 310

<212> PRT

<213> Unknown (H38g513 protein)

<220>

<223> Synthetic construct

<400> 1596

```

Met Asp Pro Gln Asn Tyr Ser Leu Val Ser Glu Phe Val Leu His Gly
1          5          10          15
Leu Cys Thr Ser Arg His Leu Gln Asn Phe Phe Phe Ile Phe Phe Phe
          20          25          30
Gly Val Tyr Val Ala Ile Met Leu Gly Asn Leu Leu Ile Leu Val Thr
          35          40          45
Val Ile Ser Asp Pro Cys Leu His Ser Ser Pro Met Tyr Phe Leu Leu
          50          55          60
Gly Asn Leu Ala Phe Leu Asp Met Trp Leu Ala Ser Phe Ala Thr Pro
65          70          75          80
Lys Met Ile Arg Asp Phe Leu Ser Asp Gln Lys Leu Ile Ser Phe Gly
          85          90          95
Gly Cys Met Ala Gln Ile Phe Phe Leu His Phe Thr Gly Gly Ala Glu
          100          105          110
Met Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Lys Pro Leu His Tyr Met Thr Leu Met Ser Trp Gln Thr Cys Ile Arg

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      130              135              140
Leu Val Leu Ala Ser Trp Val Val Gly Phe Val His Ser Ile Ser Gln
145              150              155              160
Val Ala Phe Thr Val Asn Leu Pro Tyr Cys Gly Pro Asn Glu Val Asp
      165              170              175
Ser Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Met Asp
      180              185              190
Thr Tyr Val Leu Gly Ile Ile Met Ile Ser Asp Ser Gly Leu Leu Ser
      195              200              205
Leu Ser Cys Phe Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Leu
      210              215              220
Ala Ile Arg Gln Arg Ala Ala Gly Ser Thr Ser Lys Ala Leu Ser Thr
      225              230              235              240
Cys Ser Ala His Ile Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile
      245              250              255
Phe Val Tyr Val Arg Pro Phe Ser Arg Phe Ser Val Asp Lys Leu Leu
      260              265              270
Ser Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr
      275              280              285
Thr Leu Arg Asn Glu Glu Met Lys Ala Ala Met Lys Lys Leu Gln Asn
      290              295              300
Arg Arg Val Thr Phe Gln
305              310

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<210> 1597

<211> 319

<212> PRT

<213> Unknown (H38g514 protein)

<220>

<223> Synthetic construct

<400> 1597

```

Met Glu Arg Lys Asn Gln Thr Ala Ile Thr Glu Phe Ile Ile Leu Gly
 1              5              10              15
Phe Ser Asn Leu Asn Glu Leu Gln Phe Leu Leu Phe Thr Ile Phe Phe
      20              25              30
Leu Thr Tyr Phe Cys Thr Leu Gly Gly Asn Ile Leu Ile Ile Leu Thr
      35              40              45
Thr Val Thr Asp Pro His Leu His Thr Pro Met Tyr Tyr Phe Leu Gly
      50              55              60
Asn Leu Ala Phe Ile Asp Ile Cys Tyr Thr Thr Ser Asn Val Pro Gln
      65              70              75              80
Met Met Val His Leu Leu Ser Lys Lys Lys Ser Ile Ser Tyr Val Gly
      85              90              95
Cys Val Val Gln Leu Phe Ala Phe Val Phe Phe Val Gly Ser Glu Cys
      100              105              110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
      115              120              125
Pro Leu Arg Tyr Ser Val Ile Leu Ser Lys Val Leu Cys Asn Gln Leu
      130              135              140
Ala Ala Ser Cys Trp Ala Ala Gly Phe Leu Asn Ser Val Val His Thr
      145              150              155              160
Val Leu Thr Phe Cys Leu Pro Phe Cys Gly Asn Asn Gln Ile Asn Tyr
      165              170              175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ile Leu Ser Cys Gly Asn Thr
      180              185              190
Ser Val Asn Glu Leu Ala Leu Leu Ser Thr Gly Val Phe Ile Gly Trp
      195              200              205
Thr Pro Phe Leu Cys Ile Val Leu Ser Tyr Ile Cys Ile Ile Ser Thr
      210              215              220

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Ile Leu Arg Ile Gln Ser Ser Glu Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ala Ile Val Ph Leu Phe Tyr Gly Ser Ala Ile
 245 250 255
 Phe Thr Tyr Val Arg Pro Ile Ser Thr Tyr Ser Leu Lys Lys Asp Arg
 260 265 270
 Leu Val Ser Val Leu Tyr Ser Val Val Thr Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Val Lys Thr Ile
 290 295 300
 Gly Ser Lys Trp Gln Pro Pro Ile Ser Ser Leu Asp Ser Lys Leu
 305 310 315

<210> 1598

<211> 303

<212> PRT

<213> Unknown (H38g515 protein)

<220>

<223> Synthetic construct

<400> 1598

Met Arg Glu Phe Phe Leu Ser Gly Phe Ser Gln Thr Pro Ser Ile Glu
 1 5 10 15
 Ala Gly Leu Phe Val Leu Phe Leu Phe Phe Tyr Met Ser Ile Trp Val
 20 25 30
 Gly Asn Val Leu Ile Met Val Thr Val Ala Ser Asp Lys Tyr Leu Asn
 35 40 45
 Ser Ser Pro Met Tyr Phe Leu Leu Gly Asn Leu Ser Phe Leu Asp Leu
 50 55 60
 Cys Tyr Ser Thr Val Thr Thr Pro Lys Leu Leu Ala Asp Phe Phe Asn
 65 70 75 80
 His Glu Lys Leu Ile Ser Tyr Asp Gln Cys Ile Val Gln Leu Phe Phe
 85 90 95
 Leu His Phe Val Gly Ala Ala Glu Met Phe Leu Leu Thr Val Met Ala
 100 105 110
 Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Thr Thr Val
 115 120 125
 Met Ser Arg Gly Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly
 130 135 140
 Gly Phe Val His Ser Thr Val Gln Thr Ile Leu Thr Val His Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Gln Val Glu Asn Phe Phe Cys Asp Val Pro Pro
 165 170 175
 Val Ile Lys Leu Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met
 180 185 190
 Val Ser Asn Ser Gly Leu Ile Ser Thr Ile Ser Phe Val Val Leu Ile
 195 200 205
 Ser Ser Tyr Thr Thr Ile Leu Val Lys Ile Arg Ser Lys Glu Gly Arg
 210 215 220
 Arg Lys Ala Leu Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu
 225 230 235 240
 Phe Phe Gly Pro Cys Ile Phe Ile Tyr Ala Arg Pro Phe Ser Thr Phe
 245 250 255
 Ser Val Asp Lys Met Val Ser Val Leu Tyr Asn Val Ile Thr Pro Met
 260 265 270
 Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala
 275 280 285
 Met Gln Lys Leu Trp Val Arg Asn Gly Leu Thr Trp Lys Lys Gln
 290 295 300

<210> 1599
 <211> 315
 <212> PRT
 <213> Unknown (H38g516 protein)

<220>
 <223> Synthetic construct

<400> 1599
 Met Glu Asn Val Thr Thr Met Asn Glu Phe Leu Leu Leu Gly Leu Thr
 1 5 10 15
 Gly Val Gln Glu Leu Gln Pro Phe Phe Gly Ile Phe Leu Ile Ile
 20 25 30
 Tyr Leu Ile Asn Leu Ile Gly Asn Gly Ser Ile Leu Val Met Val Val
 35 40 45
 Leu Glu Pro Gln Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Cys Leu Asp Ile Ser Tyr Ser Ser Val Thr Leu Pro Lys Leu Leu
 65 70 75 80
 Val Asn Leu Val Cys Ser Arg Arg Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Thr Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Ile Leu
 100 105 110
 Leu Ala Ile Met Ala Phe Asp Arg Phe Val Ala Ile Cys Asn Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Val Cys Ile Leu Leu Ala Ala
 130 135 140
 Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met
 145 150 155 160
 Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe
 165 170 175
 Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu
 180 185 190
 Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala
 195 200 205
 Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu
 210 215 220
 Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe
 245 250 255
 Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile
 260 265 270
 Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe
 290 295 300
 Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His
 305 310 315

<210> 1600
 <211> 322
 <212> PRT
 <213> Unknown (H38g517 protein)

<220>
 <223> Synthetic construct

<400> 1600
 Met Asn Glu Thr Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15

Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser
 20 25 30
 Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35 40 45
 Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Phe Ala Thr Pro Lys
 65 70 75 80
 Met Ile Ala Asp Phe Leu Val Glu Arg Lys Thr Ile Ser Phe Asp Ala
 85 90 95
 Cys Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100 105 110
 Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Met Thr Val Met Ser Arg Arg Val Cys Val Val Leu
 130 135 140
 Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145 150 155 160
 Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr
 180 185 190
 Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
 195 200 205
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
 210 215 220
 Val Arg Asn Arg Ser Ser Ala Ser Met Ala Lys Ala Arg Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Leu Ile Leu Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
 290 295 300
 Tyr Leu Lys Pro Ser Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
 305 310 315 320
 Leu Glu

<210> 1601

<211> 197

<212> PRT

<213> Unknown (H38g518 protein)

<220>

<223> Synthetic construct

<400> 1601

Glu Arg Leu Leu Leu Pro Met Tyr Cys Phe Leu Thr Ile Leu Ser Ala
 1 5 10 15
 Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr Met Leu Ser Ile
 20 25 30
 Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala Cys Leu Ser His
 35 40 45
 Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser Ser Val Leu Leu
 50 55 60
 Ala Met Ala Phe Asp Arg Phe Val Ala Val Ser Asn Pro Leu Arg Tyr
 65 70 75 80
 Ala Met Ile Leu Thr Asp Ser Arg Ile Ala Gln Ile Gly Val Ala Ser

<400> 1602																
Met	Ser	Pro	Glu	Asn	Gln	Ser	Ser	Val	Ser	Glu	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Leu	Pro	Ile	Arg	Pro	Glu	Gln	Gln	Ala	Val	Phe	Phe	Thr	Leu	Phe	Leu	
			20					25					30			
Gly	Met	Tyr	Leu	Thr	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Met	Leu	Leu	
		35					40					45				
Ile	Gln	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
		50				55					60					
His	Leu	Ala	Leu	Thr	Asp	Ile	Ser	Phe	Ser	Ser	Val	Thr	Val	Pro	Lys	
65					70						75				80	
Met	Leu	Met	Asp	Met	Arg	Thr	Lys	Tyr	Lys	Ser	Ile	Leu	Tyr	Glu	Glu	
				85					90					95		
Cys	Ile	Ser	Gln	Met	Tyr	Phe	Phe	Ile	Phe	Phe	Thr	Asp	Leu	Asp	Ser	
			100					105					110			
Phe	Leu	Ile	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	
			115				120					125				
Pro	Leu	His	Tyr	Thr	Val	Ile	Met	Arg	Glu	Glu	Leu	Cys	Val	Phe	Leu	
						135					140					
Val	Ala	Val	Ser	Trp	Ile	Leu	Ser	Cys	Ala	Ser	Ser	Leu	Ser	His	Thr	
145					150						155				160	
Leu	Leu	Leu	Thr	Arg	Leu	Ser	Phe	Cys	Ala	Ala	Asn	Thr	Ile	Pro	His	
				165					170					175		
Val	Phe	Cys	Asp	Leu	Ala	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Ile	
			180					185					190			
Phe	Leu	Asn	Glu	Leu	Val	Met	Phe	Thr	Val	Gly	Val	Val	Val	Ile	Thr	
		195					200					205				
Leu	Pro	Phe	Met	Cys	Ile	Leu	Val	Ser	Tyr	Gly	Tyr	Ile	Gly	Ala	Thr	
		210				215					220					
Ile	Leu	Arg	Val	Pro	Ser	Thr	Lys	Gly	Ile	His	Lys	Ala	Leu	Ser	Thr	
225					230						235				240	
Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Tyr	Tyr	Gly	Ser	Ile	Phe	
				245					250					255		
Gly	Gln	Tyr	Leu	Phe	Pro	Thr	Val	Ser	Ser	Ser	Ile	Asp	Lys	Asp	Val	
			260					265					270			
Ile	Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	
		275					280					285				

Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu
 290 295 300
 Phe Ser Arg Ala Thr Phe Phe Ser Trp
 305 310

<210> 1603
 <211> 196
 <212> PRT
 <213> Unknown (H38g520 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(196)
 <223> Xaa = Any Amino Acid

<400> 1603
 Arg Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Leu
 1 5 10 15
 Asp Leu Cys Leu Pro Ser Ile Pro Val Pro Lys Met Leu Gln Asn Leu
 20 25 30
 Leu Thr Gln Arg Xaa Thr Ile Ser Met Trp Tyr Cys Ile Val Gln Ser
 35 40 45
 Phe Phe Leu Ile Phe Ser Gly Ser Thr Glu Ala Cys Leu Leu Leu Ala
 50 55 60
 Met Ala Cys Asp His Ser Thr Ser Asn Cys His Pro Arg Leu Asn Asp
 65 70 75 80
 Val Val Met Asn Gln Pro Val Cys Val Arg Met Val Ile Ala Ala Trp
 85 90 95
 Ala Val Gly Phe Leu Asn Ser Leu Thr Lys Asn Leu Phe Ile Tyr Asn
 100 105 110
 Leu His Phe Cys Gly Pro Ser Val Ile Pro His Phe Cys Cys Glu Leu
 115 120 125
 Pro Ser Leu Phe Pro Leu Ser Cys Ile Asp Pro Ala Ala Ser Glu Val
 130 135 140
 Leu Pro Ala Gly Ser Cys Thr Leu Leu Gly Phe Val Thr Cys Arg Cys
 145 150 155 160
 Val Leu Phe Ser Tyr Ser Asn Thr Ile Ser Ala Val Leu Ala Ile Trp
 165 170 175
 Phe Ser Glu Gly Gln Gly Lys Ala Phe Ser Thr Cys Ser Ser His Leu
 180 185 190
 Thr Val Val Leu
 195

<210> 1604
 <211> 306
 <212> PRT
 <213> Unknown (H38g521 protein)

<220>
 <223> Synthetic construct

<400> 1604
 Met Ser Pro Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Arg Pro Glu Gln Gln Ala Val Phe Phe Ala Leu Phe Leu
 20 25 30
 Gly Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu
 35 40 45
 Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser

50 55 60
 His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys
 65 70 75 80
 Met Leu Met Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly
 85 90 95
 Cys Ile Ser Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser
 100 105 110
 Phe Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu
 130 135 140
 Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu His Thr
 145 150 155 160
 Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His
 165 170 175
 Tyr Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180 185 190
 Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met
 195 200 205
 Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr
 210 215 220
 Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile
 245 250 255
 Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile
 260 265 270
 Ile Ala Ser Val Ile Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu
 290 295 300
 Leu Ser
 305

<210> 1605

<211> 197

<212> PRT

<213> Unknown (H38g522 protein)

<220>

<223> Synthetic construct

<400> 1605

Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Met Asp
 1 5 10 15
 Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Ile Leu Asp Asn Phe Leu
 20 25 30
 Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr
 35 40 45
 Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu Leu Leu Ala Val Met
 50 55 60
 Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu
 65 70 75 80
 Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly
 85 90 95
 Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu
 100 105 110
 Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val
 115 120 125
 Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn Ala Leu Ala Leu Met
 130 135 140

Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu L u Leu Ile Cys L u
 145 150 155 160
 Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala
 165 170 175
 Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val
 180 185 190
 Val Val Phe Tyr Gly
 195

<210> 1606

<211> 328

<212> PRT

<213> Unknown (H38g523 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1606

Val Asn Gly Trp Ser Asn Lys Ser Val Val Thr Glu Phe Asn Leu Leu
 1 5 10 15
 Gly Leu Ser Ser Ser Trp Glu Leu Gln Val Phe Phe Phe Phe Ile Phe
 20 25 30
 Ser Val Phe Tyr Gly Ala Ala Val Leu Gly Asn Ile Leu Ile Ile Ile
 35 40 45
 Thr Val Ile Ile Asp Ser His Leu His Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Ser Asn Leu Ser Ser Ile Asp Val Cys Gln Ala Thr Phe Ala Thr Pro
 65 70 75 80
 Lys Met Ile Ala Asp Phe Leu Asn Glu His Lys Thr Thr Thr Phe Gln
 85 90 95
 Gly Cys Met Ser Gln Ile Phe Phe Leu His Val Phe Gly Gly Ser Glu
 100 105 110
 Met Val Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Met Thr Ile Met Asn Arg Arg Val Xaa Thr Val
 130 135 140
 Leu Val Gly Val Ser Trp Ala Ile Gly Ile Ser His Ser Ala Thr His
 145 150 155 160
 Leu Ala Phe Lys Val Asn Leu Pro Phe Cys Gly Pro Asn Arg Val Asp
 165 170 175
 Asn Phe Phe Cys Asp Leu Leu Leu Val Ile Lys Leu Ala Cys Leu Asp
 180 185 190
 Thr Tyr Gly Phe Glu Ile Leu Val Leu Thr Asn Ser Gly Leu Leu Ser
 195 200 205
 Leu Met Cys Phe Leu Leu Leu Leu Ile Ser Asp Thr Ile Ile Leu Ala
 210 215 220
 Thr Val His Arg Gln Ala Ser Asp Gly Met Ser Lys Ala Leu Ser Thr
 225 230 235 240
 Leu Ser Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Leu Ile
 245 250 255
 Phe Ile Tyr Ile Trp Pro Phe Glu Ser Phe Pro Ile Asp Lys Phe Ile
 260 265 270
 Ser Val Phe Phe Thr Val Phe Thr Pro Leu Leu Asn Pro Met Ile Tyr
 275 280 285
 Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Met Arg Lys Leu Arg Arg
 290 295 300
 Xaa His Val Gly Ser Lys Gln Gly Phe Xaa Thr Thr Thr Lys Lys Xaa

320

```
<221> VARIANT
<222> (1)...(260)
<223> Xaa = Any Amino Acid
```

<400> 1608


```

Tyr Tyr Tyr Tyr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Phe Leu
 1      5      10      15
Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln Leu Leu Ala Asn Leu
      20      25      30
Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln Phe
      35      40      45
Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala Thr
      50      55      60
Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr Thr
      65      70      75      80
Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp
      85      90      95
Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met Leu
      100      105      110
Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu Met
      115      120      125
Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met
      130      135      140
Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu
      145      150      155      160
Ile Leu Val Ser Tyr Gly His Ile Ala Glu Ala Gly Leu Lys Asn Lys
      165      170      175
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Phe His Val
      180      185      190

```

<210> 1609

<211> 310

<212> PRT

<213> Unknown (H38g526 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1609

```

Met Asp Ile Arg Asn Ser Ser Ile Ile Thr Glu Phe Val Leu Leu Glu
 1      5      10      15
Phe Ile Ser Thr Trp Glu Leu Glu Ile Leu Phe Leu Ile Ile Phe Leu
      20      25      30
Leu Ala Tyr Ala Ala Ile Met Ala Gly Asn Leu Thr Ala Ile Ala Val
      35      40      45
Thr Ser Asn Pro Pro Leu Cys Ser Thr Pro Met Tyr Phe Leu Leu Gly
      50      55      60
Asn Leu Ser Phe Leu Ser Met Phe Ile Ser Thr Val Thr Ile Ser Lys
      65      70      75      80
Met Val Leu Asp Val Leu Arg Glu Asn Lys Thr Thr Ser Ser Trp Gly
      85      90      95
Cys Met Ala Gln Met Leu His Phe Leu Gly Gly Ser Glu Met Thr Leu
      100      105      110
Leu Ile Phe Met Ala Val Asp Gln His Ile Ala Ile Cys Arg Pro Leu
      115      120      125
His Cys Arg Thr Ile Thr Asn Cys Arg Val Leu Met Ala Thr His Gly
      130      135      140
Leu Cys Val Leu Ser Arg Ala Val Gly Phe Val His Thr Ile Ser Gln
      145      150      155      160
Ile Val Phe Ile Ile Thr Leu Pro Phe Cys Gly Pro Ser Val Val Asp
      165      170      175
Asn Leu Phe Xaa Asp Leu Pro Leu Val Leu Lys Leu Ala Cys Thr Glu

```

<220>
<223> Synthetic construct

<400> 1611

```

Met Glu Ala Met Lys Leu Leu Asn Gln Ser Gln Val Ser Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Thr Ser Ser Gln Asp Val Glu Phe Leu Leu Phe Ala
           20           25           30
Leu Phe Ser Val Ile Tyr Val Val Thr Val Leu Gly Asn Leu Leu Ile
           35           40           45
Ile Val Thr Val Phe Asn Thr Pro Asn Leu Asn Thr Pro Met Tyr Phe
           50           55           60
Leu Leu Gly Asn Leu Ser Phe Val Asp Met Thr Leu Ala Ser Phe Ala
65           70           75           80
Thr Pro Lys Val Ile Leu Asn Leu Leu Lys Lys Gln Lys Val Ile Ser
           85           90           95
Phe Ala Gly Cys Phe Thr Gln Ile Phe Leu Leu His Leu Leu Gly Gly
           100          105          110
Val Glu Met Val Leu Leu Val Ser Met Ala Phe Asp Arg Tyr Val Ala
           115          120          125
Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Asn Lys Lys Val Cys
130          135          140
Val Leu Leu Val Val Thr Ser Trp Leu Leu Gly Leu Leu His Ser Gly
145          150          155          160
Phe Gln Ile Pro Phe Ala Val Asn Leu Pro Phe Cys Gly Pro Asn Val
           165          170          175
Val Asp Ser Ile Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys
           180          185          190
Ile Asp Ile Tyr Phe Val Gln Val Val Ile Val Ala Asn Ser Gly Ile
           195          200          205
Ile Ser Leu Ser Cys Phe Ile Ile Leu Leu Ile Ser Tyr Ser Leu Ile
210          215          220
Leu Ile Thr Ile Lys Asn His Ser Pro Thr Gly Gln Ser Lys Ala Arg
225          230          235          240
Ser Thr Leu Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro
           245          250          255
Cys Ile Phe Ile Tyr Ile Trp Pro Phe Gly Asn His Ser Val Asp Lys
           260          265          270
Phe Leu Ala Val Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Ile
           275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Met Lys Ile Ser Met Lys Lys Leu
290          295          300
Trp Arg Ala Phe Val Asn Ser Arg Glu Asp Thr
305          310          315

```

<210> 1612

<211> 317

<212> PRT

<213> Unknown (H38g529 protein)

<220>

<223> Synthetic construct

<400> 1612

```

Met Glu Pro Gln Asn Thr Ser Thr Val Thr Asn Phe Gln Leu Leu Gly
 1           5           10           15
Phe Gln Asn Leu Leu Glu Trp Gln Ala Leu Leu Phe Val Ile Phe Leu
           20           25           30
Leu Ile Tyr Cys Leu Thr Ile Ile Gly Asn Val Val Ile Ile Thr Val
           35           40           45
Val Ser Gln Gly Leu Arg Leu His Ser Pro Met Tyr Met Phe Leu Gln
           50           55           60
His Leu Ser Phe Leu Glu Val Trp Tyr Thr Ser Thr Thr Val Pro Leu

```

```

65          70          75          80
Leu Leu Ala Asn Leu Ser Trp Gly Gln Ala Ile Ser Phe Ser Ala
      85          90          95
Cys Met Ala Gln Leu Tyr Phe Phe Val Phe Leu Gly Ala Thr Glu Cys
      100         105         110
Phe Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Ser
      115         120         125
Pro Leu Arg Tyr Pro Phe Leu Met His Arg Gly Leu Cys Ala Arg Leu
      130         135         140
Val Val Val Ser Trp Cys Thr Gly Val Ser Thr Gly Phe Leu His Ser
145         150         155         160
Met Met Ile Ser Arg Leu Asp Phe Cys Gly Arg Asn Gln Ile Asn His
      165         170         175
Phe Phe Cys Asp Leu Pro Pro Leu Met Gln Leu Ser Cys Ser Arg Val
      180         185         190
Tyr Ile Thr Glu Val Thr Ile Phe Ile Leu Ser Ile Ala Val Leu Cys
      195         200         205
Ile Cys Phe Phe Leu Thr Leu Gly Pro Tyr Val Phe Ile Val Ser Ser
      210         215         220
Ile Leu Arg Ile Pro Ser Thr Ser Gly Arg Arg Lys Thr Phe Ser Thr
225         230         235         240
Cys Gly Ser His Leu Ala Val Val Thr Leu Tyr Tyr Gly Thr Met Ile
      245         250         255
Ser Met Tyr Val Cys Pro Ser Pro His Leu Leu Pro Glu Ile Asn Lys
      260         265         270
Ile Ile Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val
      275         280         285
Ile Tyr Ser Leu Arg Asn Lys Asp Phe Lys Glu Ala Val Arg Lys Val
      290         295         300
Met Arg Arg Lys Cys Gly Ile Leu Trp Ser Thr Ser Lys
305         310         315

```

<210> 1613

<211> 335

<212> PRT

<213> Unknown (H38g530 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1613

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1          5          10          15
Gly Ser Ser Glu Asp Pro Glu Trp Gln Pro Val Leu Thr Gly Leu Cys
      20         25         30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35         40         45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50         55         60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65         70         75         80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85         90         95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100        105        110
Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Glu Arg Phe Val Ala Ile
      115        120        125

```

Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
 145 150 155 160
 Leu His Asn Leu Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu
 165 170 175
 Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Tyr
 180 185 190
 Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile
 210 215 220
 Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Ile Pro Met Pro
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu
 290 295 300
 Gln Arg Pro His Gly Ser Thr Ile Ser Ser Gln Tyr Leu Leu Ile Cys
 305 310 315 320
 Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1614

<211> 330

<212> PRT

<213> Unknown (H38g531 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1614

His Thr Glu Pro Gln Asn Leu Thr Gly Ile Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Thr Leu
 35 40 45
 Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Ile Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Phe Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu Tyr Tyr Pro Val Ile Ile Asn Pro His Leu Cys Val Phe
 130 135 140
 Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Trp Ile Val Xaa Gln Phe Thr Phe Ser Lys Asn Val Glu Ile Ser

<400> 1615															
Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Asp	Val	Phe	Val	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Arg	Gln	Leu	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70					75					80
Lys	Leu	Ile	Val	Asp	Ile	Gln	Ser	Tyr	Ser	Arg	Val	Ile	Ser	Tyr	Ala
				85						90				95	
Gly	Cys	Leu	Thr	Gln	Thr	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
			100					105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Val	Tyr	Asp	Arg	Phe	Val	Ala	Ile
		115					120					125			
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Val	Met	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln
145					150					155					160
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	Glu
				165						170				175	
Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys
		180						185					190		
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile	
		195					200					205			

```

Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile
  210          215          220
Val Ser Ser Ile L u Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala
  225          230          235          240
Phe Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Thr Lys Ser Val Leu
          290          295          300
Arg Arg Pro His Gly Ser Thr Val Xaa Ser Xaa Tyr Leu Leu Ile Cys
  305          310          315          320
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val Lys
          325          330          335

```

<210> 1616
 <211> 320
 <212> PRT
 <213> Unknown (H38g533 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

```

<400> 1616
His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
          20          25          30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Cys Trp Ala Asp Ile Ser Phe Thr Ser Ala Thr Val Pro
          65          70          75          80
Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Arg Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu
          100          105          110
Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
          115          120          125
Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
          130          135          140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
          145          150          155          160
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
          165          170          175
His Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
          180          185          190
Ser Phe Ile Asn Ser Ile Phe Met Tyr Phe Asp Ser Thr Met Phe Gly
          195          200          205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
          210          215          220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
          225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly

```

<400> 1617																
Ile	Ser	Leu	Leu	Phe	Trp	Val	Leu	Leu	Leu	Val	Ile	Ser	Arg	Val	Leu	
1				5					10					15		
Val	Ala	Met	Ala	Xaa	Gly	Asn	Ser	Thr	Glu	Val	Thr	Glu	Phe	Cys	Leu	
			20					25					30			
Leu	Gly	Phe	Gly	Ala	Xaa	Gln	Glu	Phe	Trp	Cys	Ile	Leu	Phe	Ile	Ile	
		35					40					45				
Phe	Leu	Leu	Ile	Tyr	Val	Thr	Ser	Ile	Met	Gly	Asn	Ser	Gly	Ile	Ile	
	50					55					60					
Leu	Leu	Ile	Asn	Thr	Asp	Ser	Arg	Phe	Gln	Thr	Pro	Met	Tyr	Phe	Phe	
65					70					75					80	
Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Ile	Cys	Tyr	Thr	Ser	Ala	Ile	Thr	
				85					90					95		
Pro	Lys	Met	Leu	Gln	Ser	Phe	Thr	Glu	Glu	Lys	Asn	Leu	Ile	Ser	Phe	
			100					105					110			
Trp	Gly	Cys	Met	Ile	Gln	Leu	Leu	Val	Tyr	Ala	Thr	Phe	Ala	Thr	Ser	
		115					120					125				
Asp	Cys	Tyr	Leu	Leu	Ala	Met	Ile	Ala	Val	Asp	His	Tyr	Val	Ala	Ile	
	130					135				140						
Cys	Lys	Pro	Leu	His	Tyr	Thr	Val	Ile	Thr	Ser	Gln	Thr	Val	Cys	Ile	
145					150					155					160	
His	Leu	Val	Ala	Gly	Ser	Tyr	Ile	Met	Gly	Ser	Ile	Asn	Ala	Ser	Val	
				165					170					175		
His	Thr	Gly	Phe	Ala	Phe	Ser	Leu	Ser	Phe	Cys	Lys	Ser	Asn	Asn	Ile	
			180					185					190			
Asn	His	Phe	Phe	Cys	Asp	Gly	Pro	Pro	Ile	Leu	Ala	Leu	Ser	Cys	Ser	
		195				200						205				
Asn	Ile	Asp	Ile	Asn	Ile	Met	Leu	Leu	Val	Val	Phe	Val	Gly	Phe	Asn	
	210					215					220					
Leu	Met	Phe	Thr	Gly	Leu	Val	Val	Ile	Phe	Ser	Tyr	Ile	Tyr	Ile	Met	
225				230						235					240	
Ala	Thr	Ile	Leu	Lys	Met	Ser	Ser	Ser	Ala	Gly	Arg	Lys	Lys	Ser	Phe	
				245					250					255		
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Thr	Val	Ala	Ile	Phe	Tyr	Gly	Thr	
			260					265					270			
Leu	Ser	Tyr	Met	His	Leu	Gln	Ser	His	Ser	Asn	Asn	Ser	Gln	Glu	Asn	
		275					280					285				
Met	Lys	Val	Ala	Ser	Ile	Phe	Tyr	Gly	Thr	Val	Ile	Pro	Met	Leu	Asn	
	290					295					300					

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys
 305 310 315 320
 L u Ile Gly Lys Lys Phe Phe
 325

<210> 1618

<211> 309

<212> PRT

<213> Unknown (H38g535 protein)

<220>

<223> Synthetic construct

<400> 1618

Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly
 1 5 10 15
 Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu
 20 25 30
 Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu
 35 40 45
 Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65 70 75 80
 Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Met Leu Phe Gln Gly
 85 90 95
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
 100 105 110
 Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu
 130 135 140
 Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr
 145 150 155 160
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
 180 185 190
 Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile
 195 200 205
 Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
 260 265 270
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Val Ile
 290 295 300
 Gly Lys Lys Leu Phe
 305

<210> 1619

<211> 298

<212> PRT

<213> Unknown (H38g536 prot in)

<220>

<223> Synthetic construct

<400> 1619

```

Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly
 1           5           10           15
Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
          20           25           30
Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
        35           40           45
Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
      50           55           60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65           70           75           80
Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
          85           90           95
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
        100           105           110
Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
      115           120           125
Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
    130           135           140
Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
 145           150           155           160
Gly Phe Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Lys Ile Asn His
        165           170           175
Phe Phe Cys Asp Gly Leu Pro Ile Leu Ala Leu Ser Cys Ser Asn Ile
      180           185           190
Asp Ile Asn Ile Ile Leu Asp Val Val Phe Val Gly Phe Asp Leu Met
    195           200           205
Phe Thr Glu Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met Val Thr
  210           215           220
Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225           230           235           240
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
        245           250           255
Tyr Met Tyr Leu Gln Pro Gln Ser Asn Asn Ser Gln Glu Asn Met Lys
      260           265           270
Val Ala Ser Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
    275           280           285
Ile Tyr Ser Leu Arg Asn Lys Glu Gly Lys
 290           295

```

<210> 1620

<211> 148

<212> PRT

<213> Unknown (H38g537 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 1620

```

Thr Tyr Asp Gly Ala Arg Ala Gly Leu Cys Ile Val Ser Tyr Asn Thr
 1           5           10           15
Cys Lys Ser Thr Met Met Ser Ile Lys Ile Gln Leu Lys Tyr Met Xaa
          20           25           30
Xaa Lys Xaa Leu Leu Ile Tyr Ala Gly Val Tyr Leu Asn Val Thr Met
        35           40           45

```

Leu Ile Val Thr Phe Lys Tyr Thr His Ile Phe His His Pro Glu Leu
 50 55 60
 Ala Leu Cys Tyr Val Ser Phe Ser Ala Val Val Phe His Leu Thr Ala
 65 70 75 80
 Val Thr Ile Phe Phe Gly Ala Leu Ser Tyr Met Asp Leu Gln Pro Glu
 85 90 95
 Ser Thr Val Phe Gln Glu Gln Glu Lys Pro Ala Ser Ile Phe Cys Gly
 100 105 110
 Ile Met Thr Leu Val Leu Asn Phe Leu Ile Tyr Cys Leu Xaa Asn Xaa
 115 120 125
 Glu Val Lys Glu Ala Leu Gln Leu Thr Arg Lys Lys Tyr Xaa Tyr Met
 130 135 140
 Xaa Thr Glu Gly
 145

<210> 1621

<211> 296

<212> PRT

<213> Unknown (H38g538 protein)

<220>

<223> Synthetic construct

<400> 1621

Met Leu Val Ser Gln Gln Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu
 1 5 10 15
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala
 20 25 30
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 35 40 45
 Asn Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys
 50 55 60
 Met Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ser Tyr Ser Gly
 65 70 75 80
 Cys Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn
 85 90 95
 Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln
 100 105 110
 Pro Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met
 115 120 125
 Leu Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr
 130 135 140
 Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His
 145 150 155 160
 Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 165 170 175
 His Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr
 180 185 190
 Val Pro Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala
 195 200 205
 Val Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr
 210 215 220
 Cys Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met
 225 230 235 240
 Gly Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser
 245 250 255
 Arg Ala Ala Val Leu Tyr Met Val Ile Pro Thr Leu Asn Pro Phe
 260 265 270
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu
 275 280 285
 Phe Val Ser Gly Lys Thr Phe Phe

290

295

<210> 1622
 <211> 313
 <212> PPT
 <213> Unknown (H38g539 protein)

<220>
 <223> Synthetic construct

<400> 1622

```

Met Lys Arg Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Asp
 1           5           10           15
Leu Pro Ile Trp Pro Glu Gln Gln Ala Val Phe Phe Thr Leu Phe Leu
          20           25           30
Gly Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Leu
          35           40           45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Phe Phe Phe Leu Ser
          50           55           60
His Leu Ala Leu Thr Asp Ile Ser Leu Ser Ser Val Thr Val Pro Lys
          65           70           75           80
Met Leu Leu Ser Met Gln Thr Gln Asp Gln Ser Ile Leu Tyr Ala Gly
          85           90           95
Cys Val Thr Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Asn
          100          105          110
Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Thr Thr Ile Met Lys Glu Gly Leu Cys Asn Leu Leu
          130          135          140
Val Thr Val Ser Trp Ile Leu Ser Cys Thr Asn Ala Leu Ser His Thr
          145          150          155          160
Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His
          165          170          175
Phe Phe Cys Asp Leu Val Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
          180          185          190
Ser Leu Asn Glu Leu Val Ile Phe Thr Val Gly Gln Ala Val Ile Thr
          195          200          205
Leu Pro Leu Ile Cys Ile Leu Ile Ser Tyr Gly His Ile Gly Val Thr
          210          215          220
Ile Leu Lys Ala Pro Ser Thr Lys Gly Ile Phe Lys Ala Leu Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Thr Ile Ile
          245          250          255
Gly Leu Tyr Phe Leu Pro Ser Ser Ser Ala Ser Ser Asp Lys Asp Val
          260          265          270
Ile Ala Ser Val Met Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Leu Glu Arg Leu
          290          295          300
Phe Asn Arg Ala Thr Val Leu Ser Gln
          305          310

```

<210> 1623
 <211> 311
 <212> PRT
 <213> Unknown (H38g540 protein)

<220>
 <223> Synthetic construct

<400> 1623

```

Met Glu Asn Gln Ser Ser Ile Ser Glu Phe Phe Leu Arg Gly Ile Ser
 1          5          10          15
Ala Pro Pro Glu Gln Gln Ser Leu Phe Gly Ile Phe Leu Cys Met
          20          25          30
Tyr Leu Val Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala Ile Gly
          35          40          45
Ser Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu
          50          55          60
Ser Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu
          65          70          75          80
Val Asn Ile Gln Thr Arg His His Thr Ile Ser Tyr Thr Gly Cys Leu
          85          90          95
Thr Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe
          100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          115          120          125
Cys Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala
          130          135          140
Leu Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu
          145          150          155          160
Met Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe
          165          170          175
Cys Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile
          180          185          190
Asn Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro
          195          200          205
Phe Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu
          210          215          220
Arg Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser
          225          230          235          240
Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala
          245          250          255
Tyr Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala
          260          265          270
Ala Ala Met Tyr Thr Ile Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Lys Arg Leu Phe Ser
          290          295          300
His Arg Ser Ile Val Ser Ser
          305          310

```

<210> 1624

<211> 314

<212> PRT

<213> Unknown (H38g541 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1624

```

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Val Gly Pro Ala Leu Ala Ile Leu Leu Cys Gly Leu Phe Ser Val
          20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
          35          40          45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His

```

50	55	60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met		
65	70	75
Leu Ala Asn Leu Met Asn Gln Lys Ser Thr Ile Ser Phe Val Pro Cys		
85	90	95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu		
100	105	110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro		
115	120	125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala		
130	135	140
Ser Thr Cys Trp Ile Ile Ser Phe Leu Met Ala Leu Val His Ile Thr		
145	150	155
His Ile Leu Arg Pro Pro Phe Cys Gly Pro Gln Lys Ile Asn His Phe		
165	170	175
Ile Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala Gly Pro Arg		
180	185	190
Leu Asn Gln Val Val Leu Tyr Ala Gly Ser Ala Phe Ile Val Glu Gly		
195	200	205
Pro Leu Cys Leu Glu Leu Val Ser Asn Leu His Ile Leu Ser Ala Ile		
210	215	220
Leu Arg Ile Gln Asn Gly Glu Gly Arg Arg Pro Thr Tyr Ser Ser Cys		
225	230	235
Ser Ser His Leu Cys Met Val Gly Leu Leu Phe Gly Ser Thr Met Val		
245	250	255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val		
260	265	270
Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile		
275	280	285
Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu		
290	295	300
Trp Lys Gln Arg Ser Lys Xaa Gly Met Pro		
305	310	

<210> 1625

<211> 193

<212> PRT

<213> Unknown (H38g542 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(193)

<223> Xaa = Any Amino Acid

<400> 1625

Leu Lys Val Tyr Xaa Lys Ala Ile Xaa Val Gln Lys Gln Gly Lys Phe
1 5 10 15
Phe Val Ile Ile Phe Cys Xaa Xaa Cys Glu Met Xaa Gly Lys Asn Ile
20 25 30
Gln Leu Xaa Gly Cys Leu Thr Val Leu Leu Glu Thr Ser Phe Ala Leu
35 40 45
Gln Arg Pro Leu Cys Gly Asn Leu Ile Asp Asp Thr Cys Glu Ile Leu
50 55 60
Glu Val Leu Lys Leu Val Cys Ser Ser Ser Leu Leu Met Asp Met Ile
65 70 75 80
Met Met Val Val Asn Ile Leu Leu Leu Pro Ile Pro Met Tyr Leu Phe
85 90 95
Ile Thr Met Cys Ser Val Ile Leu Phe Leu Lys Arg Ser Tyr Gly Asn
100 105 110

Leu Pro Arg Glu Phe Ser Phe Cys Ile Ser Trp Ser Ile Trp Val Phe
 115 120 125
 Val Tyr Cys Leu Ala Ile Ile Phe Arg Ala Leu Tyr Lys Leu Thr Lys
 130 135 140
 Ile Trp Gly Ser Thr Met Asn Glu Ile Val Arg Trp Met Tyr Xaa Tyr
 145 150 155 160
 Xaa Thr Tyr Xaa Tyr Xaa Ile Val Xaa His Lys Leu Ala Leu Lys Tyr
 165 170 175
 Asn His Lys Leu Val Ser Thr Met Leu Gln Ala Leu Leu Ser Phe Leu
 180 185 190
 Lys

<210> 1626

<211> 314

<212> PRT

<213> Unknown (H38g543 protein)

<220>

<223> Synthetic construct

<400> 1626

Met Ala Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
 20 25 30
 Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
 35 40 45
 Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
 50 55 60
 Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
 65 70 75 80
 Met Leu Glu Asn Phe Ser Glu Asn Lys Arg Ile Ser Leu Tyr Glu
 85 90 95
 Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
 130 135 140
 Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
 145 150 155 160
 Gly Leu Val Phe Arg Leu Val Phe Cys Gly Ser Asn His Ile Asn His
 165 170 175
 Phe Tyr Cys Asp Ile Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
 180 185 190
 Tyr Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
 195 200 205
 Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
 210 215 220
 Ile Phe Lys Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Leu Ser Val Ser Leu Phe Tyr Gly Ser Leu Phe
 245 250 255
 Phe Met Tyr Val Arg Pro Asn Leu Leu Glu Glu Gly Asp Lys Asp Ile
 260 265 270
 Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Glu Val Ile Ser Val Leu Arg Lys Ile
 290 295 300
 Leu Met Lys Glu Ile Ile Ser Arg Arg Trp

305

310

<210> 1627

<211> 316

<212> PRT

<213> Unknown (H38g544 protein)

<220>

<223> Synthetic construct

<400> 1627

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1           5           10          15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
          20          25          30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
          35          40          45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
          50          55          60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
65          70          75          80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
          85          90          95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
          100         105         110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115         120         125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Cys Val Cys Ala Arg Met
          130         135         140
Ala Thr Val Ser Trp Val Thr Gly Cys Leu Thr Ala Leu Leu Glu Thr
145         150         155         160
Ser Phe Ala Leu Gln Ile Pro Leu Cys Gly Asn Leu Ile Asp His Phe
          165         170         175
Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Thr Ser Ser Leu
          180         185         190
Leu Met Asn Thr Ile Met Leu Val Val Ser Ile Leu Leu Leu Pro Ile
          195         200         205
Pro Met Leu Leu Val Cys Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile
          210         215         220
Leu Arg Ile Thr Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser Thr Cys
225         230         235         240
Gly Ala His Leu Thr Val Val Ile Leu Tyr Tyr Gly Ala Ala Leu Ser
          245         250         255
Met Tyr Leu Lys Pro Ser Ser Ser Asn Ala Gln Lys Ile Asp Lys Ile
          260         265         270
Ile Ser Leu Leu Tyr Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile
          275         280         285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Met Lys Lys Leu Leu
          290         295         300
Gly Lys Ile Thr Leu His Gln Thr His Glu His Leu
305          310          315

```

<210> 1628

<211> 312

<212> PRT

<213> Unknown (H38g545 protein)

<220>

<223> Synthetic construct

<400> 1628

Met Met Gly Arg Arg Asn Asn Thr Asn Val Ala Asp Phe Ile Leu Met
 1 5 10 15
 Gly Leu Thr L u Ser Glu Glu Ile Gln Met Ala Leu Phe M t Leu Phe
 20 25 30
 Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Il Leu
 35 40 45
 Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
 65 70 75 80
 Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
 85 90 95
 Cys Phe Ala Gln Met Phe Phe Phe Ala Phe Leu Gly Thr Ala Glu Cys
 100 105 110
 Tyr Leu Leu Ser Ser Met Ala His Asp Arg Tyr Ala Ala Ile Cys Ser
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Ser Lys Arg Leu Cys Leu Ala Leu
 130 135 140
 Ile Thr Gly Pro Tyr Val Ile Gly Phe Ile Asp Ser Phe Val Asn Val
 145 150 155 160
 Val Ser Met Ser Arg Leu His Phe Tyr Asp Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
 180 185 190
 Tyr Asn Thr Glu Ile Leu Ile Phe Ile Ile Val Gly Ser Thr Leu Met
 195 200 205
 Val Ser Leu Phe Thr Ile Ser Ala Ser Tyr Val Phe Ile Leu Phe Thr
 210 215 220
 Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Ser Thr Leu Ile
 245 250 255
 Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
 260 265 270
 Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Val Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Val Ile Arg Val
 290 295 300
 Met Gln Arg Arg Gln Asp Ser Arg
 305 310

<210> 1629

<211> 212

<212> PRT

<213> Unknown (H38g546 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1629

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Leu Cys Ile Thr
 1 5 10 15
 Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr
 20 25 30
 Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys
 35 40 45
 Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys

```

      50      55      60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
65      70      75      80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
      85      90      95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Leu Xaa Glu
      100      105      110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
      115      120      125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
      130      135      140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
145      150      155      160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
      165      170      175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
      180      185      190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
      195      200      205
Ala Leu Phe Cys
      210

```

<210> 1630

<211> 228

<212> PRT

<213> Unknown (H38g547 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(228)

<223> Xaa = Any Amino Acid

<400> 1630

```

Cys Met Phe Ser Phe Tyr Phe Asn Phe Tyr His Phe Phe Ser Thr Xaa
1      5      10      15
Lys Val Leu Gln Ser Leu Arg Asn Ala Glu Ile Asn Xaa Leu Val Xaa
      20      25      30
Ser Lys Val Ser Asp Xaa Xaa Asn Leu Leu Xaa Asn Xaa Leu Ala Phe
      35      40      45
Ser Trp Thr Ile Arg Leu Cys Thr Thr Thr Ser Tyr Ser Asn Met Gln
      50      55      60
Phe Ser Phe Gln Cys Cys Met Thr Gln Tyr Pro Ala Leu Gln Ser Thr
65      70      75      80
Phe Phe Phe Leu Gly Arg Ser Gln Val Phe Leu Leu Leu Met Ala
      85      90      95
Tyr Asp Asn Tyr Arg Ala Ile Xaa Lys Ser Leu Gln Tyr Leu Val Val
      100      105      110
Met Lys Gln Trp Leu Cys Val Val Leu Leu Val Val Pro Trp Ala Gly
      115      120      125
Gly Phe Leu His Thr Val Ile Gln Leu Gly Leu Ile His Gly Leu Pro
      130      135      140
Ser Tyr Asp Pro Asn Val Ile Gly Arg Phe Val Cys Asp Met Asp Pro
145      150      155      160
Leu Met Lys Leu Val Cys Asp Tyr Thr Leu Asn Arg Phe Val Tyr Phe
      165      170      175
Ala Gly His Asp Leu Asn Tyr Xaa Val Leu Tyr Ile Ser Phe Ile Phe
      180      185      190
Arg Leu Asp Cys Phe Leu Leu Val Ile Xaa Leu Trp Tyr Pro Phe Val
      195      200      205

```

Ile Phe Ser Leu Glu Arg His Asp Ser Ile Asn Leu Val Ile His Ser
 210 215 220
 Tyr Tyr Pro Cys
 225

<210> 1631
 <211> 299
 <212> PRT
 <213> Unknown (H38g548 protein)

<220>
 <223> Synthetic construct

<400> 1631
 Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr
 1 5 10 15
 Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe
 20 25 30
 Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr
 35 40 45
 Val Ser Glu Thr Leu Gly Ser Pro Met Ser Phe Phe Leu Ala Gly Leu
 50 55 60
 Thr Phe Ile Asp Ile Ile Tyr Ser Ser Ser Ile Ser Pro Arg Leu Ile
 65 70 75 80
 Ser Asp Leu Phe Phe Gly Asn Asn Ser Ile Ser Phe Gln Ser Phe Met
 85 90 95
 Ala Gln Leu Phe Ile Glu His Leu Phe Gly Gly Ser Glu Val Phe Leu
 100 105 110
 Leu Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val
 130 135 140
 Val Ser Trp Val Gly Gly Phe Leu Gln Ser Val Phe Gln Leu Ser Ile
 145 150 155 160
 Ile Tyr Gly Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr His Val
 180 185 190
 Ile Gly Leu Leu Val Val Ala Asn Gly Gly Leu Ser Cys Thr Ile Ala
 195 200 205
 Phe Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys
 210 215 220
 Lys Leu Ser Gln Lys Gly Arg Gln Lys Ala His Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Cys
 245 250 255
 Ala Arg Pro Ala Arg Thr Phe Ser Ile Asp Lys Ser Val Ser Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ser Glu Met Thr Ser Ala Met Lys Lys Leu
 290 295

<210> 1632
 <211> 315
 <212> PRT
 <213> Unknown (H38g549 protein)

<220>
 <223> Synthetic construct

<400> 1632

```

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu
 1          5          10          15
Ala Gly Leu Pr Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val
 20          25          30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val
 35          40          45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe
 50          55          60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile
 65          70          75          80
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe
 85          90          95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser
100          105          110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile
115          120          125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe
130          135          140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly
145          150          155          160
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val
165          170          175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys
180          185          190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu
195          200          205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile
210          215          220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala
225          230          235          240
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly
245          250          255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp
260          265          270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu
275          280          285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu
290          295          300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val
305          310          315

```

<210> 1633

<211> 260

<212> PRT

<213> Unknown (H38g550 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 1633

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1          5          10          15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
 20          25          30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
 35          40          45

```

Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Il Pro Leu Met Trp Met
 50 55 60
 Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn
 65 70 75 80
 Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe
 85 90 95
 Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr
 100 105 110
 Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu
 115 120 125
 Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala
 130 135 140
 Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val
 145 150 155 160
 Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu
 165 170 175
 Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile
 180 185 190
 Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu
 195 200 205
 Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro
 210 215 220
 Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser
 225 230 235 240
 Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn
 245 250 255
 Leu Asn Ile Arg
 260

<210> 1634

<211> 318

<212> PRT

<213> Unknown (H38g551 protein)

<220>

<223> Synthetic construct

<400> 1634

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 Leu Ser Gly His Pro Arg Leu Glu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Ser Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Val Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
 130 135 140
 Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
 165 170 175
 Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile

<400> 1635															
Met	Glu	Arg	Thr	Asn	Trp	Thr	Glu	Ile	Glu	Phe	Ile	Leu	Gln	Gly	Leu
1				5					10					15	
Ser	Gly	Tyr	Pro	Arg	Ala	Glu	Lys	Phe	Leu	Phe	Val	Met	Cys	Leu	Val
			20					25					30		
Met	Tyr	Leu	Val	Ile	Leu	Leu	Gly	Asn	Gly	Thr	Leu	Ile	Ile	Leu	Thr
		35					40					45			
Leu	Leu	Asp	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn
	50					55					60				
Leu	Ser	Phe	Leu	Asp	Ile	Trp	Tyr	Thr	Ser	Ser	Ile	Pro	Ser	Met	
65					70					75				80	
Leu	Ile	His	Phe	Leu	Ser	Glu	Lys	Lys	Thr	Ile	Ser	Phe	Thr	Arg	Cys
				85					90					95	
Val	Ile	Gln	Met	Ser	Val	Ser	Tyr	Thr	Met	Gly	Ser	Thr	Glu	Cys	Val
			100						105				110		
Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro
		115					120					125			
Leu	Arg	Tyr	Pro	Ile	Ile	Met	Gly	Lys	Ala	Leu	Cys	Ile	Gln	Met	Val
	130					135					140				
Ala	Val	Ser	Trp	Gly	Leu	Gly	Phe	Leu	Asn	Ser	Leu	Thr	Glu	Thr	Val
145					150					155					160
Leu	Ala	Ile	Arg	Leu	Pro	Phe	Cys	Gly	Lys	Asn	Val	Ile	Asn	His	Phe
				165					170					175	
Val	Cys	Glu	Ile	Leu	Ala	Phe	Val	Lys	Leu	Ala	Cys	Thr	Asp	Thr	Ser
			180					185					190		
Leu	Asn	Glu	Ile	Ile	Ile	Met	Leu	Gly	Asn	Val	Ile	Phe	Leu	Phe	Ser
		195					200					205			
Pro	Leu	Leu	Leu	Ile	Cys	Ile	Ser	Tyr	Ile	Phe	Ile	Leu	Ser	Thr	Val
	210					215					220				
Leu	Arg	Ile	Asn	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys
225					230					235					240

```

Ser Ala His Met Thr Val Val Ile Val Phe Tyr Gly Thr Ile Leu Phe
      245      250      255
Met Tyr Met Lys Ala Lys Ser Lys Asp Ser Ala Phe Asp Lys Leu Ile
      260      265      270
Ala Leu Phe Tyr Gly Ile Val Thr Pr Met Leu Asn Pro Ile Ile Tyr
      275      280      285
Ser Leu Arg Asn Thr Glu Val His Gly Ala Met Arg Lys Leu Met Ser
      290      295      300
Arg His Leu Val Leu Glu Glu Met Met Thr His Xaa His Leu Xaa Val
      305      310      315      320
Tyr Ala Gln Asn Thr Leu Thr Ser Leu Arg Gln His Phe
      325      330

```

<210> 1636

<211> 322

<212> PRT

<213> Unknown (H38g553 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1636

```

His Thr Glu Pro Trp Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Cys Leu Val Met Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Val Tyr Phe
      50      55      60
Phe Leu Ser Lys Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Ile Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Ser Phe Leu Leu Val Ser Phe Phe Leu Ser Met Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asn Ser Thr Met
      195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Cys Lys Ile
      210      215      220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Arg
      245      250      255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Ala Ser Ala Met Phe Ser Val Val Thr Pro Met Leu

```

275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala L u
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Tyr Asp Leu Phe His Pr
 305 310 315 320
 Phe Ser

<210> 1637
 <211> 312
 <212> PRT
 <213> Unknown (H38g554 protein)

<220>
 <223> Synthetic construct

<400> 1637
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
 20 25 30
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
 35 40 45
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
 65 70 75 80
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
 85 90 95
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
 130 135 140
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp
 260 265 270
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His
 290 295 300
 Leu Val Lys Arg Gln Arg Pro Ser
 305 310

<210> 1638
 <211> 310
 <212> PRT

<213> Unknown (H38g555 protein)

<220>

<223> Synthetic construct

<400> 1638

```

Met Ala Gly Asn Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1           5           10          15
Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu
           20           25           30
Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
           35           40           45
Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
           50           55           60
Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys
65           70           75           80
Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly
           85           90           95
Cys Phe Val Gln Met Tyr Phe Phe Val Gly Leu Val Cys Cys Glu Cys
           100          105          110
Phe Leu Leu Gly Ser Met Ala Tyr Asn Arg Tyr Ile Ala Ile Cys Asn
           115          120          125
Pro Leu Leu Tyr Ser Val Val Met Ser Gln Lys Val Ser Asn Trp Leu
           130          135          140
Gly Val Met Pro Tyr Val Ile Gly Phe Thr Ser Ser Leu Ile Ser Val
145          150          155          160
Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His Phe
           165          170          175
Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr Phe
           180          185          190
Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu Ser
           195          200          205
Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ile Ser Ala Ile
           210          215          220
Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
225          230          235          240
Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile Phe
           245          250          255
Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln Val
           260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
           275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile
           290          295          300
His Arg Lys Leu Phe Pro
305          310

```

<210> 1639

<211> 157

<212> PRT

<213> Unknown (H38g556 protein)

<220>

<223> Synthetic construct

<400> 1639

```

Ile Cys Ser Pro Leu Leu Tyr Ser Val Ile Ile Ser Asn Lys Ala Cys
 1           5           10          15
Phe Ser Leu Ile Leu Gly Val Tyr Ile Ile Gly Leu Val Cys Ala Ser
           20           25           30
Val His Thr Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Leu

```

35	40	45
Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Leu Leu Lys Leu Ser Cys		
50	55	60
Ser Ser Ile Tyr Val Asn Lys Leu Leu Ile Leu Cys Val Gly Ala Phe		
65	70	75
Asn Ile Leu Val Pro Ser Leu Thr Ile Leu Cys Ser Tyr Ile Phe Ile		
85	90	95
Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser Lys Ala		
100	105	110
Phe Ser Thr Cys Ser Ser His Met Leu Ala Val Val Ile Phe Phe Gly		
115	120	125
Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Ile Ser Ser Met Asp		
130	135	140
Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Ile Ile Val		
145	150	155

<210> 1640

<211> 178

<212> PRT

<213> Unknown (H38g557'protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(178)

<223> Xaa = Any Amino Acid

<400> 1640

Leu Ala Pro Ser Ser Ser Leu Ala Leu Gly Thr Trp Arg Trp Gln Trp		
1	5	10
His Ser Met Thr Glu Leu Val Leu Leu Val Leu Ser Gly Phe Gly Ser		
20	25	30
Val Arg Gly Leu Leu Phe Trp Ala Val Leu Cys Lys His Leu Val Thr		
35	40	45
Leu Leu Asp Asn Ser Leu Ile Val Val Leu Ala Leu Val Ser Leu Cys		
50	55	60
Leu Arg Trp Pro Thr His Phe Leu Leu His His Phe Ser Leu Gly Glu		
65	70	75
Val Pro Arg His Ser Gly Gly Val Ser Asp Ala Gly Arg Phe Pro Ser		
85	90	95
Pro Ala Ala Leu Ala His Arg Xaa Ala Ala Ser Arg Cys Trp Val Phe		
100	105	110
Phe Ala Leu Pro Gly Ile Ala Glu Cys Cys Leu Arg Arg Ala Met Ala		
115	120	125
Tyr Arg Arg Cys Asp Ala Ile Cys Arg Pro Leu His Ser Thr Thr Xaa		
130	135	140
Gly Ala Leu Val Phe Arg Ala Arg Phe Ala Phe Thr Leu Pro Phe Cys		
145	150	155
Gly Ala Ala Arg Thr Arg Tyr Phe Arg Leu Asp Ser Arg Pro Val Leu		
165	170	175

Arg Pro

<210> 1641

<211> 314

<212> PRT

<213> Unknown (H38g558 protein)

<220>

<223> Synthetic construct

<400> 1641

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Leu Phe Leu Phe Leu
20     25     30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Leu Gly Met Ile Leu Leu
35     40     45
Ile Arg Ile Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50     55     60
Asn Leu Ser Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys
65     70     75     80
Met Leu Ala Asp Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
85     90     95
Cys Phe Leu Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys
100    105    110
Ile Leu Phe Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
115    120    125
Pro Leu Leu Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met
130    135    140
Ala Ala Gly Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr
145    150    155    160
Ser His Val Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His
165    170    175
Phe Phe Cys Asp Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr
180    185    190
Ile Leu Lys Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val
195    200    205
Gly Thr Leu Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser
210    215    220
Ile Phe Ser Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr
225    230    235    240
Cys Ala Ser His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile
245    250    255
Tyr Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys
260    265    270
Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
275    280    285
Ile Tyr Ser Leu Arg Ser Lys Glu Val Lys Lys Ala Leu Ala Asn Val
290    295    300
Ile Ser Arg Lys Arg Thr Ser Ser Phe Leu
305    310

```

<210> 1642

<211> 314

<212> PRT

<213> Unknown (H38g559 protein)

<220>

<223> Synthetic construct

<400> 1642

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Ile Leu Leu Gly
1      5      10      15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Leu Phe Leu
20     25     30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Ile Gly Met Ile Leu Leu
35     40     45
Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Val
50     55     60
Asn Leu Ser Phe Val Asp Ile Cys Tyr Ser Thr Thr Ile Thr Pro Lys

```

65		70		75		80									
Met	Leu	Ala	Asp	Leu	Leu	Ser	Glu	Lys	Lys	Thr	Ile	Ser	Phe	Ala	Gly
		85						90						95	
Cys	Phe	Leu	Gln	Met	Tyr	Phe	Phe	Ile	Ala	Leu	Ala	Thr	Thr	Glu	Cys
		100						105						110	
Ile	Leu	Phe	Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Thr	Ile	Cys	Arg
		115						120						125	
Pro	Leu	Leu	Tyr	Ser	Leu	Ile	Met	Ser	Arg	Thr	Val	Cys	Leu	Lys	Met
		130						135						140	
Ala	Ala	Gly	Ala	Phe	Ala	Ala	Gly	Leu	Leu	Asn	Ser	Met	Val	Asn	Thr
		145						150						155	
Ser	Tyr	Val	Ser	Ser	Leu	Ser	Phe	Cys	Gly	Ser	Asn	Val	Ile	His	His
														165	
Phe	Phe	Cys	Asn	Ser	Pro	Pro	Leu	Phe	Lys	Leu	Ser	Cys	Ser	Asp	Thr
														180	
His	Leu	Lys	Glu	Ser	Ile	Phe	Ser	Thr	Phe	Ala	Gly	Val	Asn	Lys	Val
														195	
Gly	Ala	Leu	Leu	Val	Ile	Leu	Ser	Ser	Tyr	Ser	Tyr	Val	Leu	Phe	Ser
														210	
Ile	Phe	Ser	Met	His	Ser	Gly	Glu	Gly	Arg	His	Arg	Ala	Phe	Ser	Thr
														225	
Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Ile	Leu	Phe	Tyr	Thr	Thr	Ser	Ile
														240	
Tyr	Thr	Tyr	Leu	Arg	Pro	Ser	Ser	Ser	Tyr	Ser	Leu	Asn	Gln	Asp	Lys
														255	
Val	Val	Ser	Val	Phe	Tyr	Thr	Val	Val	Ile	Pro	Ile	Leu	Asn	Pro	Leu
														270	
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Lys	Ala	Leu	Ala	Asn	Val
														285	
Ile	Ser	Arg	Lys	Arg	Ile	Pro	Ser	Phe	Leu					300	
														305	

<210> 1643

<211> 314

<212> PRT

<213> Unknown (H38g560 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1643

Met	Ser	Gly	Glu	Asn	Val	Thr	Lys	Val	Ser	Thr	Phe	Ile	Leu	Val	Gly
1				5				10						15	
Leu	Pro	Thr	Ala	Pro	Gly	Leu	Gln	Tyr	Leu	Leu	Phe	Leu	Leu	Phe	Leu
				20				25						30	
Leu	Thr	Tyr	Leu	Phe	Val	Leu	Val	Glu	Asn	Leu	Ala	Ile	Ile	Leu	Ile
				35				40						45	
Val	Trp	Ser	Ser	Thr	Ser	Leu	His	Arg	Pro	Met	Tyr	Tyr	Phe	Leu	Ser
				50				55						60	
Ser	Met	Ser	Phe	Leu	Glu	Ile	Trp	Tyr	Val	Ser	Asp	Ile	Thr	Pro	Lys
				65				70						75	
Met	Leu	Glu	Gly	Phe	Leu	Leu	Gln	Gln	Lys	Arg	Ile	Ser	Phe	Val	Gly
				85				90						95	
Cys	Met	Thr	Gln	Leu	Tyr	Phe	Phe	Ser	Ser	Leu	Val	Cys	Thr	Glu	Cys
				100				105						110	
Val	Leu	Leu	Ser	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
				115				120						125	

```

Pro Leu Arg Tyr His Val Leu Val Thr Ala Gly Leu Cys Val Gln Leu
 130                135                140
Val Gly Phe Ser Phe Val Ser Gly Phe Ser Ile Ser Met Ile Lys Val
145                150                155                160
Cys Phe Ile S r Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His
                165                170                175
Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe
 180                185                190
Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val
 195                200                205
Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala
 210                215                220
Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr
225                230                235                240
Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu
                245                250                255
Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys
 260                265                270
Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu
 275                280                285
Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala
 290                295                300
Leu Gly Leu Gly Gln Thr Ser His Xaa Asp
305                310

```

<210> 1644

<211> 214

<212> PRT

<213> Unknown (H38g561 protein)

<220>

<223> Synthetic construct

<400> 1644

```

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val
 1                5                10                15
His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala
 20                25                30
Arg Leu Leu Phe Leu Leu Ile Gly Gly Cys Thr Gln Cys Ala Leu Leu
 35                40                45
Gly Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 50                55                60
Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala
 65                70                75                80
Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr
 85                90                95
Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys
100                105                110
Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser
115                120                125
Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val
130                135                140
Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys
145                150                155                160
Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser
165                170                175
His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr
180                185                190
Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val Phe
195                200                205
Tyr Pro Ile Val Thr Pro

```

210

<210> 1645

<211> 316

<212> PRT

<213> Unknown (H38g562 protein)

<220>

<223> Synthetic construct

<400> 1645

```

Met Leu Glu Ser Asn Tyr Thr Met Pro Thr Glu Phe Leu Phe Val Gly
 1           5           10           15
Phe Thr Asp Tyr Leu Pro Leu Arg Val Thr Leu Phe Leu Val Phe Leu
          20           25           30
Leu Val Tyr Thr Leu Thr Met Val Gly Asn Ile Leu Leu Ile Ile Leu
          35           40           45
Val Asn Ile Asn Ser Ser Leu Gln Ile Pro Met Tyr Tyr Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr Ala Ile Thr Pro Lys
65           70           75           80
Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser Ile Ser Pro Tyr Gly
          85           90           95
Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe Ala Asp Ala Glu Cys
          100          105          110
Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg Val Cys Val Cys Phe
          130          135          140
Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr Ser Leu Val His Val
145          150          155          160
Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Ile Val Asn His
          165          170          175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Thr Asp Thr
          180          185          190
Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys Ser Phe Ile Gln Thr
          195          200          205
Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe Cys Ile Leu Ile Thr
210          215          220
Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser Lys Thr Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe Tyr Gly Ala Leu Leu
          245          250          255
Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser Leu Asp Thr Asp Lys
          260          265          270
Val Val Ala Val Phe Tyr Thr Val Val Phe Pro Met Phe Asn Pro Ile
          275          280          285
Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Leu
290          295          300
Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp Tyr Leu
305          310          315

```

<210> 1646

<211> 314

<212> PRT

<213> Unknown (H38g563 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1646

```

Met Ser Thr His Arg Met Glu Ile Ser Gln Cys Val Pro Leu Trp Glu
 1           5           10           15
Ser Met Leu Lys Gly Leu Glu Gly Gly Leu Glu Asn Gln Ala Leu Leu
          20           25           30
Phe Ala Val Phe Pro Gly Leu Tyr Met Val Thr Ile Pro Gly Asn Leu
          35           40           45
Thr Met Thr Met Val Ile Ile Leu Asp Thr His Leu His Phe Pro Val
          50           55           60
Asn Phe Phe Leu Gly Ala Ser Pro Phe Leu Asp Leu Gly His Ala Ser
65          70           75           80
Ile Ile Pro Asn Ala Leu Val Asn Phe Ser Ser Ser Ser Lys Val Val
          85           90           95
Thr Phe Ala Gly Cys Ala Ala Arg Phe Phe Phe Ser Leu Leu Ser Thr
          100          105          110
Thr Glu Thr Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Ser Leu Val Trp Cys Pro Val Thr Thr Cys Leu Ser Ile Cys
          130          135          140
Ile Ile Leu Gly Pro Gly Thr Tyr Cys Arg Val Cys Leu Ser Ser Ile
145          150          155          160
Val Gln Thr Gly Leu Met Phe Gln Leu Pro Ser Ala Gly Thr Asn His
          165          170          175
Ile Asp His Tyr Cys Asp Met Pro Gln Leu Leu Arg Leu Ala Cys Ala
          180          185          190
Cys Leu Ala Leu Asn Glu Leu Thr Lys Phe Ser Leu Cys Gly Leu Met
          195          200          205
Met Val Asn Ala Thr Leu Val Val Leu Val Ser Phe Gly Cys Val Thr
          210          215          220
Val Thr Ile Leu Arg Thr Pro Ser Gly Ser Gln Xaa His Lys Val Phe
225          230          235          240
Thr Cys Ser Ser His Val Met Thr Val Ser Leu Phe Asp Gly Thr Val
          245          250          255
Phe Val Thr Tyr Ala Gln Pro Gly Thr Met Glu Ser Met Glu Gln Gly
          260          265          270
Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Gly Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Arg
          290          295          300
Leu Gly Gln Arg Gln Ala Leu Met Gly Arg
305          310

```

<210> 1647

<211> 252

<212> PRT

<213> Unknown (H38g564 protein)

<220>

<223> Synthetic construct

<400> 1647

```

Met Tyr Phe Phe Leu Gly Asn Leu Ser Phe Cys Asp Ile Cys Tyr Ser
 1           5           10           15
Thr Val Phe Ala Pro Lys Met Leu Val Asn Phe Leu Ser Lys His Lys
          20           25           30
Ser Ser Thr Phe Ser Gly Cys Val Leu Gln Ser Phe Pro Phe Ala Val
          35           40           45
Tyr Val Thr Thr Lys Asp Ile Leu Leu Ser Met Met Ala Tyr Asp His

```

50	55	60
Tyr Val Ala Ile Ala Asn Pro Leu Leu Tyr Thr Val Ile Met Ala Gln		
65	70	75
Lys Val Cys Ile Gln Met Val Leu Ala Ser Tyr Leu Gly Gly Leu Ile		80
	85	90
Asn Ser Leu Thr His Thr Ile Gly Leu Leu Lys Leu Asp Phe Cys Gly		95
	100	105
Pro Asn Ile Val Asn His Tyr Phe Cys Asp Val Pro Pro Leu Leu Arg		110
	115	120
Leu Ser Cys Ser Asp Ala His Ile Asn Glu Met Leu Pro Leu Val Phe		125
	130	135
Ser Gly Leu Ile Ala Met Phe Thr Phe Ile Val Ile Met Val Ser Tyr		140
145	150	155
Ile Cys Ile Ile Ile Ala Ile Gln Arg Ile His Ala Ala Glu Gly Arg		160
	165	170
Tyr Lys Ala Phe Ser Thr Cys Val Ser His Leu Thr Thr Val Thr Leu		175
	180	185
Phe Tyr Gly Ser Val Ser Phe Ser Tyr Ile Gln Pro Ser Ser Gln Tyr		190
	195	200
Ser Leu Glu Gln Glu Lys Val Leu Ala Val Phe Tyr Thr Leu Val Ile		205
	210	215
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys		220
225	230	235
Asp Ala Ala Lys Arg Leu Ile Trp Trp Gly Glu Lys		240
	245	250

<210> 1648

<211> 319

<212> PRT

<213> Unknown (H38g565 protein)

<220>

<223> Synthetic construct

<400> 1648

Met Ser Gly Glu Asn Val Thr Arg Val Gly Thr Phe Ile Leu Val Gly		
1	5	10
Phe Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu		15
	20	25
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Thr		30
	35	40
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser		45
	50	55
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys		60
65	70	75
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly		80
	85	90
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys		95
	100	105
Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His		110
	115	120
Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Cys Ala Ser Arg Leu		125
	130	135
Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val		140
145	150	155
Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His		160
	165	170
Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe		175
	180	185
Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val		190
	195	200
		205

Phe Pro Leu Leu Ala Thr Met Leu Ser Tyr Ala His Il Thr Leu Ala
 210 215 220
 Val Leu Arg Ile Pro Ser Pr Arg Gly Cys Trp Arg Ala Phe Phe Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu
 245 250 255
 Phe Met Tyr Val Arg Pro Arg Pro Leu Tyr Ser Arg Ser Ser Asn Lys
 260 265 270
 Leu Ile Ser Val Leu Tyr Thr Val Ile Thr Pro Ile Leu Asn Pro Leu
 275 280 285
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asn Ala Leu Lys Asn Ser
 290 295 300
 Arg Leu Asp Asp Cys Ala Val Glu Gly Arg Leu Ser Ser Leu Leu
 305 310 315

<210> 1649

<211> 320

<212> PRT

<213> Unknown (H38g566 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1649

Met Ala Asp Val Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Glu
 1 5 10 15
 Leu Thr Asp Arg Ala Glu Leu Lys Met Val Leu Phe Val Leu Phe Leu
 20 25 30
 Leu Ile Tyr Thr Ile Ser Leu Val Gly Asn Ile Gly Met Leu Phe Leu
 35 40 45
 Ile Tyr Val Thr Pro Lys Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Cys Leu Ser Phe Val Asp Ala Cys Tyr Ser Ser Val Phe Ala Pro Arg
 65 70 75 80
 Met Leu Leu Asn Phe Phe Val Glu Arg Glu Thr Ile Leu Phe Ser Ala
 85 90 95
 Cys Ile Val Gln Tyr Phe Leu Phe Val Ser Leu Leu Thr Thr Glu Gly
 100 105 110
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala Ile Val Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile Val Cys Ile Val Leu
 130 135 140
 Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Asn Ser Leu Thr His Thr
 145 150 155 160
 Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro Asn Val Ile Ser His
 165 170 175
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Ser Glu Thr
 180 185 190
 Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser Gly Ile Ile Ala Thr
 195 200 205
 Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile Phe Ile Val Ala Ala
 210 215 220
 Ile Leu Arg Ile Arg Xaa Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe Tyr Gly Ser Ile Ser
 245 250 255
 Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser Leu Glu Gln Glu Lys

		260						265					270				
Val	Val	Ser	Val	Phe	Tyr	Thr	Leu	Val	Val	Pro	Met	Leu	Asn	Pro	Leu		
		275						280					285				
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Glu	Ala	Val	Lys	Arg	Ala		
	290					295					300						
Ile	Glu	Met	Lys	His	Phe	Pro	Cys	Xaa	Phe	His	Ile	Ser	Ile	Ser	Lys		
305					310					315					320		

<210> 1650

<211> 313

<212> PRT

<213> Unknown (H38g567 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1650

Met	Leu	Gly	Asn	Tyr	Ser	Ser	Ala	Thr	Glu	Phe	Phe	Leu	Leu	Gly	Phe		
1			5					10						15			
Pro	Gly	Ser	Gln	Glu	Val	Arg	Arg	Ile	Leu	Phe	Val	Asn	Phe	Phe	Phe		
			20					25					30				
Leu	Tyr	Ala	Val	Thr	Val	Met	Gly	Asn	Thr	Val	Ile	Ile	Val	Thr	Val		
		35					40					45					
Cys	Val	Asp	Lys	His	Leu	Gln	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Gly	His		
	50					55					60						
Leu	Cys	Val	Leu	Glu	Ile	Leu	Ile	Thr	Ser	Thr	Ala	Ala	Pro	Phe	Met		
65					70				75						80		
Leu	Trp	Gly	Leu	Leu	Pro	Ser	Thr	Gln	Ile	Met	Ser	Leu	Thr	Ala			
			85					90					95				
Cys	Ala	Ala	Gln	Leu	Leu	Tyr	Leu	Ser	Leu	Gly	Thr	Ser	Glu	Leu	Ala		
			100					105					110				
Leu	Met	Gly	Val	Met	Ala	Val	Asp	His	Tyr	Val	Ala	Val	Cys	Asn	Pro		
	115						120					125					
Leu	Arg	Tyr	Asn	Ile	Ile	Met	Asn	Ser	Ser	Thr	Cys	Val	Trp	Met	Val		
	130					135					140						
Ile	Val	Ser	Trp	Val	Phe	Gly	Phe	Leu	Phe	Gln	Ile	Trp	Pro	Val	Tyr		
145					150					155					160		
Ala	Thr	Phe	Gln	Leu	Thr	Phe	Cys	Lys	Ser	Asn	Val	Leu	Asp	His	Phe		
			165						170					175			
Tyr	Cys	Asp	Xaa	Gly	Gln	Leu	Leu	Lys	Val	Ser	Cys	Glu	Asp	Thr	Leu		
		180						185					190				
Phe	Thr	Glu	Phe	Ile	Leu	Phe	Leu	Met	Ala	Val	Phe	Ile	Ile	Ile	Gly		
	195						200					205					
Ser	Leu	Ile	Pro	Thr	Ile	Val	Ser	Tyr	Thr	Tyr	Ile	Ile	Ser	Thr	Ile		
	210					215					220						
Leu	Lys	Ile	Pro	Leu	Ala	Ser	Gly	Trp	Arg	Lys	Ser	Phe	Ser	Thr	Cys		
225					230					235					240		
Ala	Ser	His	Phe	Thr	Cys	Val	Val	Ile	Gly	Tyr	Ser	Ser	Cys	Leu	Phe		
			245						250					255			
Leu	Tyr	Thr	Lys	Pro	Lys	Gln	Thr	Gln	Ala	Ala	Lys	Tyr	Asn	Arg	Ile		
			260					265					270				
Ala	Ser	Leu	Leu	Val	Leu	Val	Val	Thr	Pro	Phe	Leu	Asn	Pro	Phe	Ile		
	275						280					285					
Phe	Thr	Leu	Arg	Asn	Asp	Lys	Phe	Ile	Gln	Ala	Phe	Gly	Asp	Gly	Met		
	290					295					300						
Lys	His	Cys	Tyr	Gln	Leu	Leu	Arg	Ile									
305					310												

<210> 1651
 <211> 314
 <212> PRT
 <213> Unknown (H38g568 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1651
 Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu
 20 25 30
 Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile
 35 40 45
 Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile
 65 70 75 80
 Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr
 85 90 95
 His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr
 100 105 110
 Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile
 130 135 140
 Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr
 145 150 155 160
 His Leu Ser Ser Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile
 165 170 175
 Asn Arg Tyr Phe Cys Asp Ile Pro Leu Leu Phe Gln Leu Ser Cys Ser
 180 185 190
 Asn Thr Gln His Ser Lys Ile Leu Phe Thr Val Leu Ser Gly Ala Thr
 195 200 205
 Ser Val Thr Thr Phe Leu Ile Val Val Ser Ser Tyr Leu Val Ile Leu
 210 215 220
 Leu Ile Val Leu Lys Ile His Ser Thr Arg Gly Arg Asn Lys Ala Ile
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Tyr Arg Thr
 245 250 255
 Val Ile Phe Thr Tyr Leu Gly Ala Asn Pro Gly Tyr Ser Gln Asp Arg
 260 265 270
 Pro Lys Ile Leu Pro Val Glu Cys Thr Leu Leu Leu Ser Ile Leu Asn
 275 280 285
 Leu Leu Ile Tyr Ser Val Arg Asn Arg Glu Val Lys Glu Ala Ile Lys
 290 295 300
 Ile Ile Ile Lys Arg Lys Ile Leu Pro Gln
 305 310

<210> 1652
 <211> 314
 <212> PRT
 <213> Unknown (H38g569 protein)

<220>

<223> Synthetic construct

<400> 1652

```

Met Leu Met Asn Tyr Ser Ser Ala Thr Glu Phe Tyr Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Glu Glu Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
          20           25           30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Met Ile Val
          35           40           45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
          50           55           60
Leu Ser Ala Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Val Met
65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Gly Met Gln Thr Ile Tyr Leu Ser Ala
          85           90           95
Cys Val Val Gln Leu Phe Leu Tyr Leu Ala Val Gly Thr Thr Glu Phe
          100          105          110
Ala Leu Leu Gly Ala Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
          115          120          125
Pro Leu Arg Tyr Asn Ile Ile Met Asn Arg His Thr Cys Asn Phe Val
          130          135          140
Val Leu Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val
          145          150          155          160
Tyr Val Met Phe Gln Leu Thr Tyr Cys Lys Ser Asn Val Val Asn Asn
          165          170          175
Phe Phe Cys Asp Arg Gly Gln Leu Leu Lys Leu Ser Cys Asn Asn Thr
          180          185          190
Leu Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Val Leu Phe
          195          200          205
Gly Ser Leu Ile Pro Thr Ile Val Ser Asn Ala Tyr Ile Ile Ser Thr
          210          215          220
Ile Leu Lys Ile Pro Ser Ser Ser Gly Arg Arg Lys Ser Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Gly Ser Cys Leu
          245          250          255
Phe Leu Tyr Val Lys Pro Lys Gln Thr Gln Ala Ala Asp Tyr Asn Trp
          260          265          270
Val Val Ser Leu Met Val Ser Val Val Thr Pro Phe Leu Asn Pro Phe
          275          280          285
Ile Phe Thr Leu Arg Asn Asp Lys Val Ile Glu Ala Leu Arg Asp Gly
          290          295          300
Val Lys Arg Cys Cys Gln Leu Phe Arg Asn
          305          310

```

<210> 1653

<211> 312

<212> PRT

<213> Unknown (H38g570 protein)

<220>

<223> Synthetic construct

<400> 1653

```

Met Met Gly Arg Arg Asn Asp Thr Asn Val Ala Asp Phe Ile Leu Thr
 1           5           10           15
Gly Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Met Leu Phe
          20           25           30
Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Leu Leu
          35           40           45
Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60

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Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
65          70          75          80
Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
          85          90          95
Cys Phe Ala Gln Met Phe Cys Phe Val Phe Leu Gly Thr Ala Glu Cys
          100         105         110
Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Ser
          115         120         125
Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu Cys Leu Ala Leu
          130         135         140
Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser Phe Val Asn Val
145          150         155         160
Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn Ile Ile His His
          165         170         175
Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
          180         185         190
Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly Ser Thr Leu Met
          195         200         205
Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr
          210         215         220
Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
225          230         235         240
Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile
          245         250         255
Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
          260         265         270
Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
          275         280         285
Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala Leu Ile Arg Val
          290         295         300
Met Gln Arg Arg Gln Asp Ser Arg
305          310

```

<210> 1654

<211> 245

<212> PRT

<213> Unknown (H38g571 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 1654

```

Met Ser Xaa Xaa Ile Phe Cys Leu Pro Lys Ile Ile Ile Thr Leu Leu
1          5          10          15
Gln Xaa Glu Trp Asp Ala Leu Asn Leu Glu Thr Arg Val Phe Leu Glu
          20          25          30
Glu Asp Phe Pro Cys Gly Phe Ser Leu Trp Ile Val Arg Gln Leu Ser
          35          40          45
Phe Phe Leu Glu Ile Asn Xaa Phe Ala His Leu Lys Lys Xaa Cys Arg
          50          55          60
Lys His Thr Ser Thr Phe Ser Leu Ser Asn Leu Ala Phe Xaa Asp Phe
65          70          75          80
Cys Tyr Ala Ser Val Ile Thr Ser Lys Met Phe Gly Ser Phe Leu Tyr
          85          90          95
Lys Gln Lys Lys Leu Thr Phe Asn Ala Leu Gly Cys Ser Leu Thr Phe
          100         105         110
Met Thr Thr Glu Cys Leu Leu Leu Ala Phe Met Ala Cys Asp Gln Tyr

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      115              120              125
Leu Val Ile Cys Asn Pro Pro Leu Tyr Met Val Thr Met Ser Pro Pro
 130              135              140
Gln Gly Val Cys Ile Gln Leu Met Pro Ala Ser Tyr Ser Tyr Ser Phe
145              150              155              160
Leu Met Thr Leu Ser His Tyr Leu Ser Ala Phe Arg Leu Pro Tyr Cys
      165              170              175
Pro Ser Val Ser Leu Met Phe Asn Gly Ser Leu Phe Leu Tyr Cys Thr
      180              185              190
Xaa Cys Ser Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe
      195              200              205
Tyr Thr Val Val Ile Pro Met Leu Ser Pro Leu Ile Trp Ser Leu Arg
      210              215              220
Asn Lys Asp Val Lys Asp Ala Leu Arg Lys Val Ile Val Asn Arg Asn
225              230              235              240
Gln Ala Leu Phe Cys
      245

```

<210> 1655

<211> 312

<212> PRT

<213> Unknown (H38g572 protein)

<220>

<223> Synthetic construct

<400> 1655

```

Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly
 1              5              10              15
Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
      20              25              30
Val Leu Tyr Val Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu
      35              40              45
Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg
      50              55              60
His Leu Ala Ile Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys
      65              70              75              80
Met Leu Met Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu
      85              90              95
Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val
      100              105              110
Met Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn,
      115              120              125
Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu
      130              135              140
Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser
      145              150              155              160
Pro Cys Ile Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His
      165              170              175
Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
      180              185              190
Tyr Ile Pro Glu Thr Ile Val Phe Ile Ser Ala Ala Thr Asn Leu Phe
      195              200              205
Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser
      210              215              220
Ile Leu Arg Ile Arg Ser Pro Glu Gly Arg Lys Lys Ala Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Met Ile Ala Val Thr Val Phe Tyr Gly Thr Met Leu
      245              250              255
Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser Leu Asp Thr Asp Lys
      260              265              270

```

Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Asp Val Asn Val Ala Leu Lys Lys Phe
 290 295 300
 Met Glu Asn Pro Cys Tyr Ser Phe
 305 310

<210> 1656
 <211> 161
 <212> PRT
 <213> Unknown (H38g573 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(161)
 <223> Xaa = Any Amino Acid

<400> 1656
 Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser
 20 25 30
 Ile Val Ile Arg Asn Tyr Val Ile Ile Val Cys Val Glu Lys Cys
 35 40 45
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu
 50 55 60
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr
 65 70 75 80
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu
 85 90 95
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val
 100 105 110
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn
 115 120 125
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu
 130 135 140
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu
 145 150 155 160
 Pro

<210> 1657
 <211> 324
 <212> PRT
 <213> Unknown (H38g574 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1657
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser

```

      35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
 50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met
65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Glu Gly Cys Leu Thr Gln Met Phe Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu Asn Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Ile Leu Met Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
      195      200      205
Phe Ala Phe Leu Pro Ile Ser Ala Ile Leu Leu Ser Tyr Tyr Lys Ile
      210      215      220
Val Thr Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225      230      235      240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245      250      255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290      295      300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
      305      310      315      320
Phe Phe Leu Cys

```

<210> 1658

<211> 320

<212> PRT

<213> Unknown (H38g575 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1658

```

His Thr Lys Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
      20      25      30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu
      50      55      60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65      70      75      80

```


Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Thr Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Phe Ile Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Val Val Leu Gln Phe Thr Phe Phe Asn Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Val Asn Leu Ala Ser Ser Asp
 180 185 190
 Ser Val Val Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Leu Gly Val Leu Leu Ser His Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Val Phe Ala
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly
 245 250 255
 Ile Asp Met Tyr Leu Thr Ser Ala Val Ser Pro Pro His Arg Asn Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Phe Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg
 290 295 300
 Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315 320

<210> 1659

<211> 270

<212> PRT

<213> Unknown (H38g576 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(270)

<223> Xaa = Any Amino Acid

<400> 1659

Val Ser Leu Ile Thr Tyr Leu Ile Thr Val Met Ser Asn Leu Gly Met
 1 5 10 15
 Asn Ile Leu Thr Lys Leu Asp Ser His Leu Tyr Thr Pro Val Val Tyr
 20 25 30
 Phe Leu Ile Lys His Ile Phe Phe Ile Asp Phe Tyr Asn Cys Ile Val
 35 40 45
 Ile Tyr Thr Asn Lys Met Leu Asn Phe Val Val Asp Gln Asn Asn Ile
 50 55 60
 Ser Tyr Tyr Ala Cys Ala Thr His Met Thr Phe Phe Met Phe Ile Ile
 65 70 75 80
 Thr Glu Leu Leu Ile Leu Val Ser Met Ala Tyr Asp Cys Tyr Val Val
 85 90 95
 Asn Ser Asn Pro Leu Phe Tyr Ile Val Ile Met Cys Leu Xaa Leu Xaa
 100 105 110
 His Val Leu Met Ser Ile Pro Tyr Leu Cys Asn Thr Phe Gln Ser Leu
 115 120 125
 Ile Ile Thr Ile Asp Leu Phe Leu Thr Phe Cys Ser Phe Ile Ile Ser

130	135	140
His Phe Tyr Cys Tyr Asp Val Leu Phe Phe His Met Leu Cys Ser Asn		
145	150	155
Ala Gln Glu Arg Glu Leu Leu Ile Thr Leu Leu Thr Ala Phe Asn Leu		
	165	170
Ile Pro Ser Leu Leu Val Leu Leu Val Leu Asn Ile Leu Ile Leu Leu		
	180	185
Ala Ile Cys Xaa Met His Ser Ala Leu Gly Arg Lys Lys Ala Phe Ser		
	195	200
Met Cys Gly Ser His Leu Thr Met Val Val Met Phe Tyr Gly Ser Leu		
	210	215
Leu Phe Asp Met Asp Lys Val Ala Ser Leu Phe Tyr Thr Leu Met Ile		
225	230	235
Leu Arg Phe Asn Leu Leu Ile Tyr Ser Phe Ser Asn Leu Gly Val Lys		
	245	250
Asn Val Phe Tyr Arg Val Phe Lys Asn Xaa Cys Lys Leu Cys		
	260	265
		270

<210> 1660

<211> 128

<212> PRT

<213> Unknown (H38g577 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(128)

<223> Xaa = Any Amino Acid

<400> 1660

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe	
1	5
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg	
	20
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr	
	35
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe	
	50
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val	
65	70
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Asn Phe Val	
	85
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu	
	100
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile Cys	
	115
	120
	125

<210> 1661

<211> 307

<212> PRT

<213> Unknown (H38g578 protein)

<220>

<223> Synthetic construct

<400> 1661

Met Gly Gln His Asn Leu Thr Val Leu Thr Glu Phe Ile Leu Met Glu	
1	5
Leu Thr Arg Arg Pro Glu Leu Gln Ile Pro Leu Phe Gly Val Phe Leu	
	20
	25
	30

Val Ile Tyr Leu Ile Thr Val Val Gly Asn Leu Thr Met Ile Ile Leu
 35 40 45
 Thr Lys Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Ser Ile Arg
 50 55 60
 His Leu Ala Ser Val Asp Leu Gly Asn Ser Thr Val Ile Cys Pro Lys
 65 70 75 80
 Val Leu Ala Asn Phe Val Val Asp Arg Asn Thr Ile Ser Tyr Tyr Ala
 85 90 95
 Cys Ala Ala Gln Leu Ala Phe Phe Leu Met Phe Ile Ile Ser Glu Phe
 100 105 110
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Tyr Val Ile Met Ser Gln Arg Leu Cys His Val Leu
 130 135 140
 Val Gly Ile Gln Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Phe Thr
 145 150 155 160
 Ile Lys Ile Phe Thr Leu Thr Phe Cys Gly Ser Asn Val Ile Ser His
 165 170 175
 Phe Tyr Cys Asp Asp Val Pro Leu Leu Pro Met Leu Cys Ser Asn Ala
 180 185 190
 Gln Glu Ile Glu Leu Leu Ser Ile Leu Phe Ser Val Phe Asn Leu Ile
 195 200 205
 Ser Ser Phe Leu Ile Val Leu Val Ser Tyr Met Leu Ile Leu Leu Ala
 210 215 220
 Ile Cys Gln Met His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Val Val Phe Tyr Gly Ser Leu Leu
 245 250 255
 Phe Met Tyr Met Gln Pro Asn Ser Thr His Phe Phe Asp Thr Asp Lys
 260 265 270
 Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Glu Glu Val Lys Asn Ala Phe Tyr Lys Leu
 290 295 300
 Phe Glu Asn
 305

<210> 1662

<211> 218

<212> PRT

<213> Unknown (H38g579 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1662

Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Val Ile Phe Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ala Gln Leu His Asn Leu

```
<210> 1663
<211> 227
<212> PRT
<213> Unknown (H38g580 protein)
```

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<221> VARIANT
<222> (1)...(227)
<223> Xaa = Any Amino Acid
```

908

<210> 1664
 <211> 194
 <212> PRT
 <213> Unknown (H38g581 protein)

<220>
 <223> Synthetic construct

<400> 1664
 Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ile
 1 5 10 15
 Ser Cys Val Pro Gly Met Leu Val Asn Leu Trp Glu Pro Lys Lys Thr
 20 25 30
 Ile Ile Leu Leu Gly Cys Ser Val Gln Phe Phe Ile Phe Leu Ser Leu
 35 40 45
 Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr
 50 55 60
 Met Ala Ile Cys Gln Pro Leu His Tyr Ala Thr Ile Val His Pro Leu
 65 70 75 80
 Leu Cys Trp Gln Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Glu
 85 90 95
 Ser Val Val Gln Thr Pro Ser Thr Leu His Leu Pro Phe Cys Pro Asp
 100 105 110
 Arg Gln Val Asp Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu
 115 120 125
 Ser Cys Glu Asp Thr Ser Tyr Asn Glu Ile Gln Leu Ala Val Ala Ser
 130 135 140
 Val Phe Ile Leu Ala Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly
 145 150 155 160
 Ala Ile Ala Trp Ala Val Leu Arg Thr Asn Ser Ala Lys Gly Gln Arg
 165 170 175
 Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe
 180 185 190
 Tyr Ser

<210> 1665
 <211> 320
 <212> PRT
 <213> Unknown (H38g582 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1665
 Met Val Ser Ser Asn Gln Thr Ser Pro Val Leu Gly Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
 20 25 30
 Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Thr Ile Leu Asp Ser Arg Leu Asp Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Val Leu
 65 70 75 80
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala

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<210> 1666
<211> 318
<212> PRT
<213> Unknown (H38g583 protein)
```

<220>
<223> Synthetic construct

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<400> 1666
Met Val Ser Ala Asn Gln Thr Ala Ser Val Thr Glu Phe Ile Leu Leu
  1          5          10          15
Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
  20          25          30
Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
  35          40          45
Met Thr Val Ser Asn Ser His Leu His Met Pro Met Tyr Phe Phe Leu
  50          55          60
Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Tyr Ser Val Pro
  65          70          75          80
Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser
  85          90          95
Ala Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu
  100          105          110
Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
  115          120          125
Asn Pro Leu Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Met Pro
  130          135          140
Met Ala Val Gly Ser Trp Val Ala Gly Ser Thr Ala Ser Met Val Gln
  145          150          155          160
Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Ile Ile Asn
  165          170          175

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His Phe Thr Cys Glu Ile Leu Ala Val Gln Lys Leu Ala Cys Ala Asp
 180 185 190
 Ile Ser Val Asn Val Ile Ser Met Gly Val Thr Asn Val Ile Phe Leu
 195 200 205
 Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Ala
 210 215 220
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
 260 265 270
 Lys Gln Asp Phe Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val
 275 280 285
 Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val
 290 295 300
 Lys Ala Ala Val Arg Asp Leu Ile Phe Gln Lys Cys Phe Ala
 305 310 315

<210> 1667

<211> 321

<212> PRT

<213> Unknown (H38g584 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1667

Met Asn Arg Ser Asn Glu Ala Ser Pro Val Leu Gly Phe Val Leu Leu
 1 5 10 15
 Gly Leu Ser Ala His Pro Xaa Leu Glu Lys Thr Phe Phe Val Phe Ile
 20 25 30
 Leu Leu Val Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Leu
 65 70 75 80
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala
 85 90 95
 Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu
 100 105 110
 Leu Ser Met Met Ala Phe Asp His Tyr Leu Asp Met Cys Asn Pro Leu
 115 120 125
 Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Met Pro Met Ala Val
 130 135 140
 Gly Ser Trp Ala Ala Gly Ile Thr Asn Ser Val Val Gln Ile Ser Leu
 145 150 155 160
 Ala Met Xaa Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr
 165 170 175
 Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Cys Ile
 180 185 190
 Asn Val Ile Ser Met Val Val Thr Asn Met Ile Phe Leu Ala Leu Pro
 195 200 205
 Val Leu Phe Ile Phe Val Ser Tyr Val Phe Ile Ile Ala Thr Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser

```

225          230          235          240
Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Met Ile Leu Phe Met
          245          250          255
Tyr Gly Lys Pro Lys Ser Lys Asp Pro Met Gly Ala Asp Lys Gln Asp
          260          265          270
Leu Ala Asp Lys Leu Ile Ser Ile Phe Tyr Gly Val Val Thr Pro Ile
          275          280          285
Leu Asn Pro Ile Ile Tyr Ser Pro Arg Asn Lys Asp Leu Lys Ala Ala
          290          295          300
Met Arg Asn Leu Val Ala Gln Lys His Leu Thr Glu Xaa Leu Ser Gln
305          310          315          320
Ile

```

<210> 1668
 <211> 125
 <212> PRT
 <213> Unknown (H38g585 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(125)
 <223> Xaa = Any Amino Acid

```

<400> 1668
Arg Leu Asn Val Ile Ser His Leu Pro Phe Tyr Gly Asp Ile Ile Asn
 1          5          10          15
His Leu Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
          20          25          30
Ile Ser Ile Asn Met Ile Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala
          35          40          45
His Leu Thr Val Val Val Ile Phe Tyr Arg Thr Ile Leu Phe Thr His
          50          55          60
Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Phe
65          70          75          80
Ala Asp Lys Leu Ile Ser Leu Ser Tyr Gly Val Val Thr Pro Met Leu
          85          90          95
Asn Thr Ile Ile Tyr Ser Leu Arg Lys Lys Gly Val Lys Ala Ala Val
          100          105          110
Lys Asn Leu Val Phe Gln Lys Pro Leu Thr Glu Xaa Gln
          115          120          125

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<210> 1669
 <211> 216
 <212> PRT
 <213> Unknown (H38g586 protein)

<220>
 <223> Synthetic construct

```

<400> 1669
Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val
 1          5          10          15
Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr
          20          25          30
Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu
          35          40          45
Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys
          50          55          60

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Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu
 65 70 75 80
 Cys Trp Val L u Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
 115 120 125
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
 130 135 140
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
 145 150 155 160
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
 180 185 190
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Ile Val Thr Pro
 210 215

<210> 1670

<211> 319

<212> PRT

<213> Unknown (H38g587 protein)

<220>

<223> Synthetic construct

<400> 1670

Met Glu Lys Ala Asn Glu Thr Ser Pro Val Met Gly Phe Val Leu Leu
 1 5 10 15
 Arg Leu Ser Ala His Pro Glu Leu Glu Lys Thr Phe Phe Val Leu Ile
 20 25 30
 Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Phe Thr Thr Ser Ser Val Pro
 65 70 75 80
 Leu Val Leu Asp Ser Phe Leu Thr Pro Gln Glu Thr Ile Ser Phe Ser
 85 90 95
 Ala Cys Ala Val Gln Met Ala Leu Ser Phe Ala Met Ala Gly Thr Glu
 100 105 110
 Cys Leu Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Ala Ala Tyr Met Pro
 130 135 140
 Met Ala Ala Ser Ser Trp Ala Ile Gly Gly Ala Ala Ser Val Val His
 145 150 155 160
 Thr Ser Leu Ala Ile Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
 165 170 175
 His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 Ile Ser Ile Asn Val Ile Ser Met Glu Val Thr Asn Val Ile Phe Leu
 195 200 205
 Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Thr
 210 215 220
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu

				245					250					255	
Phe	Phe	Met	Tyr	Gly	Lys	Pro	Lys	Ser	Lys	Asp	Ser	Met	Gly	Ala	Asp
			260					265					270		
Lys	Glu	Asp	Leu	Ser	Asp	Lys	Leu	Ile	Pro	Leu	Phe	Tyr	Gly	Val	Val
		275					280					285			
Thr	Pro	Met	Leu	Asn	Pro	Ile	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val
	290					295					300				
Lys	Ala	Ala	Val	Arg	Arg	Leu	Leu	Arg	Pro	Lys	Gly	Phe	Thr	Gln	
305					310					315					

<210> 1671

<211> 218

<212> PRT

<213> Unknown (H38g588 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1671

Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro	Lys	Met	Ile	Val
1				5				10					15		
Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu	Glu	Ser	Met	Leu
	35					40					45				
Leu	Ser	Val	Ile	Ala	Tyr	Glu	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
	50				55					60					
Tyr	His	Ser	Ala	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu
65				70				75						80	
Leu	Ser	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln	Leu	His	Asn	Leu
			85					90					95		
Ile	Ala	Leu	Gln	Arg	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe
		100					105						110		
Phe	Cys	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Tyr	Cys	Gly	Thr	Phe
	115					120					125				
Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu
	130				135						140				
Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Asn	Lys	Ile	Val	Phe	Ser	Ile
145				150				155						160	
Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys
			165					170					175		
Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly	Thr	Gly	Ile	Gly
	180						185					190			
Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser	Pro	Arg	Lys	Ala	Ala	Val	
	195					200					205				
Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Ile	Pro						
	210					215									

<210> 1672

<211> 216

<212> PRT

<213> Unknown (H38g589 protein)

<220>

<223> Synthetic construct

<400> 1672

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Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
 1           5           10           15
Asn His Ile L u Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
          20           25           30
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu
          35           40           45
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50           55           60
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly
          65           70           75           80
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met
          85           90           95
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys
          100          105          110
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115          120          125
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe
          130          135          140
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg
          145          150          155          160
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser
          165          170          175
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr
          180          185          190
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala
          195          200          205
Val Met Tyr Pro Val Val Thr Pro
          210          215

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<210> 1673

<211> 329

<212> PRT

<213> Unknown (H38g590 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1673

```

Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1           5           10           15
Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
          20           25           30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
          35           40           45
Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
          50           55           60
Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
          65           70           75           80
Met Leu Ile Asn Phe Leu Ser Lys Asn His Met Leu Ser Met Ala Lys
          85           90           95
Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln Phe
          130          135          140
Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His Val

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145          150          155          160
Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His Tyr
      165          170          175
Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn Pro
      180          185          190
Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln Val
      195          200          205
Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser Ala
      210          215          220
Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ala His Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu Phe
      245          250          255
Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala Lys
      260          265          270
Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Asp Ala Leu Arg Arg Ile
      290          295          300
Met Lys Lys Xaa Ile Val Arg Gln His Ser Asn His Phe Phe Phe
305          310          315          320
Ile Phe Cys Xaa Arg Lys Pro Gln Val
      325

```

<210> 1674

<211> 212

<212> PRT

<213> Unknown (H38g591 protein)

<220>

<223> Synthetic construct

<400> 1674

```

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly
 1          5          10          15
Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe
      20          25          30
Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala
      35          40          45
Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr
      50          55          60
Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys
65          70          75          80
Gly Phe Leu Asn Ala Ser Leu Arg Ile Val Asp Ile Phe Ser Leu Ser
      85          90          95
Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro
      100          105          110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
      115          120          125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
      130          135          140
Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
145          150          155          160
Gln Gly His Leu Lys Ala Leu Ser Thr Cys Ala Ser His Leu Ile Ala
      165          170          175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
      180          185          190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
      195          200          205
Val Phe Ile Ser
      210

```

<210> 1675
 <211> 314
 <212> PRT
 <213> Unknown (H38g592 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1675
 Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1 5 10 15
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
 20 25 30
 Leu Tyr Leu Phe Ser Leu Leu Gly Asn Gly Val Ile Phe Gly Leu Ile
 35 40 45
 Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65 70 75 80
 Leu Ala Asn Leu Val Asn Gln Lys Arg Thr Ile Ser Phe Ile Ser Cys
 85 90 95
 Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Val Cys Leu
 100 105 110
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Val Leu Ala
 130 135 140
 Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val His Leu Val
 145 150 155 160
 Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
 165 170 175
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
 180 185 190
 Leu Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly
 195 200 205
 Xaa Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu Ala Ala Ile
 210 215 220
 Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val
 245 250 255
 Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg Arg Lys Ile
 260 265 270
 Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu
 290 295 300
 Trp Lys Gln Arg Ser Ile Glu Glu Ser Phe
 305 310

<210> 1676
 <211> 216
 <212> PRT
 <213> Unknown (H38g593 protein)

<220>

<223> Synthetic construct

<400> 1676

```

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1           5           10           15
Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr
          20           25           30
Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
          35           40           45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          50           55           60
Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
          65           70           75           80
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
          85           90           95
Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys
          100          105          110
Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn
          115          120          125
Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe
          130          135          140
Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
          145          150          155          160
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser
          165          170          175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
          180          185          190
Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala
          195          200          205
Met Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 1677

<211> 312

<212> PRT

<213> Unknown (H38g594 protein)

<220>

<223> Synthetic construct

<400> 1677

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1           5           10           15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
          20           25           30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35           40           45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
          65           70           75           80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85           90           95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
          145          150          155          160

```

Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pr Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Arg Ile Ser
 305 310

<210> 1678

<211> 128

<212> PRT

<213> Unknown (H38g595 protein)

<220>

<223> Synthetic construct

<400> 1678

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
 1 5 10 15
 Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
 20 25 30
 Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
 35 40 45
 Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala
 65 70 75 80
 Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
 85 90 95
 Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
 100 105 110
 Asp Thr Glu Cys Ser Met Gln Leu Met Pro Lys Val Asn Gln Asn Val
 115 120 125

<210> 1679

<211> 270

<212> PRT

<213> Unknown (H38g596 protein)

<220>

<223> Synthetic construct

<400> 1679

Met Thr Ile Val Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro
 1 5 10 15
 Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr
 20 25 30
 Thr Gly Ser Ile Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys

```

      35              40              45
Thr Ile Ser Tyr Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala
50              55              60
Leu Gly Gly Val Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg
65              70              75              80
Tyr Ala Ala Val Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro
85              90              95
Arg Leu Cys Gly Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly
100              105              110
Asn Ser Leu Ile Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly
115              120              125
His Arg Arg Val Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly
130              135              140
Met Ala Cys Val Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu
145              150              155              160
Ala Ile Phe Ile Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr
165              170              175
Gly Tyr Val Gly Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg
180              185              190
Lys Lys Ala Phe Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu
195              200              205
Phe Tyr Gly Thr Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr
210              215              220
Ser Gln Asp Gln Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr
225              230              235              240
Pro Ser Val Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys
245              250              255
Glu Ala Met Lys Lys Val Leu Gly Lys Gly Ser Ala Glu Ile
260              265              270

```

<210> 1680

<211> 114

<212> PRT

<213> Unknown (H38g597 protein)

<220>

<223> Synthetic construct

<400> 1680

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys
1              5              10              15
Val Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys
20              25              30
Ala His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala
35              40              45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
50              55              60
Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr Ile
65              70              75              80
Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg Val
85              90              95
Leu Leu Ala Val Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala
100              105              110
Tyr Ser

```

<210> 1681

<211> 212

<212> PRT

<213> Unknown (H38g598 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1681

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Val
 1           5           10           15
Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
          20           25           30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
          35           40           45
Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
          50           55           60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65          70          75          80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
          85          90          95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
          100         105         110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
          115         120         125
Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
          130         135         140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145         150         155         160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
          165         170         175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg
          180         185         190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
          195         200         205
Thr Ile Thr Pro
          210

```

<210> 1682

<211> 212

<212> PRT

<213> Unknown (H38g599 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1682

```

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 1           5           10           15
Asn Leu Val Ala Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
          20           25           30
Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Cys Met Leu
          35           40           45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
          50           55           60
Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
65          70          75          80
Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu

```

```
<210> 1684
<211> 114
<212> PRT
<213> Unknown (H38g601 protein)
```

<220>

<223> Synthetic construct

<400> 1684

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Met Arg Lys Arg Val Cys
 1           5           10           15
Ala Leu Met Ile Thr Gly Ser Trp Met Ile Gly Ser Ile Asn Ser Cys
          20           25           30
Ala His Thr Val Tyr Ala Leu Arg Ile Pro Tyr Cys Lys Ser Arg Ala
          35           40           45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
          50           55           60
Thr Asp Thr Trp Val Tyr Glu Cys Thr Val Phe Leu Ser Thr Thr Ile
65           70           75           80
Phe Leu Val Phe Pro Phe Ile Cys Ile Ala Cys Ser Tyr Gly Arg Ile
          85           90           95
Leu Leu Ala Val Tyr His Met His Ser Ala Glu Gly Arg Lys Lys Ala
          100          105          110
Tyr Ser

```

<210> 1685

<211> 216

<212> PRT

<213> Unknown (H38g602 protein)

<220>

<223> Synthetic construct

<400> 1685

```

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1           5           10           15
His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
          20           25           30
Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
          35           40           45
Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg
          50           55           60
Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr
65           70           75           80
Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr
          85           90           95
Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys
          100          105          110
Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn
          115          120          125
Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe
          130          135          140
Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys
145          150          155          160
Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser
          165          170          175
His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr
          180          185          190
Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser
          195          200          205
Val Phe Tyr Ala Ile Leu Thr Pro
          210          215

```

<210> 1686

<211> 212

<212> PRT
 <213> Unknown (H38g603 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(212)
 <223> Xaa = Any Amino Acid

<400> 1686

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
 1             5             10             15
Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
      20             25             30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu
      35             40             45
Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
      50             55             60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65             70             75             80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Val Leu Thr
      85             90             95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
      100            105            110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
      115            120            125
Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
      130            135            140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145            150            155            160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
      165            170            175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
      180            185            190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
      195            200            205
Thr Ile Thr Pro
      210
  
```

<210> 1687
 <211> 114
 <212> PRT
 <213> Unknown (H38g604 protein)

<220>
 <223> Synthetic construct

<400> 1687

```

Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys
 1             5             10             15
Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu
      20             25             30
Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile
      35             40             45
Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys
      50             55             60
Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe S r Gly Ser
65             70             75             80
Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val
      85             90             95
  
```

Leu Phe Ala Ile Leu Lys Arg Lys S r Asp Lys Gly Val Arg Lys Ala
 100 105 110
 Phe Ser

<210> 1688

<211> 111

<212> PRT

<213> Unknown (H38g605 protein)

<220>

<223> Synthetic construct

<400> 1688

Ile Cys Asn Pro Leu Arg Tyr Pro Ile Ile Met Ser Arg His Val Cys
 1 5 10 15
 Val Gln Met Ala Ala Ile Ser Trp Val Thr Gly Cys Leu Thr Ala Leu
 20 25 30
 Leu Val Thr Ser Cys Ala Leu Gln Ile Pro Leu Cys Gly Asn Val Ile
 35 40 45
 Asp His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Val
 50 55 60
 Ser Ser Leu Leu Val Asp Met Val Met Leu Val Val Ser Ile Leu Leu
 65 70 75 80
 Leu Pro Ile Pro Met Leu Leu Ile Cys Ile Ser Tyr Gly Phe Ile Leu
 85 90 95
 Ser Thr Ile Leu Arg Ile Gly Ser Thr Glu Gly Arg Asn Lys Ala
 100 105 110

<210> 1689

<211> 223

<212> PRT

<213> Unknown (H38g606 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1689

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Cys Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Gly Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Ser Phe Cys Phe Val Ser Val Phe Leu Ser Leu Leu Asp Ser
 85 90 95
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Gly Phe Lys Asp Val
 100 105 110
 Asp Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Leu His Leu Ala
 115 120 125
 Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala
 130 135 140
 Val Phe Gly Phe Leu Pro Ile Leu Gly Thr Phe Phe Ser Tyr Cys Lys

```

145          150          155          160
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
          165          170          175
Ala Phe Ser Thr Cys Gly Ser His Leu Pro Val Val Cys Xaa Phe Cys
          180          185          190
Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
          195          200          205
Arg Lys Ser Ala Val Pro Ser Val Met Tyr Pro Val Val Thr Ser
          210          215          220

```

<210> 1690
 <211> 215
 <212> PRT
 <213> Unknown (H38g607 protein)

<220>
 <223> Synthetic construct

```

<400> 1690
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1          5          10          15
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Asp Cys Ile Thr
          20          25          30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
          35          40          45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
          65          70          75          80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
          85          90          95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
          100          105          110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
          115          120          125
Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
          130          135          140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
          145          150          155          160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
          165          170          175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Ser Leu Gly Val Tyr
          180          185          190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
          195          200          205
Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 1691
 <211> 278
 <212> PRT
 <213> Unknown (H38g608 protein)

<220>
 <223> Synthetic construct

```

<400> 1691
Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe
 1          5          10          15
Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile
          20          25          30

```

Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln
 35 40 45
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly
 50 55 60
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg
 65 70 75 80
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly
 85 90 95
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly
 100 105 110
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly
 115 120 125
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn
 130 135 140
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu
 145 150 155 160
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr
 165 170 175
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg
 180 185 190
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile
 195 200 205
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser
 210 215 220
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val
 225 230 235 240
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys
 245 250 255
 Arg Ala Leu Cys Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp
 260 265 270
 Pro Lys Lys Gly Ser Arg
 275

<210> 1692

<211> 314

<212> PRT

<213> Unknown (H38g609 protein)

<220>

<223> Synthetic construct

<400> 1692

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
 20 25 30
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
 35 40 45
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val
 65 70 75 80
 Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
 85 90 95
 Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
 100 105 110
 Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
 130 135 140
 Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val

```

145          150          155          160
His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
          165          170          175
Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
          180          185          190
Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
          195          200          205
Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
          210          215          220
Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
          245          250          255
Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
          260          265          270
Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn
          275          280          285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
          290          295          300
Lys Val Leu Arg Ser Lys Val Asp Ser Ser
305          310

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<210> 1693

<211> 316

<212> PRT

<213> Unknown (H38g610 protein)

<220>

<223> Synthetic construct

<400> 1693

```

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
1          5          10          15
Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
          20          25          30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
          35          40          45
Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
50          55          60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65          70          75          80
Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
          85          90          95
Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
          100          105          110
Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
115          120          125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
130          135          140
Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
145          150          155          160
Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
          165          170          175
Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
          180          185          190
Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
          195          200          205
Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
210          215          220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
225          230          235          240

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Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
 245 250 255
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
 260 265 270
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
 290 295 300
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
 305 310 315

<210> 1694

<211> 309

<212> PRT

<213> Unknown (H38g611 protein)

<220>

<223> Synthetic construct

<400> 1694

Met Lys Arg Glu Asn Phe Thr Leu Ile Thr Asp Phe Val Phe Gln Gly
 1 5 10 15
 Phe Ser Ser Phe His Glu Gln Gln Ile Thr Leu Phe Gly Val Phe Leu
 20 25 30
 Ala Leu Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile
 35 40 45
 Ile Arg Ile Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ser Thr Ser Glu Thr Val Tyr Thr Leu Val Ile Leu Pro Arg
 65 70 75 80
 Met Leu Ser Ser Leu Val Gly Met Ser Gln Pro Met Ser Leu Ala Gly
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Val Thr Phe Gly Ile Thr Asn Cys
 100 105 110
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Met Val Ile Met Asn Lys Arg Leu Arg Ile Gln Leu
 130 135 140
 Val Leu Gly Ala Cys Ser Ile Gly Leu Ile Val Ala Ile Thr Gln Val
 145 150 155 160
 Thr Ser Val Phe Arg Leu Pro Phe Cys Ala Arg Lys Val Pro His Phe
 165 170 175
 Phe Cys Asp Ile Arg Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
 180 185 190
 Val Asn Glu Ile Leu Thr Leu Ile Ile Ser Val Leu Val Leu Val Val
 195 200 205
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Ile
 210 215 220
 Leu Lys Ile Ala Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Val Val Ile Val His Tyr Ser Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Lys Pro Lys Ser Glu Asn Thr Arg Glu His Asp Gln Leu
 260 265 270
 Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val
 290 295 300
 Gly Gly Lys Phe Ser
 305

<210> 1695
 <211> 216
 <212> PRT
 <213> Unknown (H38g612 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(216)
 <223> Xaa = Any Amino Acid

<400> 1695
 Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Ala Pro Lys Met Ile Val
 1 5 10 15
 Asp Met Gln Ser His Arg Arg Ala Ile Ser His Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Phe Leu Phe Leu Cys Ala Cys Val Glu Gly Met Leu Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Cys Phe Val Asp Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Pro Val Ile Gly Asn Pro His Phe Cys Val Phe Phe Val Gly Val
 65 70 75 80
 Ser Phe Leu Leu Ser Leu Trp Asp Ser Gln Leu His Ser Trp Ile Val
 85 90 95
 Leu Gln Ile Thr Ile Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys
 100 105 110
 Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Gly Val Ile Asn
 115 120 125
 Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile
 130 135 140
 Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg
 145 150 155 160
 Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Gln Ala Val Val Cys Xaa Phe Tyr Arg Thr Gly Ile Gly Met Tyr
 180 185 190
 Leu Thr Ser Ala Val Ser Pro Pro Arg Asn Gly Val Val Ala Ser
 195 200 205
 Leu Ile Tyr Ala Leu Val Thr Pro
 210 215

<210> 1696
 <211> 214
 <212> PRT
 <213> Unknown (H38g613 protein)

<220>
 <223> Synthetic construct

<400> 1696
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu
 65 70 75 80

Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
 100 105 110
 Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 1697

<211> 212

<212> PRT

<213> Unknown (H38g614 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1697

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 1 5 10 15
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
 20 25 30
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
 50 55 60
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
 65 70 75 80
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu
 85 90 95
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
 100 105 110
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser
 115 120 125
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Ser Glu Ile Ser Ser Leu
 130 135 140
 Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro Ser Thr
 145 150 155 160
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
 165 170 175
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 180 185 190
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 195 200 205
 Val Val Ile Pro
 210

<210> 1698
 <211> 212
 <212> PRT
 <213> Unkn wn (H38g615 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(212)
 <223> Xaa = Any Amino Acid

<400> 1698
 Leu Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Arg
 1 5 10 15
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
 20 25 30
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Val Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
 50 55 60
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
 65 70 75 80
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu
 85 90 95
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
 100 105 110
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser
 115 120 125
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
 130 135 140
 Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Arg Thr Pro Ser Thr
 145 150 155 160
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
 165 170 175
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 180 185 190
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 195 200 205
 Val Val Ile Pro
 210

<210> 1699
 <211> 312
 <212> PRT
 <213> Unknown (H38g616 protein)

<220>
 <223> Synthetic construct

<400> 1699
 Met Ser Ile Ser Asn Ile Thr Val Tyr Met Pro Ser Val Leu Thr Leu
 1 5 10 15
 Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
 20 25 30
 Phe Cys Ala Ile Tyr Leu Ile Ala Met Ile Gly Asn Ser Leu Leu Leu
 35 40 45
 Ser Ile Ile Lys Ser Glu Arg Ser Leu His Glu Pro Leu Tyr Ile Phe
 50 55 60
 Leu Gly Met Leu Gly Ala Thr Asp Ile Ala Leu Ala Ser Ser Ile Met
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Val Pro Glu Ile Tyr Phe
 85 90 95
 Asp Ser Cys Leu Leu Gln Met Trp Phe Ile His Thr Leu Gln Gly Ile
 100 105 110
 Glu Ser Gly Ile Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg His Ala Asn Ile Phe Thr His Gln Leu Val Ile
 130 135 140
 Gln Ile Gly Thr Met Val Val Leu Arg Ala Ala Ile Leu Val Ala Pro
 145 150 155 160
 Cys Leu Val Leu Ile Lys Cys Arg Phe Gln Phe Tyr His Thr Thr Val
 165 170 175
 Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
 180 185 190
 Ala Asn Val Gln Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Thr
 195 200 205
 Val Ala Gly Phe Asp Leu Thr Phe Ile Thr Leu Ser Tyr Ile Gln Ile
 210 215 220
 Phe Ile Thr Val Phe Arg Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
 225 230 235 240
 Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
 245 250 255
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ser His Ile Pro
 260 265 270
 Pro Tyr Ile His Ile Leu Phe Ser Ser Ile Tyr Leu Leu Val Pro Pro
 275 280 285
 Phe Leu Asn Pro Leu Val Tyr Gly Ala Lys Thr Thr Gln Ile Arg Ile
 290 295 300
 His Val Val Lys Met Phe Cys Ser
 305 310

<210> 1700

<211> 318

<212> PRT

<213> Unknown (H38g617 protein)

<220>

<223> Synthetic construct

<400> 1700

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1 5 10 15
 Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
 20 25 30
 Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
 35 40 45
 Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Ile Ile Leu Lys
 65 70 75 80
 Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
 100 105 110
 Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
 130 135 140
 Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
 145 150 155 160
 Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His

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                165                170                175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
                180                185                190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu Leu
                195                200                205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
                210                215                220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225                230                235                240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
                245                250                255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
                260                265                270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
                275                280                285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
290                295                300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305                310                315

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<210> 1701

<211> 294

<212> PRT

<213> Unknown (H38g618 protein)

<220>

<223> Synthetic construct

<400> 1701

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Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
1                5                10                15
Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu
                20                25                30
Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
                35                40                45
Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
50                55                60
Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
65                70                75                80
Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe
                85                90                95
Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser Ser
                100                105                110
Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile
                115                120                125
Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp
130                135                140
Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala
145                150                155                160
Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro
                165                170                175
Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser
                180                185                190
Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val
                195                200                205
Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile
210                215                220
Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala
225                230                235                240
Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Il
                245                250                255

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Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro
 260 265 270
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys
 275 280 285
 Leu Leu Gln Ala Leu Pro
 290

<210> 1702
 <211> 295
 <212> PRT
 <213> Unknown (H38g619 protein)

<220>
 <223> Synthetic construct

<400> 1702
 Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
 1 5 10 15
 Ser Phe Pro Glu Leu Arg His Leu Gln Gly Leu Leu Phe Gly Leu Leu
 20 25 30
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
 35 40 45
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
 50 55 60
 Ala Lys Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
 65 70 75 80
 Lys Leu Leu Ala Gly Leu Pro Gly Thr Ser Asp Asp His Leu Ile Ser
 85 90 95
 Phe Ser Gly His Leu Thr Trp Leu Leu Phe Leu Ser Leu Ser Ser
 100 105 110
 Ser Glu Cys Ile Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val
 115 120 125
 Ile Cys His Leu Leu His Tyr Pro Ala His His Gly Leu His Ala Ala
 130 135 140
 Arg Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro
 145 150 155 160
 Ala Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser
 165 170 175
 Pro Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu
 180 185 190
 Ser Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln
 195 200 205
 Val Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His
 210 215 220
 Ile Leu Ala Arg Ser Leu Arg Ile Pro Ala Lys Ala Gln Gln Leu Lys
 225 230 235 240
 Ala Phe Pro Thr Tyr Ala Ser His Leu Gly Trp Arg Pro Ser Asn Leu
 245 250 255
 Ile Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys
 260 265 270
 Pro Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala
 275 280 285
 Lys Leu Leu Gln Ala Leu Pro
 290 295

<210> 1703
 <211> 175
 <212> PRT
 <213> Unknown (H38g620 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(175)

<223> Xaa = Any Amino Acid

<400> 1703

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Leu Leu Met Ala Ala Asp Asn His Thr Arg Val Glu Ala Phe Val Leu
 1           5           10           15
Gln Gly Phe Ser Glu Asp Leu Pro Leu Gln Gly Cys Cys Phe Ala Phe
      20           25           30
Phe Leu Leu Tyr Leu Met Ala Leu Val Gly Asn Ile Leu Met Val Met
      35           40           45
Ala Ile Ser Leu Asn Pro Gly Leu His Thr Pro Val Tyr Phe Phe Leu
      50           55           60
Thr Asn Leu Ala Leu Leu Asp Ile Val Cys Thr Ser Met Asp Asn Ser
      65           70           75           80
Arg Val Val Ala Val Leu Tyr Thr Val Val Ser Pro Thr Leu Asn Pro
      85           90           95
Ser Pro Thr Pro Cys Gly Thr Arg Thr Tyr Gln Xaa His Xaa Gly Glu
      100          105          110
Cys Phe Leu Ala Ser Gly Lys Arg Lys Gly Ser Phe Xaa Cys Glu Met
      115          120          125
Phe Gln Val Leu Thr Asn Xaa Phe Gln His Met Thr Leu Arg Ile Ser
      130          135          140
Cys Lys Gln Gln Gly Thr Arg Lys Xaa Leu Met Pro His Ile Tyr Lys
      145          150          155          160
Xaa Cys Ala Pro Ala Arg Gly Cys His His Ser Met Trp Asn Ser
      165          170          175

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<210> 1704

<211> 317

<212> PRT

<213> Unknown (H38g621 protein)

<220>

<223> Synthetic construct

<400> 1704

```

Met Glu Arg Thr Asn Asp Ser Thr Ser Thr Glu Phe Phe Leu Val Gly
 1           5           10           15
Leu Ser Ala His Pro Lys Leu Gln Thr Val Phe Phe Val Leu Ile Leu
      20           25           30
Trp Met Tyr Leu Met Ile Leu Leu Gly Asn Gly Val Leu Ile Ser Val
      35           40           45
Ile Ile Phe Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
      50           55           60
Asn Leu Ser Phe Leu Asp Val Cys Tyr Thr Ser Ser Ser Val Pro Leu
      65           70           75           80
Ile Leu Ala Ser Phe Leu Ala Val Lys Lys Lys Val Ser Phe Ser Gly
      85           90           95
Cys Met Val Gln Met Phe Ile Ser Phe Ala Met Gly Ala Thr Glu Cys
      100          105          110
Met Ile Leu Gly Thr Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Tyr
      115          120          125
Pro Leu Arg Tyr Pro Val Ile Met Ser Lys Gly Ala Tyr Val Ala Met
      130          135          140
Ala Ala Gly Ser Trp Val Thr Gly Leu Val Asp Ser Val Val Gln Thr
      145          150          155          160
Ala Phe Ala Met Gln Leu Pro Phe Cys Ala Asn Asn Val Ile Lys His
      165          170          175

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Phe Val Cys Glu Ile Leu Ala Ile Leu Lys Leu Ala Cys Ala Asp Il
 180 185 190
 Ser Ile Asn Val Ile Ser Met Thr Gly Ser Asn Leu Ile Val Leu Val
 195 200 205
 Ile Pro Leu Leu Val Ile Ser Ile Ser Tyr Ile Phe Ile Val Ala Thr
 210 215 220
 Ile Leu Arg Ile Pro Ser Thr Glu Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
 245 250 255
 Phe Met Tyr Ala Lys Pro Glu Ser Lys Ala Ser Val Asp Ser Gly Asn
 260 265 270
 Glu Asp Ile Ile Glu Ala Leu Ile Ser Leu Phe Tyr Gly Val Met Thr
 275 280 285
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Asn Ile Leu Cys Arg Lys Asn Phe Ser
 305 310 315

<210> 1705

<211> 318

<212> PRT

<213> Unknown (H38g622 protein)

<220>

<223> Synthetic construct

<400> 1705

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met
 130 135 140
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His
 165 170 175
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu
 195 200 205
 Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser
 210 215 220
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp

Leu Val Val Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Thr Ile Met Asn Arg Gln Val Cys Phe Leu Leu Leu Val
 130 135 140
 Val Ala Met Ile Gly Gly Phe Val His Ser Ala Phe Gln Ile Val Val
 145 150 155 160
 Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Val His Phe Ser Cys
 165 170 175
 Asp Met His Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Phe Ile
 180 185 190
 Gly Leu Thr Val Val Val Asn Ser Gly Ala Ile Cys Met Val Ile Phe
 195 200 205
 Asn Leu Leu Ile Ser Tyr Gly Val Ile Leu Ser Ser Leu Lys Thr
 210 215 220
 Tyr Ser Gln Glu Lys Arg Gly Lys Ala Leu Ser Thr Cys Ser Ser Gly
 225 230 235 240
 Ser Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Ile Tyr Val
 245 250 255
 Arg Pro Val Ser Asn Phe Pro Thr Asp Lys Phe Met Thr Val Phe Tyr
 260 265 270
 Thr Ile Ile Thr His Met Leu Ser Pro Leu Ile Tyr Thr Leu Arg Asn
 275 280 285
 Ser Glu Met Arg Asn Ala Ile Glu Lys Leu Leu Gly Lys Lys Leu Thr
 290 295 300
 Ile Phe Ile Ile Gly Gly Val Ser Val Leu Met
 305 310 315

<210> 1708

<211> 117

<212> PRT

<213> Unknown (H38g625 protein)

<220>

<223> Synthetic construct

<400> 1708

Arg Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala
 1 5 10 15
 Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln
 20 25 30
 Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile
 35 40 45
 Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe
 50 55 60
 Ser Gly Gly Arg Gln Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr
 65 70 75 80
 Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro
 85 90 95
 Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr
 100 105 110
 Thr Val Val Thr Pro
 115

<210> 1709

<211> 313

<212> PRT

<213> Unknown (H38g626 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1709

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Gly Leu Ser Asn Asn Val Thr Glu Phe Val Leu Leu Gly Asn Thr Gln
 1           5           10           15
Cys Pro Asp Val Gln Asn Ala Leu Phe Val Met Val Leu Leu Thr Tyr
          20           25           30
Val Val Ser Met Ala Gly Asn Leu Ala Val Val Ala Ile Ile Ser
          35           40           45
Ser Pro Ser Phe Gly Ser Pro Met Tyr Phe Phe Leu Thr Cys Leu Leu
          50           55           60
Phe Ile Tyr Ala Ala Tyr Ser Asn Thr Ile Ser Pro Lys Leu Ile Ile
65           70           75           80
Gly Leu Leu His Asp Lys Lys Thr Ile Phe Phe Thr Ala Cys Met Gly
          85           90           95
Gln Leu Phe Ile Asp His Leu Phe Gly Ala Glu Val Phe Leu Leu
          100          105          110
Val Gly Met Ser Tyr Asp Phe Tyr Val Ala Ile Ser Lys Pro Leu His
          115          120          125
Tyr Leu Thr Ile Met Asn Gln Gln Val Cys Ile Leu Leu Leu Val Val
          130          135          140
Ala Val Thr Gly Gly Phe Val Ser Cys Val Phe Gln Ile Val Val Val
          145          150          155          160
Tyr Thr Leu Ser Phe Cys Gly Pro Asn Val Thr Asp His Phe Val Cys
          165          170          175
Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe Ile
          180          185          190
Gly Leu Thr Val Val Ala Asn Gly Leu Ala Ile Cys Met Val Val Phe
          195          200          205
Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Asn Phe Lys Thr
          210          215          220
Tyr Ser Gln Glu Gly Arg Leu Lys Ala Leu Ser Ala Cys Ile Ser Tyr
          225          230          235          240
Ile Thr Val Thr Val Leu Phe Leu Val Pro Cys Ile Phe Leu Phe Val
          245          250          255
Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Met Thr Val Phe Tyr
          260          265          270
Thr Val Ile Ile His Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Leu Glu Met Arg Ile Ala Val Lys Ser Asn Val Lys Lys Leu Trp His
          290          295          300
Xaa Lys Leu Asn Tyr Ser Xaa Asn Glu
          305          310

```

<210> 1710

<211> 323

<212> PRT

<213> Unknown (H38g627 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1710

```

Met Arg Leu Ser Ser Asp Val Thr Ala Phe Val Leu Leu Gly Leu Thr
 1           5           10           15

```

Gln Asp Pro Asp Val Xaa Asn Ala Leu Phe Val Val His Leu Leu Thr
 20 25 30
 Tyr Ile Met Thr Met Val Gly Asn L u Pro Ile Val Val Thr Ile Ile
 35 40 45
 Ala Thr Pro Thr Leu Gly Ser Pro Val Tyr Phe Phe Ile Val Cys Leu
 50 55 60
 Ser Phe Ile Asp Val Val Tyr Ser Thr Thr Ile Pro Pro Lys Leu Ile
 65 70 75 80
 Val Ser Tyr Leu His Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Gly Gln Pro Phe Ile Asp His Leu Val Gly Gly Ala Glu Ala Phe Ile
 100 105 110
 Leu Leu Val Met Ala Tyr Asn Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Phe Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val
 130 135 140
 Val Ala Val Thr Ala Gly Phe Val His Ser Val Phe Gln Ile Leu Val
 145 150 155 160
 Ala Tyr Ser Leu Leu Phe Cys Gly Pro Asn Ile Ile Asp His Phe Phe
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala His Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Val Ala Asn Gly Gly Gly Ile Cys Met Val Leu
 195 200 205
 Phe Ile Leu Leu Leu Ile Ser Cys Gly Val Ile Leu Ile Ser Leu Lys
 210 215 220
 Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Pro Ile Asn Lys Phe Ile Thr Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Xaa Glu Met Lys Asn Ala Ile Gly Asn Leu Trp Cys Lys Tyr Xaa
 290 295 300
 Leu Xaa Ile Glu Xaa Glu Gly Thr Phe Ser Cys Arg Tyr Arg Val Met
 305 310 315 320
 Gln Val Lys

<210> 1711

<211> 235

<212> PRT

<213> Unknown (H38g628 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 1711

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Cys Tyr
 1 5 10 15
 Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe Ile Ser Glu Arg
 20 25 30
 Asn Ile Ile Ser Phe Pro Gly Cys Ile Thr Gln Leu Phe Phe Phe Cys
 35 40 45
 Phe Phe Val His Ser Glu Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp

50	55	60
Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Met Val Thr Thr Ser		
65	70	75
Pro Gln Ile Cys Ser Leu Leu Met Leu Gly Ser Tyr Val Met Gly Phe		80
	85	90
Ala Gly Ala Met Val His Thr Glu Cys Met Met Lys Leu Ile Phe Cys		95
	100	105
Asp Ser Asn Val Ile Asn His Asn Met Cys Asp Ile Phe Pro Leu Leu		110
	115	120
Gln Leu Ser Cys Ser Ser Thr Xaa Ala Asn Glu Leu Val Met Ser Val		125
	130	135
Ile Val Gly Thr Val Val Ile Val Ser Ser Leu Ile Ile Leu Ile Ser		140
	145	150
Tyr Ala Leu Ile Leu Phe Asn Ile Leu His Met Ser Ser Ala Glu Gly		155
	165	170
Trp Phe Lys Ala Ile Gly Thr Cys Gly Ser His Ile Ile Thr Val Gly		175
	180	185
Leu Phe Tyr Glu Phe Gly Leu Ile Thr His Val Lys Leu Ser Ser Asp		190
	195	200
Trp Tyr Met Gly Gln Gly Lys Phe Leu Ser Val Phe Tyr Thr Asn Val		205
	210	215
Val Pro Met Leu Asn Pro Phe Ile Tyr Cys Leu		220
225	230	235

<210> 1712

<211> 308

<212> PRT

<213> Unknown (H38g629 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1712

Met Arg Gln Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser	
1	5
Gln Tyr Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Ile	10
	20
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Ser Ile Ile	25
	35
Ala Ser Pro Phe Leu Gly Ser Pro Val Tyr Phe Phe Leu Ala Cys Leu	40
	50
Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Ser Pro Val Leu Ile	55
	65
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met	60
	75
Gly Gln Leu Phe Ile Glu His Leu Phe Gly Asp Thr Asp Val Phe Leu	80
	85
Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Lys Pro Leu	90
	100
Arg Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val	105
	115
Val Ala Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Leu Val	120
	130
Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Tyr His Phe Phe	135
	145
Cys Asn Ile Tyr Pro Leu Leu Asp Leu Glu Cys Thr Asp Thr Tyr Phe	150
	165
	170
	180
	185
	190

Val Gly Leu Ala Val Val Phe Asn Gly Gly Ala Ile Cys Met Val Ile
 195 200 205
 Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys
 210 215 220
 Thr Tyr Ser Pro Glu Gly Arg His Lys Ala Pro Phe Ile Cys Ser Ser
 225 230 235 240
 His Phe Ile Met Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Leu Thr Val Phe
 260 265 270
 Tyr Ser Val Ile Thr Pro Lys Leu Asn Pro Phe Ile Tyr Met Leu Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Ala Ile Glu Asn Leu Leu Gly Tyr Gln Ser
 290 295 300
 Gly Lys Thr Gly
 305

<210> 1713

<211> 230

<212> PRT

<213> Unknown (H38g630 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(230)

<223> Xaa = Any Amino Acid

<400> 1713

Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser Leu Pro Asp Ile Gly Phe
 1 5 10 15
 Thr Ser Ser Met Val Pro Lys Met Ile Val Asp Ile Xaa Ser His Ser
 20 25 30
 Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr Pro Met Ser Leu Phe Ala
 35 40 45
 Ile Phe Gly Gly Met Glu Glu Asn Met Leu Leu Ser Val Ile Ala Tyr
 50 55 60
 Asp Pro Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met
 65 70 75 80
 Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu Ser Phe Phe Ser Gln
 85 90 95
 Ser Leu Leu Asp Ala Gln Val His Asn Leu Ile Ala Leu Gln Met Thr
 100 105 110
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln
 115 120 125
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met
 130 135 140
 Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu
 145 150 155 160
 Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Arg Arg Val Ser Ser Ser
 165 170 175
 Gly Gly Lys Tyr Lys Ala Cys Ser Thr Cys Gly Ser His Leu Ser Val
 180 185 190
 Val Cys Xaa Phe Tyr Gly Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp
 195 200 205
 Val Ser Ser Ser Pro Gly Lys Ala Ala Val Ala Ser Val Met Tyr Thr
 210 215 220
 Val Val Thr Pro Met Leu
 225 230

<210> 1714
 <211> 227
 <212> PRT
 <213> Unknown (H38g632 protein)

<220>
 <223> Synthetic construct

<400> 1714
 Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu
 1 5 10 15
 Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala
 20 25 30
 Thr Gln Met Tyr Phe Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu
 35 40 45
 Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
 50 55 60
 His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala
 65 70 75 80
 Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp
 85 90 95
 Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe
 100 105 110
 Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu
 115 120 125
 Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro
 130 135 140
 Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu
 145 150 155 160
 Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser
 165 170 175
 Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr
 180 185 190
 Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu
 195 200 205
 Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu
 210 215 220
 Leu Ser Trp
 225

<210> 1715
 <211> 192
 <212> PRT
 <213> Unknown (H38g633 protein)

<220>
 <223> Synthetic construct

<400> 1715
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1 5 10 15
 Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu
 20 25 30
 Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu
 35 40 45
 His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asp Ile
 50 55 60
 Ala Tyr Ala Cys Asn Thr Val Pro Arg Met Leu Val Asn Leu Leu His
 65 70 75 80
 Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu
 85 90 95

Phe Ser Thr Phe Ala Val Thr Glu Cys Leu Leu Leu Val Val Met Ser
 100 105 110
 Tyr Asp Leu Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile
 115 120 125
 Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys
 130 135 140
 Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Arg Glu Ile Asn His Phe Leu Cys Glu Ile Leu Ala
 165 170 175
 Val Leu Arg Leu Gly Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile
 180 185 190

<210> 1716

<211> 308

<212> PRT

<213> Unknown (H38g634 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1716

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
 145 150 155 160
 Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
 165 170 175
 Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys
 180 185 190
 Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
 210 215 220
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Arg Gly Val Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu

275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
 290 295 300
 Arg Arg Pro Gln
 305

<210> 1717
 <211> 238
 <212> PRT
 <213> Unknown (H38g635 protein)

<220>
 <223> Synthetic construct

<400> 1717
 Met Tyr Leu Phe Leu Arg Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr
 1 5 10 15
 Ser Thr Ile Val Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg
 20 25 30
 Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser Leu Phe Ala Ile
 35 40 45
 Phe Gly Gly Met Glu Asp Asn Met Leu Leu Ser Val Met Ala Tyr Asp
 50 55 60
 Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met Asn
 65 70 75 80
 Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu Ser Phe Phe Phe Phe Leu
 85 90 95
 Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr
 100 105 110
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln
 115 120 125
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Val
 130 135 140
 Tyr Phe Pro Ala Val Ile Phe Val Phe Leu Pro Ile Ser Gly Thr Leu
 145 150 155 160
 Phe Ser Leu Lys Leu Phe Val Ser Ser Ile Leu Arg Val Ser Ser Ser
 165 170 175
 Gly Gly Lys Tyr Lys Thr Phe Ser Thr Cys Gly Ser His Leu Ser Val
 180 185 190
 Ile Cys Leu Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp
 195 200 205
 Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys
 210 215 220
 Met Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Arg
 225 230 235

<210> 1718
 <211> 321
 <212> PRT
 <213> Unknown (H38g636 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1718
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly
 1 5 10 15

```

Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys
      20                      25                      30
Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile
      35                      40                      45
Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala
      50                      55                      60
Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr
      65                      70                      75                      80
Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly
      85                      90                      95
Cys Leu Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser
      100                     105                     110
Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser
      115                     120                     125
Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met
      130                     135                     140
Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu
      145                     150                     155                     160
Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His
      165                     170                     175
Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr
      180                     185                     190
Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly
      195                     200                     205
Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr
      210                     215                     220
Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr
      225                     230                     235                     240
Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile
      245                     250                     255
Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe
      260                     265                     270
Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn
      275                     280                     285
Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val
      290                     295                     300
Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile
      305                     310                     315                     320
Pro

```

<210> 1719

<211> 291

<212> PRT

<213> Unknown (H38g637 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(291)

<223> Xaa = Any Amino Acid

<400> 1719

```

Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe Leu
  1                      5                      10                      15
Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      20                      25                      30
Met Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu Ser
      35                      40                      45
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Gln

```

50	55	60
Met Thr Val Asp Ile Gln Ser Arg Ser Arg Val Ile Ser Tyr Ala Gly		
65	70	75
Cys Leu Thr Gln Lys Ser Leu Phe Ala Ile Phe Gly Gly Thr Glu Glu		
	85	90
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys		
	100	105
His Pro Leu Tyr His Ser Ala Ile Met Asn Leu Cys Phe Cys Gly Phe		
	115	120
Leu Val Leu Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu		
	130	135
Tyr Asn Leu Ile Ala Leu Leu Met Thr Cys Phe Lys Glu Val Asp Ile		
145	150	155
Pro Asn Phe Phe Cys Asp Leu Ser Gln Leu Pro His Leu Ala Cys Cys		
	165	170
Asp Thr Phe Ile Asn Asn Ile Ile Met Tyr Phe Pro Thr Ala Ile Phe		
	180	185
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		
	195	200
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe		
	210	215
Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Arg		
225	230	235
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys		
	245	250
Gly Ala Val Ala Val Met Tyr Thr Val Val Thr Ser Met Leu Asn		
	260	265
Pro Phe Ile Tyr Ser Leu Gly Asn Arg Asp Ile Lys Ser Val Leu Arg		
	275	280
Arg Pro Gln		285
290		

<210> 1720

<211> 216

<212> PRT

<213> Unknown (H38g638 protein)

<220>

<223> Synthetic construct

<400> 1720

Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Thr Val Ile Ala		
1	5	10
Gly Leu Val Ile Gly Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala Ala		
	20	25
Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val Glu Asn Phe Leu Leu		
	35	40
Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val Cys Lys Pro Leu His		
	50	55
Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala Cys Leu Ala Ile Ile		
65	70	75
Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile His Ile Gly Glu Thr		
	85	90
Leu Ser Leu Phe Leu Tyr Gly Pro Asn Glu Val His Cys Phe Phe Cys		
	100	105
Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys Asp Arg His Val Asn		
	115	120
Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn Ile Phe Ser Ala Ile		
	130	135
Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Lys		
145	150	155
		160

```

Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Thr Cys Ala Ser
      165      170      175
His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr
      180      185      190
Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser
      195      200      205
Val Phe Tyr Thr Met Ile Ile Pro
      210      215

```

<210> 1721

<211> 216

<212> PRT

<213> Unknown (H38g639 protein)

<220>

<223> Synthetic construct

<400> 1721

```

Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala
 1      5      10      15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
      20      25      30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu
      35      40      45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
      50      55      60
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
      65      70      75      80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
      85      90      95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
      100      105      110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
      115      120      125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
      130      135      140
Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys
      145      150      155      160
Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr
      180      185      190
Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr
      195      200      205
Val Leu Tyr Thr Val Val Thr Pro
      210      215

```

<210> 1722

<211> 157

<212> PRT

<213> Unknown (H38g640 protein)

<220>

<223> Synthetic construct

<400> 1722

```

Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His Cys
 1      5      10      15
Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser Thr
      20      25      30
Ile His Thr Gly Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn Val

```

35	40	45
Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser Cys		
50	55	60
Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala Ph		
65	70	75
Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe Ile		
85	90	95
Ile Ala Ser Ile Leu Arg Ile Arg Ser Thr Glu Gly Arg Ser Lys Ala		
100	105	110
Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Gly Phe Phe Gly		
115	120	125
Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp		
130	135	140
Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Ile Val Val		
145	150	155

<210> 1723

<211> 325

<212> PRT

<213> Unknown (H38g641 protein)

<220>

<223> Synthetic construct

<400> 1723

Met Lys Thr Leu Cys Ser Phe Leu Gln Ile Ser Arg Asn Met His Gln		
1	5	10
Glu Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Leu Ser Asn		
20	25	30
Gln Ala Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Ser Met Tyr		
35	40	45
Val Val Thr Val Val Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu		
50	55	60
Asp Ile Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Tyr Leu Ser		
65	70	75
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val		
85	90	95
Asn Ile Gln Thr Asn Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr		
100	105	110
Gln Met Tyr Phe Ser Ile Val Phe Val Val Thr Asp Asn Leu Leu Leu		
115	120	125
Gly Thr Met Ala Phe Asp His Phe Val Ala Ile Cys His Pro Leu Asn		
130	135	140
Tyr Thr Thr Phe Met Arg Ala Arg Phe Gly Thr Leu Leu Thr Val Ile		
145	150	155
Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu		
165	170	175
Ile Gln Leu Leu Phe Cys Asp His Asn Thr Leu Pro His Phe Phe Cys		
180	185	190
Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Met Ile Asn		
195	200	205
Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe		
210	215	220
Val Leu Ile Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Gly		
225	230	235
Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser		
245	250	255
His Leu Thr Ile Ala Leu Leu Phe Tyr Gly Thr Thr Val Gly Val Tyr		
260	265	270
Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala		
275	280	285

Val Leu Phe Thr Val Val Thr Pro Met Met Asn Pro Phe Il Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gly Ala L u Arg Lys Leu Ile Asn Arg
 305 310 315 320
 Lys Ile Ser Ser Leu
 325

<210> 1724
 <211> 315
 <212> PRT
 <213> Unknown (H38g642 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1724
 Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asp Pro Gly Met Gln Lys Glu Leu Phe Val Met Phe Leu Phe Thr
 20 25 30
 Tyr Val Val Thr Val Leu Gly Asn Gln Leu Ile Val Val Thr Ile Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
 50 55 60
 Ser Phe Ile Asp Ala Ala Tyr Phe Thr Val Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Gln Thr Phe Met
 85 90 95
 Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Ala Phe Leu
 100 105 110
 Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Thr Leu
 115 120 125
 His Tyr Leu Thr Ile Met Thr Arg Gln Val Cys Ile Leu Ala Leu Leu
 130 135 140
 Val Ala Ala Thr Gly Gly Phe Val His Ser Val Phe Gln Ile Val Val
 145 150 155 160
 Val Tyr Ser Leu Pro Phe Cys Gly Ala Asn Val Ile Asp His Phe Ser
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Xaa Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Leu Cys Met Val Ile
 195 200 205
 Phe Thr Leu Leu Ile Ile Ser Tyr Arg Val Ile Leu Asn Ser Leu Lys
 210 215 220
 Thr Tyr Thr Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Ile Val Leu Phe Phe Ile Pro Cys Ile Ser Ile Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Ser Ile Asp Thr Phe Met Thr Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Tyr Thr Phe Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Val Ile Glu Lys Leu Leu Val Lys Lys Val
 290 295 300
 Thr Ile Phe Arg Ile Thr Gly Ser Ile Leu Met
 305 310 315

<210> 1725
 <211> 314
 <212> PRT
 <213> Unknown (H38g643 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1725
 Met Arg Gln Asn Lys Asn Asn Thr Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asp Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Thr
 20 25 30
 Xaa Leu Val Thr Thr Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Val Tyr Phe Xaa Leu Ala Cys Leu
 50 55 60
 Ser Cys Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Val Glu Leu Leu Ile Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Gly Gln Leu Phe Ile Glu His Leu Phe Gly Gly Thr Glu Ile Phe Ile
 100 105 110
 Leu Met Met Met Ala Cys Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val
 130 135 140
 Leu Ala Val Thr Gly Gly Phe Val His Ser Met Phe Gln Thr Val Val
 145 150 155 160
 Val Tyr Asn Leu Pro Phe Ser Gly Pro Asn Val Ile Asp Ile Asp His
 165 170 175
 Phe Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Phe Thr Asp Thr
 180 185 190
 Tyr Phe Ile Gly Leu Thr Val Val Val Asn Gly Gly Ala Met Cys Met
 195 200 205
 Val Ile Phe Thr Ile Leu Leu Ile Ser Tyr Gly Ile Ile Leu Asn Ser
 210 215 220
 Leu Lys Thr Tyr Ser Gln Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ser Pro His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Arg Pro Val Ser Thr Phe Pro Ile Asp Lys Phe Met Thr
 260 265 270
 Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn Ser Glu Met Arg Asn Ser Ile Glu Asn Leu Leu Cys Lys
 290 295 300
 Lys Ala Ile Cys Ser Xaa Asn Lys Ser Val
 305 310

<210> 1726
 <211> 315
 <212> PRT
 <213> Unknown (H38g644 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1726

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Glu Xaa Met Arg Gln Asn Asn Ser Ser Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Phe Ser Gln Asp Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu
 20          25          30
Leu Thr Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Thr
 35          40          45
Ile Ile Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala
 50          55          60
His Leu Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Ser Pro Val
 65          70          75          80
Leu Ile Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Xaa Ala
 85          90          95
Cys Met Gly Gln Leu Phe Ile Asp His Leu Phe Gly Gly Ser Glu Val
 100          105          110
Phe Leu Leu Val Val Met Ala Cys Asp Arg Cys Val Ala Ile Cys Lys
 115          120          125
Pro Leu His Tyr Leu Thr Ile Met Asn Arg Gln Val Cys Ile Leu Leu
 130          135          140
Leu Val Leu Ala Val Thr Gly Gly Phe Val His Pro Val Phe Gln Val
 145          150          155          160
Val Val Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His
 165          170          175
Phe Phe Cys Asp Ile Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr
 180          185          190
Tyr Phe Ile Gly Leu Thr Val Val Phe Asn Gly Gly Ala Met Arg Met
 195          200          205
Val Ile Leu Thr Leu Leu Leu Val Phe Tyr Gly Val Ile Leu Asn Ser
 210          215          220
Leu Lys Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys
 225          230          235          240
Ser Ser His Val Thr Val Val Ile Leu Phe Phe Ala Ser Cys Ile Phe
 245          250          255
Ile Tyr Val Arg Pro Val Ser Asn Phe Pro Val Asp Lys Phe Met Thr
 260          265          270
Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Phe Ile Cys Met
 275          280          285
Leu Arg Asn Ser Glu Met Arg Asn Ala Ile Glu Lys Leu Leu Cys Lys
 290          295          300
Met Asn Cys Ser Xaa Asn Lys Ser Val Pro Ser
 305          310          315

```

<210> 1727

<211> 313

<212> PRT

<213> Unknown (H38g645 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1727

Met Gly Leu Ser Asn Asn Val Thr Glu Leu Phe Leu Leu Gly Leu Thr

1		5		10		15									
Gln	Asp	Leu	Asp	Val	Gln	Asn	Ala	Leu	Phe	Val	Met	Phe	Leu	Leu	Thr
		20						25					30		
Tyr	Ile	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Val	Val	Thr	Ile	Ile
		35					40					45			
Ala	Thr	Pro	Ser	Leu	Gly	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ala	Cys	Leu
		50				55					60				
Ser	Phe	Ile	Asp	Ala	Val	Tyr	Ser	Thr	Thr	Ile	Tyr	Pro	Lys	Leu	Val
		65			70					75				80	
Val	Asp	Xaa	Leu	His	Asn	Xaa	Lys	Thr	Ile	Leu	Phe	Pro	Thr	Cys	Met
			85						90					95	
Gly	Gln	Pro	Leu	Thr	Asp	His	Leu	Phe	Gly	Gly	Val	Glu	Val	Phe	Phe
		100						105					110		
Leu	Leu	Val	Met	Ala	Cys	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu
		115					120					125			
His	Tyr	Phe	Thr	Ile	Met	Asn	Arg	Gln	Val	Phe	Ile	Leu	Leu	Leu	Val
		130				135					140				
Val	Ala	Val	Thr	Gly	Gly	Phe	Val	Arg	Ser	Val	Phe	Gln	Ile	Val	Val
		145			150					155				160	
Val	Tyr	Ser	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His	Phe	Phe
			165					170						175	
Cys	Asn	Met	Tyr	Pro	Leu	Met	Glu	Met	Ala	Xaa	Thr	Asp	Thr	Tyr	Phe
			180					185					190		
Ile	Gly	Leu	Thr	Val	Val	Phe	Lys	Val	Glu	Ala	Ile	Cys	Val	Val	Ile
		195					200					205			
Phe	Thr	Leu	Leu	Leu	Ile	Ser	Ser	Gly	Val	Ile	Leu	Ile	Ser	Leu	Lys
		210				215					220				
Thr	Tyr	Ser	Gln	Glu	Gly	Arg	His	Lys	Ala	Leu	Phe	Thr	Cys	Ser	Ser
		225			230					235				240	
Arg	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Val	Pro	Cys	Ile	Phe	Met	Tyr
			245						250					255	
Val	Arg	Pro	Val	Phe	Asn	Phe	Pro	Ile	Asp	Lys	Phe	Ile	Ile	Val	Phe
			260					265					270		
Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Met	Leu	Arg
		275					280				285				
Asn	Ser	Xaa	Thr	Arg	Asn	Ala	Ile	Glu	Asn	Pro	Xaa	Cys	Lys	Lys	Leu
		290				295					300				
Thr	Val	Asp	Arg	Ile	Arg	Val	Tyr	Ile							
		305			310										

<210> 1728

<211> 315

<212> PRT

<213> Unknown (H38g646 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1728

Met	Arg	Pro	Asn	Asn	Ser	Ile	Thr	Glu	Phe	Val	Leu	Leu	Gly	Phe	Ser
1				5					10					15	
Gln	Asp	Pro	Asp	Met	Gln	Asn	Thr	Leu	Phe	Val	Met	Phe	Leu	Leu	Thr
			20					25					30		
Tyr	Ile	Val	Thr	Val	Val	Gly	Asn	Leu	Leu	Val	Ala	Val	Thr	Ile	Ile
		35				40						45			
Val	Ser	Pro	Ser	Leu	Ser	Ser	Pro	Met	Xaa	Phe	Phe	Leu	Ala	Cys	Leu
		50				55						60			

```

Ser Leu Ile Asp Ala Val Leu Ser Thr Thr Ile Ser Pro Ile Leu Ile
65          70          75          80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
          85          90          95
Gly Gln Leu Phe Thr Asp His Leu Phe Gly Gly Thr Glu Ile Phe Leu
          100         105         110
Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
          115         120         125
His Tyr Leu Thr Ile Met Asn Arg Gln Val Ser Ile Leu Leu Leu Val
          130         135         140
Val Ala Met Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Ala Val
145         150         155         160
Leu Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
          165         170         175
Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Ser
          180         185         190
Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Met Cys Met Val Ile
          195         200         205
Phe Ala Leu Leu Leu Ile Ser Tyr Gly Val Ser Leu Asn Ser Leu Lys
          210         215         220
Thr Tyr Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser
225         230         235         240
His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
          245         250         255
Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Val Thr Val Phe
          260         265         270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Phe Leu Tyr Thr Leu Arg
          275         280         285
Asn Ser Glu Met Ile Asn Ala Ile Lys His Leu Leu Cys Lys Lys Leu
          290         295         300
Thr Ile Val Arg Ile Arg Val Ser Leu Leu Met
305          310          315

```

<210> 1729

<211> 322

<212> PRT

<213> Unknown (H38g647 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1729

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Met Gly Ser Ser Asn Asn Val Thr Glu Phe Val Leu Leu Ala Leu Thr
1          5          10          15
Gln Ala Pro Asp Val Gln Lys Val Leu Phe Val Met Phe Leu Phe Thr
          20          25          30
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Thr Val Val Thr Ile Phe
          35          40          45
Ala Ser Pro Ser Leu Gly Ser Pro Val Xaa Leu Phe Leu Ala Cys Leu
          50          55          60
Ser Leu Met Asp Ala Val Tyr Ser Thr Ser Phe Ser Pro Lys Leu Met
65          70          75          80
Ile Asp Leu Leu Cys Asp Lys Lys Thr Val Ser Phe Pro Ala Cys Met
          85          90          95
Gly Gln Leu Phe Ala Asp His Leu Phe Gly Gly Val Glu Val Phe Leu
          100         105         110
Phe Val Gly Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu

```

115	120	125
His Tyr Leu Ile Ile Val	Asn Arg Leu Val Cys	Ile Leu Leu Leu Val
130	135	140
Val Ala Val Thr Gly Gly	Phe Xaa His Ser Met	Phe Leu Phe Phe Xaa
145	150	155
Ile Tyr Leu Phe Phe Tyr	Val Asn Ser Met Phe	Gln Ile Val Val Val
165	170	175
Tyr Ser Leu Pro Phe Cys	Gly Ser Asn Val Ile	Asp His Ile Val Cys
180	185	190
Asp Met Tyr Pro Leu Leu	Glu Leu Ala Cys Ala	Asp Thr Tyr Phe Ile
195	200	205
Gly Leu Thr Val Ile Ala	Asn Gly Gly Ala Ile	Cys Met Val Ile Phe
210	215	220
Cys Leu Leu Leu Thr Ser	Tyr Gly Val Ile Leu	Asn Phe Leu Lys Thr
225	230	235
Tyr Ser Gln Glu Gly Arg	His Arg Thr Leu Ser	Thr Cys Ser Ser His
245	250	255
Ile Thr Val Val Val Leu	Phe Phe Val Pro Cys	Ile Phe Met Tyr Val
260	265	270
Arg Pro Val Ser Asn Phe	Pro Ile Asp Lys Phe	Ile Thr Glu Phe Tyr
275	280	285
Thr Val Ile Thr Pro Lys	Leu Asn Pro Leu Ile	Gln Pro Leu Arg Asn
290	295	300
Xaa Glu Met Arg Ile Thr	Met Lys Lys Leu Trp	Cys Xaa Thr Xaa Thr
305	310	315
Ile Val		320

<210> 1730

<211> 310

<212> PRT

<213> Unknown (H38g648 protein)

<220>

<223> Synthetic construct

<400> 1730

Met Lys Asn Lys	Asn Asn Val Thr	Glu Phe Ile Leu	Leu Gly Leu Thr
1	5	10	15
Gln Asn Pro Glu	Gly Gln Lys Val	Leu Phe Val Thr	Phe Leu Leu Ile
20	25	30	
Tyr Met Val Thr	Ile Met Gly Asn	Leu Leu Ile Ile	Val Thr Ile Met
35	40	45	
Ala Ser Gln Ser	Leu Gly Ser Pro	Met Tyr Phe Phe	Leu Ala Ser Leu
50	55	60	
Ser Phe Ile Asp	Thr Val Tyr Ser	Thr Ala Phe Ala	Pro Lys Met Ile
65	70	75	80
Val Asp Leu Leu	Ser Glu Lys Lys	Thr Ile Ser Phe	Gln Gly Cys Met
85	90	95	
Ala Gln Leu Phe	Met Asp His Leu	Phe Ala Gly Ala	Glu Val Ile Leu
100	105	110	
Leu Val Val Met	Ala Tyr Asp Arg	Tyr Met Ala Ile	Cys Lys Pro Leu
115	120	125	
His Glu Leu Ile	Thr Met Asn Arg	Arg Val Cys Val	Leu Met Leu Leu
130	135	140	
Ala Ala Trp Ile	Gly Gly Phe Leu	His Ser Leu Val	Gln Phe Leu Phe
145	150	155	160
Ile Tyr Gln Leu	Pro Phe Cys Gly	Pro Asn Val Ile	Asp Asn Phe Leu
165	170	175	
Cys Asp Leu Tyr	Pro Leu Leu Lys	Leu Ala Cys Thr	Asn Thr Tyr Val
180	185	190	

Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Ala Val Thr
 195 200 205
 Phe Ph Thr Ile Leu Leu Ser Tyr Gly Val Ile Leu His Ser Leu Lys
 210 215 220
 Thr Gln Ser Leu Glu Gly Lys Arg Lys Ala Phe Tyr Thr Cys Ala Ser
 225 230 235 240
 His Val Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Ala Arg Pro Asn Ser Thr Phe Pro Ile Asp Lys Ser Met Thr Val Val
 260 265 270
 Leu Thr Phe Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Lys
 275 280 285
 Asn Ala Glu Met Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Val
 290 295 300
 Ser Leu Ala Gly Lys Trp
 305 310

<210> 1731

<211> 275

<212> PRT

<213> Unknown (H38g649 protein)

<220>

<223> Synthetic construct

<400> 1731

Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser
 1 5 10 15
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp
 20 25 30
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu
 35 40 45
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe
 50 55 60
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met
 65 70 75 80
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn
 85 90 95
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Leu Val Val Ala Met Ile
 100 105 110
 Gly Gly Phe Val His Ser Val Val Gln Ile Val Phe Leu Tyr Ser Leu
 115 120 125
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr
 130 135 140
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr
 145 150 155 160
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu
 165 170 175
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln
 180 185 190
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val
 195 200 205
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val
 210 215 220
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile
 225 230 235 240
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met
 245 250 255
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg
 260 265 270
 Lys Arg Val

275

<210> 1732
 <211> 218
 <212> PRT
 <213> Unknown (H38g650 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1732

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Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr
           20           25           30
Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
           35           40           45
Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile Cys His Pro Leu
           50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
           65           70           75           80
Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln Val His Asn Leu
           85           90           95
Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
           100          105          110
Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
           115          120          125
Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu
           130          135          140
Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile
           145          150          155          160
Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Leu Ser Thr Cys
           165          170          175
Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly
           180          185          190
Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val
           195          200          205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
           210          215

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<210> 1733
 <211> 216
 <212> PRT
 <213> Unknown (H38g651 protein)

<220>
 <223> Synthetic construct

<400> 1733

```

Ser Met Ala Leu Met Leu Ile Cys Thr Thr Gly Pro Lys Met Ala Phe
 1           5           10           15
Asn Tyr Leu Ser Gly Ser Lys Ser His Phe Tyr Gly Cys Cys Ala Thr
           20           25           30
Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu
           35           40           45
Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His Pro Leu Arg
           50           55           60

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Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met Thr Ala Phe
 65 70 75 80
 Ser Trp Il Leu Gly Ser Thr Asp Gly Ile Ile Asp Val Val Ala Thr
 85 90 95
 Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr Ser Ile Phe
 115 120 125
 Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val
 130 135 140
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
 145 150 155 160
 Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser
 165 170 175
 His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr
 180 185 190
 Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Met Val Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1734

<211> 212

<212> PRT

<213> Unknown (H38g652 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1734

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
 1 5 10 15
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
 20 25 30
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu
 35 40 45
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
 50 55 60
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
 65 70 75 80
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
 85 90 95
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Glu His Tyr Phe Cys
 100 105 110
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
 115 120 125
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
 130 135 140
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
 145 150 155 160
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
 180 185 190
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
 195 200 205
 Thr Ile Thr Pro

210

<210> 1735
 <211> 223
 <212> PRT
 <213> Unknown (H38g653 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(223)
 <223> Xaa = Any Amino Acid

<400> 1735
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Xaa Gly Arg Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Val Cys
 65 70 75 80
 Cys Pro Cys Phe Phe Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser
 85 90 95
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 100 105 110
 Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala
 115 120 125
 Cys Cys Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala
 130 135 140
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys
 145 150 155 160
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Arg Tyr Lys
 165 170 175
 Ala Leu Ser Thr Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr
 180 185 190
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro
 195 200 205
 Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ala Val Thr Pro
 210 215 220

<210> 1736
 <211> 216
 <212> PRT
 <213> Unknown (H38g654 protein)

<220>
 <223> Synthetic construct

<400> 1736
 Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1 5 10 15
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20 25 30
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35 40 45
 Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50 55 60

Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65 70 75 80
 Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp L u Ser Thr Leu Thr
 85 90 95
 Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100 105 110
 Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115 120 125
 Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130 135 140
 Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145 150 155 160
 Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165 170 175
 His Leu Ile Val Val Ser Leu Phe Asn Ser Thr Ala Val Ser Val Tyr
 180 185 190
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195 200 205
 Leu Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 1737

<211> 218

<212> PRT

<213> Unknown (H38g655 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1737

Leu Pro Asp Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln Leu His Asn Leu
 85 90 95
 Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
 100 105 110
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
 115 120 125
 Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
 130 135 140
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser Ile
 145 150 155 160
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr
 165 170 175
 Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly
 180 185 190
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Pro Arg Lys Thr Ala Val
 195 200 205
 Ala Ser Val Met Tyr Thr Val Val Thr Pro

210

215

<210> 1738
 <211> 221
 <212> PRT
 <213> Unknown (H38g656 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(221)
 <223> Xaa = Any Amino Acid

<400> 1738
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Pro Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Asp Thr Glu Glu Asn Met Phe
 35 40 45
 Leu Ser Val Val Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Ser
 65 70 75 80
 Leu Ser Leu Val Phe Phe Phe Phe Ser Leu Leu Asp Ser Gln Leu
 85 90 95
 His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile
 100 105 110
 Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 115 120 125
 Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala Ile Phe
 130 135 140
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Cys Tyr Lys Ile Val
 145 150 155 160
 Ser Phe Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe
 165 170 175
 Ser Ala Cys Gly Ser His Leu Ser Val Val Tyr Xaa Phe Tyr Gly Thr
 180 185 190
 Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys
 195 200 205
 Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
 210 215 220

<210> 1739
 <211> 216
 <212> PRT
 <213> Unknown (H38g657 protein)

<220>
 <223> Synthetic construct

<400> 1739
 Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
 1 5 10 15
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
 20 25 30
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu L u
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr
 50 55 60

```

Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
65          70          75          80
Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met
          85          90          95
Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys
          100         105         110
Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn
          115         120         125
Glu Leu Leu Leu Phe Val Ala Ala Ala Phe Met Ala Val Ala Pro Leu
          130         135         140
Val Phe Ile Ser Val Pro Tyr Ala His Val Val Ala Ala Val Leu Gln
          145         150         155         160
Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
          165         170         175
His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr
          180         185         190
Met Arg Leu Gly Ser Val Glu Ser Ser Asp Lys Asp Lys Gly Val Gly
          195         200         205
Val Phe Met Thr Val Ile Asn Pro
          210         215

```

<210> 1740

<211> 212

<212> PRT

<213> Unknown (H38g658 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1740

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
1          5          10          15
Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
          20          25          30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
          35          40          45
Thr Val Met Ala Phe Asp Arg Cys Ala Ala Ile Cys Gln Pro Leu Arg
          50          55          60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65          70          75          80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
          85          90          95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
          100         105         110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
          115         120         125
Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
          130         135         140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
          145         150         155         160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
          165         170         175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
          180         185         190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
          195         200         205
Thr Ile Thr Pro

```

210

<210> 1741
 <211> 216
 <212> PRT
 <213> Unknown (H38g659 protein)

<220>
 <223> Synthetic construct

<400> 1741

```

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1           5           10           15
Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr
      20           25           30
Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
      35           40           45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50           55           60
Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
      65           70           75           80
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
      85           90           95
Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys
      100          105          110
Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn
      115          120          125
Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe
      130          135          140
Leu Leu Ile Leu Gly Ser Tyr Ala Arg Val Val Ser Ser Ile Leu Lys
      145          150          155          160
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser
      165          170          175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
      180          185          190
Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala
      195          200          205
Met Met Tyr Thr Val Val Thr Pro
      210          215

```

<210> 1742
 <211> 146
 <212> PRT
 <213> Unknown (H38g660 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(146)

<223> Xaa = Any Amino Acid

<400> 1742

```

Thr Leu Gln Asn Ile Thr Ser Thr Ser Ile Ile Phe Leu Leu Thr Gly
 1           5           10           15
Val Pro Gly Leu Glu Ala Phe His Thr Trp Ile Ser Ile Pro Phe Cys
      20           25           30
Phe Leu Ser Val Thr Ala Leu Leu Gly Asn Ser Leu Ile Leu Phe Ala
      35           40           45
Thr Ile Thr Gln Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser
      50           55           60

```

Met Leu Ser Ala Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr
 65 70 75 80
 Met Leu Ser Ile Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala
 85 90 95
 Cys Leu Ser His Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser
 100 105 110
 Ser Val Leu Leu Ala Met Ala Phe Asp Arg Leu Val Pro Ser Leu Ser
 115 120 125
 Pro Xaa Tyr Ala Met Ile Xaa Leu Thr Gln Ile Ala Lys Met Ser Ala
 130 135 140
 Val Tyr
 145

<210> 1743

<211> 334

<212> PRT

<213> Unknown (H38g661 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1743

Ala Gly Val Glu Asn Asp Asn Thr Ser Ser Phe Glu Gly Phe Ile Leu
 1 5 10 15
 Val Gly Phe Ser Asp Arg Pro His Leu Glu Leu Ile Val Phe Val Val
 20 25 30
 Val Leu Ile Phe Tyr Leu Leu Thr Leu Leu Gly Asn Met Thr Ile Val
 35 40 45
 Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Gly Ser Ile
 65 70 75 80
 Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr
 85 90 95
 Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Gly Val
 100 105 110
 Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Val
 115 120 125
 Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro Arg Leu Cys Gly
 130 135 140
 Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly Asn Ser Leu Ile
 145 150 155 160
 Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly His Arg Arg Val
 165 170 175
 Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly Met Ala Cys Val
 180 185 190
 Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu Ala Ile Phe Ile
 195 200 205
 Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Val Gly
 210 215 220
 Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe
 225 230 235 240
 Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr
 245 250 255
 Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr Ser Gln Asp Gln
 260 265 270
 Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr Pro Ser Val Asn

275	280	285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Met Lys		
290	295	300
Lys Val Leu Gly Lys Gly Ser Ala Glu Ile Xaa Xaa Gly Val Ile Lys		
305	310	315
Leu Trp Asp Cys Ile Leu Thr His Leu Leu Tyr Met Leu Leu		
325	330	

<210> 1744

<211> 275

<212> PRT

<213> Unknown (H38g662 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 1744

Leu Tyr Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Tyr		
1	5	10
Phe Leu Thr Met Leu Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr		
20	25	30
Met Pro Thr Val Met Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser		
35	40	45
Ser Val Gly Cys Phe Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val		
50	55	60
Val Glu Ser Gly Ser Leu Leu Ala Met Ala Tyr Asp Arg Leu Ile Ala		
65	70	75
Ile Arg Asn Pro Leu Arg Tyr Ala Ser Ile Ser Thr Asn Thr Arg Val		
85	90	95
Ile Ala Leu Gly Val Gly Leu Phe Leu Arg Gly Leu Val Ser Ile Leu		
100	105	110
Pro Val Ile Leu Arg Leu Phe Pro Phe Pro Tyr Gly Lys Ser His Val		
115	120	125
Ile Thr Arg Ala Phe Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys		
130	135	140
Ala Asp Ile Thr Ser Asn Lys Leu Tyr Pro Val Ile Leu Ile Ser Leu		
145	150	155
Thr Ile Ser Leu Asn Ser Leu Ile Thr Pro Ser Ser Tyr Ile Leu Ile		
165	170	175
Leu Asn Thr Val Ile Gly Ile Ala Ser Gly Glu Glu Lys Thr Lys Ala		
180	185	190
Leu Asn Thr Cys Ile Ser His Ile Ser Cys Val Leu Ile Ser Tyr Val		
195	200	205
Thr Val Met Gly Leu Thr Phe Ile Tyr Lys Phe Gly Lys Asn Val Pro		
210	215	220
Lys Val Val His Ile Ile Ile Ser Tyr Ile Tyr Phe Leu Phe Pro Pro		
225	230	235
Leu Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr		
245	250	255
Gly Ile Ile Arg Leu Leu Ser Lys His Arg Phe Ser Arg Xaa Thr Arg		
260	265	270
Ile Trp Lys		
275		

<210> 1745

<211> 219

<212> PRT

<213> Unkn wn (H38g663 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1745

```

Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Asn Met Leu
          35           40           45
Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr Cys Ser Ala Ile Phe Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
          65           70           75           80
Leu Ser Phe Phe Phe Phe Phe Leu Ser Leu Ser Asp Ser Gln Leu His
          85           90           95
Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro
          100          105          110
Asn Phe Phe Trp Glu Pro Ser Gln Leu Ser His Leu Ala Cys Cys Asp
          115          120          125
Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
          130          135          140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser
          145          150          155          160
Ile Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr
          165          170          175
Arg Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Ile
          180          185          190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Ala Ala
          195          200          205
Val Ala Ser Val Met Tyr Thr Val Ala Ile Pro
          210          215

```

<210> 1746

<211> 218

<212> PRT

<213> Unknown (H38g664 protein)

<220>

<223> Synthetic construct

<400> 1746

```

Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro Lys Met Val Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu
          35           40           45
Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu
          65           70           75           80
Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met
          85           90           95
Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe

```

<220>
<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amin Acid

<400> 1748

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
          35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
          65           70           75           80
Leu Ser Phe Phe Phe Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu
          85           90           95
Lys Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp
          100          105          110
Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Lys
          115          120          125
Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
          130          135          140
Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile Leu Arg Val
          145          150          155          160
Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
          165          170          175
Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly Gly Tyr Leu
          180          185          190
Ser Ser Asp Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser
          195          200          205
Val Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 1749

<211> 217

<212> PRT

<213> Unknown (H38g667 protein)

<220>

<223> Synthetic construct

<400> 1749

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
          20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
          35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
          50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
          65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
          85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
          100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
          115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro

```

130 135 140
 Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
 145 150 155 160
 Gly Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 165 170 175
 Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
 180 185 190
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
 195 200 205
 Ser Leu Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 1750
 <211> 216
 <212> PRT
 <213> Unknown (H38g668 protein)

<220>
 <223> Synthetic construct

<400> 1750
 Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Thr Val Ile Ala
 1 5 10 15
 Gly Leu Val Ile Gly Asp Glu Val Ile Ser Tyr Ser Ala Cys Ala Ala
 20 25 30
 Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val Glu Asn Phe Leu Leu
 35 40 45
 Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val Cys Lys Pro Leu His
 50 55 60
 Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala Cys Leu Ala Ile Ile
 65 70 75 80
 Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile His Ile Gly Glu Thr
 85 90 95
 Leu Ser Leu Phe Leu Asn Gly Pro Asn Glu Val His Cys Ile Phe Cys
 100 105 110
 Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys Asp Arg His Val Asn
 115 120 125
 Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn Ile Phe Ser Ala Ile
 130 135 140
 Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Glu
 145 150 155 160
 Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Asn Cys Ala Ser
 165 170 175
 His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr
 180 185 190
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser
 195 200 205
 Val Phe Tyr Thr Met Ile Ile Pro
 210 215

<210> 1751
 <211> 311
 <212> PRT
 <213> Unknown (H38g669 protein)

<220>
 <223> Synthetic construct

<400> 1751
 Met Ala Ala Glu Asn Ser Ser Ph Val Thr Gln Phe Ile Leu Ala Gly
 1 5 10 15

Leu Thr Asp Gln Pr Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr
 50 55 60
 Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Ser Glu Ser
 100 105 110
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu
 130 135 140
 Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr
 145 150 155 160
 Ala Cys Met Met Gly Val Thr Phe Cys Ala Asn Asn Leu Val Asn His
 165 170 175
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Cys Ala Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Leu Val Val Phe Val Val Val Gly Ile Asp Ile Gly
 195 200 205
 Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser
 210 215 220
 Ile Phe His Ile Asp Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
 245 250 255
 Phe Met Tyr Leu Lys Pro Phe Ser Leu Leu Ala Met Asn Gln Gly Lys
 260 265 270
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Lys Lys Ile
 290 295 300
 Leu Asn Lys Asn Ala Phe Ser
 305 310

<210> 1752

<211> 309

<212> PRT

<213> Unknown (H38g670 protein)

<220>

<223> Synthetic construct

<400> 1752

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
 85 90 95
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr

Val	Leu	Val	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro
	115						120					125			
Leu	Leu	Tyr	Met	Val	Thr	Met	Ser	Pro	Arg	Val	Cys	Phe	Leu	Leu	Met
	130					135					140				
Phe	Gly	Ser	Tyr	Val	Val	Gly	Phe	Ala	Gly	Ala	Met	Ala	His	Thr	Gly
145					150					155					160
Ser	Met	Leu	Arg	Leu	Thr	Phe	Cys	Asp	Ser	Asn	Val	Ile	Asp	His	Tyr
			165					170					175		
Leu	Cys	Asp	Val	Leu	Pro	Leu	Leu	Gln	Leu	Ser	Cys	Thr	Ser	Thr	His
		180						185					190		
Val	Ser	Glu	Leu	Val	Phe	Phe	Ile	Val	Val	Gly	Val	Ile	Thr	Met	Leu
	195						200					205			
Ser	Ser	Ile	Ser	Ile	Val	Ile	Ser	Tyr	Ala	Leu	Ile	Leu	Ser	Asn	Ile
	210				215						220				
Leu	Cys	Ile	Pro	Ser	Ala	Glu	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Thr	Trp
225					230					235					240
Gly	Ser	His	Ile	Ile	Ala	Val	Ala	Leu	Phe	Phe	Gly	Ser	Gly	Thr	Phe
			245					250						255	
Thr	Tyr	Leu	Thr	Thr	Ser	Phe	Pro	Gly	Ser	Met	Asn	His	Gly	Arg	Phe
		260						265					270		
Ala	Ser	Val	Phe	Tyr	Thr	Asn	Val	Val	Pro	Met	Leu	Asn	Pro	Ser	Ile
	275						280					285			
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Asp	Lys	Leu	Ala	Leu	Gly	Lys	Thr	Leu
	290					295					300				
Lys	Arg	Val	Leu	Phe											
305															

<210> 1753

<211> 297

<212> PRT

<213> Unknown (H38g671 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(297)

<223> Xaa = Any Amino Acid

<400> 1753

Met	Lys	Xaa	Met	Ala	Val	Glu	Asn	Asn	Ser	Ser	Val	Thr	Glu	Phe	Ile
1				5					10					15	
Leu	Val	Arg	Leu	Thr	Asn	Ser	Arg	Cys	Pro	Ser	Val	Leu	Phe	Leu	Met
		20					25					30			
Trp	Ser	Leu	Trp	Gly	Glu	Phe	Glu	His	Asn	Phe	Met	Ser	Leu	Asn	Ser
	35					40					45				
His	Leu	His	Thr	Pro	Thr	His	Phe	Phe	Leu	Phe	Thr	Leu	Ser	Phe	Ile
	50				55						60				
Asp	Val	Cys	Tyr	Ser	Phe	Val	Cys	Thr	Thr	Lys	Ile	Pro	Met	Gly	Phe
65					70				75						80
Ile	Ser	Glu	Arg	Asn	Ile	Ile	Ser	Phe	Val	Gly	Trp	Pro	Thr	Xaa	Leu
			85					90						95	
Tyr	Phe	Phe	Cys	Ile	Phe	Val	Lys	Glu	Pro	Lys	Asn	Gly	Val	Ile	Val
		100						105					110		
Gly	Ile	Met	Phe	Ser	Ala	Lys	Met	Leu	Val	Cys	Arg	Glu	Ile	Met	Asp
	115						120					125			
Xaa	Ser	Leu	Met	Xaa	Asn	Xaa	Lys	Met	His	Met	Ala	Leu	Glu	Arg	Ser
	130					135					140				
Asp	Phe	Arg	Met	Gly	Xaa	Thr	Gly	Ser	Ala	Thr	Lys	Lys	His	Leu	Ile
145					150					155					160

```

Ile Phe Leu Tyr Tyr Ser Asp Tyr Phe Gln Arg Xaa Xaa Gly Cys Arg
      165      170      175
Ala Leu Gly Gln Gly Ser Leu Ala Lys Gln Asp Thr Thr Leu Xaa Asn
      180      185      190
Cys Thr Cys Thr Leu Lys Ser Leu Leu His Ile Ile Ile Cys Phe Tyr
      195      200      205
Ile Trp Lys Gln Lys Lys Ile Ser Tyr Leu Tyr His Lys Ser Xaa Lys
      210      215      220
Met Asp Leu Tyr Lys Ile Cys His Val Leu Trp Val Thr His Lys Lys
      225      230      235      240
Asn Phe Leu Arg Pro Ser Ser Thr Ser Gln Met Val Gln Gly Lys Met
      245      250      255
Leu Leu Lys Gly Tyr Ile Xaa Phe Trp Arg Met Ser Leu Pro Met Cys
      260      265      270
Ala Ile Phe Ile Phe Val Arg Arg Tyr Tyr Tyr Leu Leu Lys Lys Leu
      275      280      285
Lys Thr Leu Leu Tyr Lys Asn Ser Tyr
      290      295

```

<210> 1754

<211> 313

<212> PRT

<213> Unknown (H38g672 protein)

<220>

<223> Synthetic construct

<400> 1754

```

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
  1      5      10      15
Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
      20      25      30
Val Val Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Ile Leu
      35      40      45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
      50      55      60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
      65      70      75      80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Tyr Val Gly
      85      90      95
Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
      100      105      110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
      130      135      140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
      145      150      155      160
Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
      165      170      175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
      180      185      190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
      195      200      205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
      210      215      220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
      245      250      255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val

```

<400>	1755															
Met	Asn	Trp	Val	Asn	Lys	Ser	Val	Pro	Gln	Glu	Phe	Ile	Leu	Leu	Val	
1				5				10						15		
Phe	Ser	Asp	Gln	Pro	Trp	Leu	Glu	Ile	Pro	Pro	Phe	Val	Met	Phe	Leu	
			20					25					30			
Phe	Ser	Tyr	Ile	Leu	Thr	Ile	Phe	Gly	Asn	Leu	Thr	Ile	Ile	Leu	Val	
		35					40					45				
Ser	His	Val	Asp	Phe	Lys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ser	Leu	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Ser	Thr	Val	Pro	Gln	
65					70					75					80	
Met	Leu	Val	Asn	Ile	Cys	Asn	Thr	Arg	Lys	Val	Ile	Ser	Tyr	Gly	Gly	
				85					90					95		
Cys	Val	Ala	Gln	Leu	Phe	Ile	Phe	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	
			100					105					110			
Leu	Leu	Leu	Ala	Val	Met	Cys	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	Arg	
			115				120					125				
Pro	Leu	His	Tyr	Ser	Ile	Ile	Met	His	Gln	Arg	Leu	Cys	Phe	Gln	Leu	
	130					135						140				
Ala	Ala	Ala	Ser	Trp	Ile	Ser	Gly	Phe	Ser	Asn	Ser	Val	Leu	Gln	Ser	
145					150					155					160	
Thr	Trp	Thr	Leu	Lys	Met	Pro	Leu	Cys	Gly	His	Lys	Glu	Val	Asp	His	
				165					170					175		
Phe	Phe	Cys	Glu	Val	Pro	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Val	Asp	Thr	
			180					185					190			
Thr	Ala	Asn	Glu	Ala	Glu	Leu	Phe	Phe	Ile	Ser	Val	Leu	Phe	Leu	Leu	
		195					200					205				
Ile	Pro	Val	Thr	Leu	Ile	Leu	Ile	Ser	Tyr	Ala	Phe	Ile	Val	Gln	Ala	
	210					215					220					
Val	Leu	Arg	Ile	Gln	Ser	Ala	Glu	Gly	Gln	Arg	Lys	Ala	Phe	Gly	Thr	
225					230					235					240	
Cys	Gly	Ser	His	Leu	Ile	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ala	Ile	
				245					250					255		
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Pro	Ser	Ser	Lys	Asp	Arg	Gly	Lys	
			260					265					270			
Met	Val	Ser	Leu	Phe	Cys	Gly	Ile	Ile	Ala	Pro	Met	Leu	Asn	Pro	Leu	
			275				280					285				
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Glu	Ala	Phe	Lys	Arg	Leu	
	290					295					300					
Val	Ala	Lys	Ser	Leu	Leu	Asn	Gln	Glu	Ile	Arg	Asn	Met	Gln	Met	Ile	
305					310					315					320	

Gln Arg Lys Phe Pro
355

<210> 1756

<211> 331

<212> PRT

<213> Unknown (H38g674 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1756

Met	Ala	Pro	Gly	Asn	Gly	Phe	Phe	Met	Thr	Lys	Ile	Ile	Leu	Leu	Glu
1				5				10					15		
Leu	Thr	Asp	Gln	Pro	Asp	Leu	Gln	Leu	Pro	Leu	Phe	Phe	Leu	Phe	Leu
		20					25						30		
Val	Tyr	Gly	His	Cys	Val	Gly	Lys	Phe	Gly	Leu	Val	Thr	Leu	Val	Val
	35					40					45				
Leu	Asn	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Asn	Leu
	50				55					60					
Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Thr	Pro	Gln	Met	Leu
65				70					75					80	
Met	Asn	Phe	Ile	Thr	Gln	Lys	Asp	Ile	Ile	Ser	His	Met	Gly	Cys	Met
			85					90					95		
Ser	Gln	Leu	Phe	Phe	Ala	Leu	Phe	Phe	Phe	Gly	Ile	Ser	Glu	Cys	
		100					105					110			
Tyr	Val	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Ala	Cys	His	His	Asp	His
	115					120						125			
His	Val	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Asn	Ile	Ala	Met	Ser	Pro
	130				135					140					
Lys	Val	Tyr	Ser	His	Leu	Met	Leu	Gly	Leu	Tyr	Leu	Leu	Ala	Phe	Ser
145				150					155						160
Ser	Ala	Met	Ala	His	Thr	Gly	Cys	Met	Leu	Arg	Leu	Thr	Phe	Cys	Asp
			165					170						175	
Ala	Asn	Thr	Ile	His	Pro	Tyr	Leu	Cys	Asp	Ile	Leu	Pro	Leu	Leu	Gln
		180					185					190			
Leu	Ser	Cys	Thr	Gly	Thr	Tyr	Ile	Asn	Glu	Leu	Val	Val	Ser	Thr	Ala
	195					200						205			
Ala	Val	Ile	Ile	Ser	Thr	Val	Thr	Ile	Phe	Ile	Ser	Cys	Gly	Cys	Ser
	210					215					220				
Ser	Tyr	Ile	Ile	Leu	His	Ile	Asn	Ser	Lys	Glu	Gly	Arg	Ser	Lys	Ala
225				230					235					240	
Leu	Asn	Thr	Cys	Ser	Ser	Asn	Leu	Ile	Ala	Val	Ser	Leu	Met	Phe	Gly
			245					250						255	
Ser	Cys	Ala	Phe	Met	Cys	Leu	Lys	Pro	Ser	Ser	Ala	Gly	Ser	Met	Asp
		260						265					270		
Glu	Gly	Lys	Ile	Ser	Ser	Val	Phe	Tyr	Thr	Asn	Thr	Ala	Pro	Leu	Met
	275					280						285			
Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Met	Asn	Lys	Met	Phe	Asn	Phe	Leu	Xaa
	290					295					300				
Glu	Lys	Asn	Pro	Ser	Arg	Lys	Lys	Phe	Xaa	Leu	Glu	Ile	Val	Ser	Phe
305				310					315						320
Cys	Ala	Cys	Ile	Phe	Arg	Thr	Gly	Ser	Phe	Cys					
			325					330							

<210> 1757

<211> 332

<212> PRT

<213> Unknown (H38g675 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(332)

<223> Xaa = Any Amino Acid

<400> 1757

```

Met Ala Pro Gly Asn Gly Ser Leu Met Asn Glu Phe Ile Leu Val Gly
 1           5           10           15
Leu Thr Asp Xaa Pro Asp Leu Xaa Leu Pro Leu Phe Phe Met Phe Leu
          20           25           30
Val Met Tyr Val Val Thr Val Ile Arg Asn Phe Val Leu Val Ile Leu
          35           40           45
Thr Met Arg Asn Ser Arg Leu His Thr Pro Lys Tyr Phe Phe Leu Ser
          50           55           60
Lys Leu Phe Phe Thr Asp Leu Cys Tyr Ser Ser Val Phe Ile Leu Gln
          65           70           75           80
Leu Pro Arg Lys Cys Ile Ser Glu Glu Asn Val Ile Ser Tyr Met Val
          85           90           95
Cys Met Ile Xaa Leu Phe Phe Phe Phe Phe Phe Phe Phe Phe Xaa
          100          105          110
Phe Ile Ser Glu Cys Tyr Met Leu Thr Ser Met Ala Tyr Asp Cys Cys
          115          120          125
Val Ala Ile Cys Tyr Pro Leu Leu Tyr His Ile Ala Met Ser Pro Lys
          130          135          140
Val Cys Phe Ser Leu Met Leu Gly Ser Tyr Phe Leu Ser Phe Ser Gly
          145          150          155          160
Ala Met Ala His Thr Gly Cys Met Leu Arg Leu Thr Cys Asp Ala Asn
          165          170          175
Thr Ile Asn His Tyr Phe Arg Asp Ile Leu Pro Val Phe Gln Leu Ser
          180          185          190
Cys Thr Ser Thr Tyr Ile Asn Glu Leu Val Val Phe Ile Val Ala Gly
          195          200          205
Ile Asn Thr Ile Val Pro Thr Val Thr Val Phe Ile Ser Tyr Gly Asp
          210          215          220
Ile Leu Ser Arg Ile Leu His Ile Ser Ser Asn Glu Gly Arg Ser Lys
          225          230          235          240
Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe
          245          250          255
Gly Leu Ser Ala Phe Met Tyr Leu Lys Pro Ser Ser Ala Gly Ser Met
          260          265          270
Asp Glu Gly Lys Phe Ser Ser Val Phe Tyr Met Asn Gly Leu Pro Met
          275          280          285
Met Ser Ser Leu Ile Tyr Ser Leu Arg Arg Lys Asp Val Lys Phe Ala
          290          295          300
Met Gly Lys Ser Leu Ser Arg Arg Met Phe Leu Pro Xaa Thr Thr Phe
          305          310          315          320
Leu Cys Val Cys Ser Tyr Arg Met Gly Ile Leu Cys
          325          330

```

<210> 1758

<211> 313

<212> PRT

<213> Unknown (H38g676 protein)

<220>

<223> Synthetic construct

<400> 1758

```

Met Asp Ser Leu Asn Gln Thr Arg Val Thr Glu Phe Val Phe Leu Gly
 1          5          10          15
Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala Phe Ser
          20          25          30
Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile Ala
          35          40          45
Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val Pro Lys
65          70          75          80
Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe Asp Asn
          85          90          95
Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile
          100          105          110
Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr
          115          120          125
Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu
130          135          140
Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly Gln Thr
145          150          155          160
Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser
          165          170          175
Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu
          195          200          205
Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser
210          215          220
Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys Ile Phe
          245          250          255
Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser
          260          265          270
Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Thr
          275          280          285
Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg Gln Arg
290          295          300
Gln Val Phe Phe Thr Lys Ser Tyr Thr
305          310

```

<210> 1759

<211> 331

<212> PRT

<213> Unknown (H38g677 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1759

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Met Ala Pro Gly Asn Ile Ser Thr Val Ala Glu Leu Ile Leu Val Gly
 1          5          10          15
Leu Lys Asp Gln Thr Asp Leu Gln Pro Pro Leu Phe Phe Leu Phe Leu
          20          25          30
Val Met Gly Val Val Ala Gly Xaa Gly Asn Leu Gly Leu Val Thr Leu

```

```

      35              40              45
Ile Val Phe Ser Ser His Phe His Ala Pro Met Tyr Phe Phe Leu Phe
  50              55              60
Ser Leu Ala Phe Ile Asp His Phe Tyr Ser Ser Val Phe Ile Pro Lys
  65              70              75              80
Met Leu Met Asn Phe Ile Thr Glu Lys Asn Ile Ile Ser Tyr Ala Gly
      85              90              95
Cys Met Ser Ala Phe Phe Ser Phe Phe Phe Cys Phe Phe Val Ile
      100              105              110
Ser Glu Cys Tyr Val Leu Thr Ser Met Val Ser Asp His Tyr Val Ala
      115              120              125
Met Ala Ile Cys Asn Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro Lys
      130              135              140
Val Cys Ser Ser His Met Leu Gly Ser Tyr Phe Trp Pro Phe Ser Gly
      145              150              155              160
Ala Met Ala His Thr Arg Cys Met Leu Lys Leu Thr Ser Cys Glu Ala
      165              170              175
Asn Thr Ile Asn His Tyr Phe Cys Asp Thr Leu His Leu Leu Gln Leu
      180              185              190
Ser Cys Thr Ser Thr Tyr Val Ser Glu Leu Met Val Phe Ile Ala Ala
      195              200              205
Gly Ile Ile Phe Thr Val Pro Ser Ile Thr Ile Phe Ile Ser Tyr Phe
      210              215              220
Phe Thr Ser Pro Leu Ser Tyr His Phe Thr Glu Gly Trp Ser Lys Phe
      225              230              235              240
Phe Ser Thr Cys Ser Phe His Lys Ile Ala Ile Ser Leu Phe Phe Gly
      245              250              255
Leu Gly Ala Ser Leu Cys Leu Lys Leu Ser Ser Thr Gly Thr Ile Asn
      260              265              270
Glu Gly Lys Ile Ser Ser Val Phe His Ile Asp Val Val Pro Met Ile
      275              280              285
Asn Ser Ser Ile Tyr Ser Leu Arg Asn Asn Asp Val Lys Leu Ala Trp
      290              295              300
Arg Lys Ile Leu Ser Trp Arg Lys Phe Pro Phe Glu Thr Ile Ser Leu
      305              310              315              320
His Ala Tyr Ser Tyr Arg Thr Arg Arg Phe Cys
      325              330

```

<210> 1760

<211> 322

<212> PRT

<213> Unknown (H38g678 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1760

```

Met Ser Val Val Glu Ala Asn Asn Ile Ser Gly Pro Val Ser Glu Phe
  1              5              10              15
Ile Leu Leu Gly Phe Pro Cys Arg Cys Arg Glu Thr Lys Ile Leu Leu
      20              25              30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Met Gly Asn Thr
      35              40              45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met
      50              55              60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Ile Ser
      65              70              75              80

```

Ser Asp Val Pro Asn Met Leu Ala Asn Leu Ile Ser His Il Lys S r
 85 90 95
 Ile Ser Tyr Ala Gly Cys Leu Leu Gln Phe Phe Tyr Phe Ser Met Cys
 100 105 110
 Ala Ala Glu Gly Tyr Phe Leu Ser Val Met Ser Phe Asp Arg Phe Leu
 115 120 125
 Thr Ile Cys Arg Pro Leu His Tyr Pro Thr Val Met Thr His His Leu
 130 135 140
 Cys Val Xaa Leu Val Ala Phe Cys Arg Ala Gly Gly Phe Leu Ser Ile
 145 150 155 160
 Leu Met Pro Ala Val Leu Met Ser Arg Val Pro Phe Cys Gly Pro Asn
 165 170 175
 Ile Thr Asp His Phe Phe Cys Asn Leu Gly Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ala Pro Val Pro Lys Thr Thr Leu Thr Cys Ala Thr Val Ser Ser
 195 200 205
 Leu Ile Ile Phe Ile Thr Phe Leu Tyr Ile Leu Gly Ser His Ile Leu
 210 215 220
 Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr
 245 250 255
 Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pro
 260 265 270
 Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr Ala Thr Pro Phe
 275 280 285
 Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala
 290 295 300
 Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Tyr Trp Asn Thr
 305 310 315 320
 Leu Lys

<210> 1761

<211> 335

<212> PRT

<213> Unknown (H38g679 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1761

Met Glu Glu Ala Ile Leu Leu Asn Gln Thr Ser Leu Val Thr Tyr Phe
 1 5 10 15
 Arg Leu Arg Gly Leu Ser Val Asn His Lys Ala Arg Ile Ala Met Phe
 20 25 30
 Ser Met Phe Leu Ile Phe Tyr Val Leu Thr Leu Ile Gly Asn Val Leu
 35 40 45
 Ile Val Ile Thr Ile Ile Tyr Asp His Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ser Asn Leu Ser Phe Ile Asp Val Cys His Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Met Leu Arg Asp Val Trp Ser Glu Glu Lys Leu Ile
 85 90 95
 Ser Phe Asp Ala Cys Val Thr Gln Met Phe Phe Leu His Leu Phe Ala
 100 105 110
 Cys Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val

115	120	125
Ala Ile Cys Lys Pro Leu Gln Tyr Met Ile Val Met Asn Trp Lys Val		
130	135	140
Cys Val Leu Leu Ala Val Ala Leu Trp Thr Gly Gly Thr Ile His Ser		
145	150	155
Ile Ala Leu Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro Asp		
165	170	175
Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala		
180	185	190
Cys Ile Asp Thr Pro Tyr Val Leu Glu Ile Leu Ile Val Ser Asn Ser		
195	200	205
Gly Leu Ile Ser Val Val Cys Phe Val Val Leu Val Val Ser Tyr Ala		
210	215	220
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Lys Gly Lys Trp Lys		
225	230	235
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu		
245	250	255
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Thr Ser Leu Pro Glu		
260	265	270
Asp Lys Ala Val Ser Val Phe Phe Thr Ala Val Thr Pro Leu Leu Asn		
275	280	285
Pro Ile Ile Tyr Thr Leu Arg Asn Glu Glu Met Lys Ser Ala Leu Asn		
290	295	300
Lys Leu Val Gly Arg Lys Glu Arg Lys Glu Glu Lys Xaa Lys Cys Pro		
305	310	315
Thr Ser Leu Gly Tyr Val Val Leu Gln Ile Lys Glu Ala Pro Cys		
325	330	335

<210> 1762

<211> 161

<212> PRT

<213> Unknown (H38g680 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(161)

<223> Xaa = Any Amino Acid

<400> 1762

Thr Gly Thr Gly Xaa Trp Leu Cys His Ala Met Ile Leu Thr Pro Leu	
1	5
Thr Phe Gln Leu Pro Tyr Cys Gly Leu Thr Arg Trp Asp Tyr Tyr Phe	
20	25
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu	
35	40
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys	
50	55
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser	
65	70
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser	
85	90
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile	
100	105
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile	
115	120
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu	
130	135
Arg Asn Lys Asp Val Lys Ser Asp Gln Pro Xaa Gly Met Tyr Phe Pro	
145	150
	155
	160

Arg

<210> 1763
 <211> 134
 <212> PRT
 <213> Unknown (H38g681 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(134)
 <223> Xaa = Any Amino Acid

<400> 1763
 Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His
 1 5 10 15
 Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe
 20 25 30
 Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu
 35 40 45
 Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly
 50 55 60
 Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly
 65 70 75 80
 Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe
 85 90 95
 Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa
 100 105 110
 Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr
 115 120 125
 Phe Leu Arg Val Leu Ser
 130

<210> 1764
 <211> 311
 <212> PRT
 <213> Unknown (H38g682 protein)

<220>
 <223> Synthetic construct

<400> 1764
 Met Ala Thr Ser Asn His Ser Ser Gly Ala Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr Gln Arg Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Phe Leu
 35 40 45
 Ile Ala Leu Ser Ser Gln Leu Tyr Pro Pro Val Tyr Tyr Phe Leu Ser
 50 55 60
 His Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Pro Glu Glu Asn Ile Ile Ser Phe Leu Glu
 85 90 95
 Cys Ile Thr Gln Leu Tyr Phe Phe Leu Ile Phe Val Ile Ala Glu Gly
 100 105 110
 Tyr Leu Leu Thr Ala Met Glu Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu Leu Tyr Asn Ile Val Met Ser His Arg Val Cys Ser Ile Met

130	135	140
Met Ala Val Val Tyr Ser Leu Gly Phe Leu Trp Ala Thr Val His Thr		
145	150	155
Thr Arg Met Ser Val Leu Ser Phe Cys Arg Ser His Thr Val Ser His		160
	165	170
Tyr Phe Cys Asp Ile Leu Pro Leu Leu Thr Leu Ser Cys Ser Ser Thr		175
	180	185
His Ile Asn Glu Ile Leu Leu Phe Ile Ile Gly Gly Val Asn Thr Leu		190
	195	200
Ala Thr Thr Leu Ala Val Leu Ile Ser Tyr Ala Phe Ile Phe Ser Ser		205
	210	215
Ile Leu Gly Ile His Ser Thr Glu Gly Gln Ser Lys Ala Phe Gly Thr		220
225	230	235
Cys Ser Ser His Leu Leu Ala Val Gly Ile Phe Phe Gly Ser Ile Thr		240
	245	250
Phe Met Tyr Phe Lys Pro Pro Ser Ser Thr Thr Met Glu Lys Glu Lys		255
	260	265
Val Ser Ser Val Phe Tyr Ile Thr Ile Ile Pro Met Leu Asn Pro Leu		270
	275	280
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Met		285
	290	295
Thr Arg Gly Arg Gln Ser Ser		300
305	310	

<210> 1765

<211> 316

<212> PRT

<213> Unknown (H38g683 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1765

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val	
1	5
Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met	10
	20
Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile	25
	30
Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe	35
	40
50	55
Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile	60
65	70
Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser	75
	80
	85
Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala	90
	95
	100
Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala	105
	110
	115
Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys	120
	125
	130
Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala	135
145	150
Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu	155
	160
	165
Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys	170
	175
	180
	185
	190

```

Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
   195                               200               205
Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val
   210                               215               220
Leu Ser Ala Ile L u Arg Ile Pr Ser Cys Thr Gly Gln Lys Lys Ala
  225                               230               235               240
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly
                               245               250               255
Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu
                               260               265               270
Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe
   275                               280               285
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu
   290                               295               300
Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu
  305                               310               315

```

<210> 1766

<211> 315

<212> PRT

<213> Unknown (H38g684 protein)

<220>

<223> Synthetic construct

<400> 1766

```

Pro Val Arg Thr Leu Glu Thr Thr Asn Ile Thr Gly Phe Val Asn Glu
  1                               5               10               15
Phe Ile Leu Leu Gly Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu
   20                               25               30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr
   35                               40               45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met
   50                               55               60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser
  65                               70               75               80
Ser Asp Val Pro Ile Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser
   85                               90               95
Ile Ser Cys Ala Gly Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys
  100                               105              110
Ala Ala Glu Cys Leu Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro
  115                               120              125
Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Leu Met Thr His His Val
  130                               135              140
Cys Ala His Phe Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu
  145                               150              155              160
Leu Thr Pro Leu Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn
  165                               170              175
Thr Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser
  180                               185              190
Cys Ala Pro Ile Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala
  195                               200              205
Leu Ile Ile Phe Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys
  210                               215              220
Val Leu Ser Thr Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys
  225                               230              235              240
Ala Phe Ser Thr Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr
  245                               250              255
Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His
  260                               265              270
Gly Ile Lys Lys Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe

```

275 280 285
 Phe Asn Pro Leu Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala
 290 295 300
 Leu Lys Lys Phe Leu Arg Asn Arg His Thr Val
 305 310 315

<210> 1767
 <211> 316
 <212> PRT
 <213> Unknown (H38g685 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(316)
 <223> Xaa = Any Amino Acid

<400> 1767
 Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Lys Phe Ile Leu Met
 1 5 10 15
 Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr
 20 25 30
 Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile
 35 40 45
 Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe
 50 55 60
 Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Ala
 65 70 75 80
 Pro Asn Met Leu Trp Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe
 85 90 95
 Leu Gly Cys Ala Thr Xaa Met Tyr Phe Val Phe Phe Phe Gly Val Ala
 100 105 110
 Glu Cys Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Leu Ala
 130 135 140
 Lys Leu Ala Ala Thr Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val
 145 150 155 160
 Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val
 165 170 175
 Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala
 180 185 190
 Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val
 195 200 205
 Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr His Ile Ala
 210 215 220
 Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser
 245 250 255
 Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly
 260 265 270
 Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser
 290 295 300
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu
 305 310 315

<210> 1768

<211> 324
 <212> PRT
 <213> Unknown (H38g686 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1768
 Met Ala Val Glu Asn Asp Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Gln Pro Glu Ile Xaa Leu Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Val Asn Tyr Met Thr Thr Met Val Gly Asn Leu Ser Leu Ile Asn Leu
 35 40 45
 Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Phe Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Ile Ser Glu Arg Asn Ile Ile Ser Phe Pro Gly
 85 90 95
 Cys Val Thr Gln Leu Phe Phe Phe Cys Phe Phe Val His Ser Glu Cys
 100 105 110
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Met Val Thr Thr Ser Pro Gln Ile Cys Ser Leu Leu
 130 135 140
 Met Leu Gly Ser Tyr Val Met Gly Phe Ala Gly Ala Met Val His Thr
 145 150 155 160
 Glu Cys Met Met Lys Leu Ile Phe Cys Asp Ser Asn Val Ile Asn His
 165 170 175
 Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Ser Ser Thr
 180 185 190
 Xaa Ala Asn Glu Leu Val Met Ser Val Ile Val Gly Thr Val Val Ile
 195 200 205
 Val Ser Ser Leu Ile Ile Leu Ile Ser Tyr Ala Leu Ile Leu Phe Asn
 210 215 220
 Ile Leu His Met Ser Ser Ala Glu Gly Trp Phe Lys Ala Ile Gly Thr
 225 230 235 240
 Cys Gly Ser His Ile Ile Thr Val Gly Leu Phe Tyr Glu Phe Gly Leu
 245 250 255
 Ile Thr His Val Lys Leu Ser Ser Asp Trp Tyr Met Gly Gln Gly Lys
 260 265 270
 Phe Leu Ser Val Phe Tyr Thr Asn Glu Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Glu Thr
 290 295 300
 Leu Asn Lys Ile Thr Asn Xaa Val Glu Pro Met Val Leu Pro Xaa Pro
 305 310 315 320
 Leu Ser Asn Cys

<210> 1769
 <211> 331
 <212> PRT
 <213> Unknown (H38g687 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1769

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Met Arg Xaa Ile Asn Gln Thr Gln Val Ile Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
 20           25           30
Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
 35           40           45
Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50           55           60
Asn Leu Ser Leu Ala Asp Leu Tyr Phe Ser Thr Asn Ile Leu Pro Gln
 65           70           75           80
Ala Leu Val His Leu Leu Ser Ile Asn Asn Leu Ile Ala Phe Thr Leu
 85           90           95
Ser Leu Thr Gln Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
100           105           110
Ala Leu Ile Ala Val Met Ser Tyr Asn Pro Tyr Val Ala Ile Cys Asn
115           120           125
Pro Leu His Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu
130           135           140
Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
145           150           155           160
Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
165           170           175
Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr
180           185           190
His Ala Ser Glu Met Ala Ile Tyr Leu Thr Gly Val Val Ile Leu Leu
195           200           205
Ile Pro Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr
210           215           220
Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
225           230           235           240
Cys Gly Ser His Leu Met Val Val Ile Leu Leu Asn Gly Ser Ala Ile
245           250           255
Leu Thr Cys Met Thr Pro Lys Ser Ser Lys Gln Gln Xaa Lys Ser Val
260           265           270
Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
275           280           285
Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
290           295           300
Arg Asn Phe Pro Xaa Arg Leu Gly Ile His Thr Asp Ser Glu Leu Arg
305           310           315           320
Glu Pro Phe Gly Phe Leu Leu Pro Lys Thr Cys
325           330

```

<210> 1770

<211> 183

<212> PRT

<213> Unknown (H38g688 protein)

<220>

<223> Synthetic construct

<400> 1770

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1           5           10           15

```

Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
 20 25 30
 Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
 35 40 45
 Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50 55 60
 Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
 65 70 75 80
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
 85 90 95
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
 100 105 110
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile
 130 135 140
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu
 145 150 155 160
 Thr Ile Ser Val Pro Phe Cys Gly Pro Asn Asp Ile Asp His Tyr Ser
 165 170 175
 Arg Asp Val Tyr Pro Leu Leu
 180

<210> 1771

<211> 224

<212> PRT

<213> Unknown (H38g689 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400> 1771

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ser Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Arg His Ala
 35 40 45
 Pro Glu Val Met Ala Tyr Asp Leu Phe Val Ala Ile Cys His Leu Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Phe Val Arg Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Leu Leu Leu Val Phe Phe Phe Phe Leu Ile Ser Leu Leu Asp
 85 90 95
 Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp
 100 105 110
 Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu
 115 120 125
 Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met Tyr Phe Pro Ala
 130 135 140
 Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys
 145 150 155 160
 Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr
 165 170 175
 Lys Pro Ser Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
 180 185 190
 Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Phe

195 200 205
 Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr Thr Val Val Thr
 210 215 220

<210> 1772
 <211> 215
 <212> PRT
 <213> Unknown (H38g690 protein)

<220>
 <223> Synthetic construct

<400> 1772
 Met Asp Val Arg Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe Asn
 1 5 10 15
 Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr Gln
 20 25 30
 Ile Phe Phe Cys Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu Ala
 35 40 45
 Val Met Ser Tyr Asp Cys Tyr Ile Ala Ile Cys His Pro Leu Arg Tyr
 50 55 60
 Thr Asn Leu Met Arg Pro Lys Ile Cys Arg Leu Met Thr Ala Phe Ser
 65 70 75 80
 Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Tyr Ala Val Ala Thr Phe
 85 90 95
 Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys Glu
 100 105 110
 Leu Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe Glu
 115 120 125
 Lys Val Ile Phe Ile Cys Ser Ile Val Met Leu Val Phe Pro Val Ala
 130 135 140
 Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala Val Ile His Met
 145 150 155 160
 Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser His
 165 170 175
 Leu Met Val Val Gly Met Phe Tyr Gly Ala Gly Leu Phe Met Tyr Ile
 180 185 190
 Gln Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Leu Val Ser Val
 195 200 205
 Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1773
 <211> 127
 <212> PRT
 <213> Unknown (H38g691 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(127)
 <223> Xaa = Any Amino Acid

<400> 1773
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser
 1 5 10 15
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu
 20 25 30
 Phe Gln Asn His Lys Leu Phe Leu Leu Phe Ala Gly Met Asn Val Phe
 35 40 45

Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Il Cys His Pro
 50 55 60
 Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val
 65 70 75 80
 Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg
 85 90 95
 Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile
 100 105 110
 Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn
 115 120 125

<210> 1774
 <211> 216
 <212> PRT
 <213> Unknown (H38g692 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(216)
 <223> Xaa = Any Amino Acid

<400> 1774
 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 1 5 10 15
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
 20 25 30
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
 50 55 60
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
 65 70 75 80
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu
 85 90 95
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
 100 105 110
 Glu His Ala Ala Val Val Ala Val Ser Trp Ser Asp Pro Cys Val Ser
 115 120 125
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Gly Leu
 130 135 140
 Val Ile Ile Leu Thr Pro Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
 145 150 155 160
 Thr Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser
 165 170 175
 His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
 180 185 190
 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser
 195 200 205
 Val Leu Tyr Thr Val Val Ile Pro
 210 215

<210> 1775
 <211> 215
 <212> PRT
 <213> Unknown (H38g693 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400> 1775

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Met Gln Ser His Ser Arg Ile Ile Ser His Ala Gly Cys Leu Thr
          20           25           30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
          35           40           45
Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys His Pro Leu His
          50           55           60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Met
65           70           75           80
Ser Ile Phe Leu Ser Leu Leu Asp Ser Xaa Leu His Asn Ser Val Leu
          85           90           95
Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys
          100          105          110
Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Phe Ile Ser Asn
          115          120          125
Ile Phe Ile Arg Leu Asp Ser Thr Ile Phe Gly Phe Leu Pro Ile Ser
          130          135          140
Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
145          150          155          160
Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
          165          170          175
Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu
          180          185          190
Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val Ala Ser Val
          195          200          205
Leu Tyr Ala Met Val Thr Pro
210          215

```

<210> 1776

<211> 217

<212> PRT

<213> Unknown (H38g694 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 1776

```

Leu Pro Asp Ile Gly Phe Thr Pro Thr Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly Cys Leu Thr Val
          20           25           30
Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu Leu
          35           40           45
Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu Tyr
          50           55           60
His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu
65           70           75           80
Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met Ile
          85           90           95
Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
          100          105          110

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Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
   115                               120                               125
Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro
   130                               135                               140
Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile Val Ser Ser Ile Leu
  145                               150                               155                               160
Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala Phe Ala Thr Cys Gly
   165                               170                               175
Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly
   180                               185                               190
Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala
   195                               200                               205
Ser Val Met Tyr Ala Val Val Thr Pro
   210                               215

```

<210> 1777

<211> 230

<212> PRT

<213> Unknown (H38g695 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(230)

<223> Xaa = Any Amino Acid

<400> 1777

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala Lys Met Ile Val
  1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
   20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
   35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
   50           55           60
Tyr Arg Ser Ala Ile Leu Ser Arg Asp Ser Val Pro Ser Xaa Ile Cys
   65           70           75           80
Cys Leu Cys Phe Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe
   85           90           95
Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
  100           105           110
Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Leu Trp Glu Pro Ser
  115           120           125
Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
  130           135           140
Met Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Pro
  145           150           155           160
Phe Leu Leu Gln Trp Ser Lys Ile Val Ser Ser Thr Leu Arg Val Ser
  165           170           175
Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
  180           185           190
Ser Val Val Cys Xaa Phe Cys Gly Thr Gly Val Gly Gly Tyr Leu Gly
  195           200           205
Ser Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met
  210           215           220
Tyr Thr Val Val Thr Pro
  225           230

```

<210> 1778

<211> 313

<212> PRT
 <213> Unknown (H38g696 protein)

<220>
 <223> Synthetic construct

<400> 1778

```

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
 1           5           10          15
Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
 20          25          30
Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
 35          40          45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
 50          55          60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
 65          70          75          80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
 85          90          95
Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
100         105         110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115         120         125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
130         135         140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145         150         155         160
Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
165         170         175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
180         185         190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
195         200         205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210         215         220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225         230         235         240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245         250         255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
260         265         270
Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
290         295         300
Ile Lys Ile Gln Arg Arg Asn Ile Phe
305         310

```

<210> 1779
 <211> 308
 <212> PRT
 <213> Unknown (H38g697 protein)

<220>
 <223> Synthetic construct

<400> 1779

```

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
 1           5           10          15
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe L u Leu Phe Leu
 20          25          30

```


Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly M t Ile Leu Leu
 35 40 45
 Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
 85 90 95
 Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
 130 135 140
 Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
 145 150 155 160
 Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
 180 185 190
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
 195 200 205
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
 210 215 220
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
 245 250 255
 Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val
 290 295 300
 Leu Val Gly Lys
 305

<210> 1780

<211> 328

<212> PRT

<213> Unknown (H38g698 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1780

Met Ala Pro Gly Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr His Gln Pro Asp Leu Gln Ser Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Val Ile Tyr Val Val Thr Leu Leu Gly Asn Leu Gly Leu Val Thr Leu
 35 40 45
 Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Met Asn Phe Ile Ser Glu Lys Asn Ile Ile Ser Phe Lys Gly

<210> 1781
<211> 314
<212> PRT
<213> Unknown (H38g699 protein)

<400> 1781																
Met	Lys	Pro	Gly	Asn	Glu	Thr	Gln	Ile	Ser	Gln	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Leu	Ser	Glu	Glu	Pro	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Thr	Ile	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ser	Phe	Ala	Asp	Ile	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys	
65					70					75					80	
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Ser	Arg	Val	Ile	Thr	Tyr	Ala	Asp	
				85					90					95		
Cys	Ile	Thr	Gln	Met	Cys	Phe	Phe	Ile	Leu	Phe	Val	Val	Leu	Asp	Ser	
			100					105					110			
Leu	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	His	Tyr	Thr	Val	Ile	Met	Asn	Ser	Trp	Leu	Cys	Gly	Leu	Leu	
	130					135					140					
Val	Leu	Val	Ser	Trp	Ile	Val	Ser	Ile	Leu	Tyr	Ser	Leu	Leu	Gln	Ser	
145					150					155					160	

```

Ile Met Ala Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His
      165                      170                      175
Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr
      180                      185                      190
Phe Ile Asn Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly
      195                      200                      205
Gly Cys Leu Ala Gly Ile Leu Tyr Thr Tyr Phe Lys Ile Leu Cys Cys
      210                      215                      220
Ile Cys Ser Ile Ser Ser Ala Gln Gly Met Asn Lys Ala Leu Ser Thr
      225                      230                      235                      240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val
      245                      250                      255
Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala
      260                      265                      270
Ala Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe
      275                      280                      285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Arg Ala Leu Asn Arg Phe
      290                      295                      300
Phe Arg Glu Gln Lys Gln Glu Gly His Phe
      305                      310

```

<210> 1782

<211> 324

<212> PRT

<213> Unknown (H38g700 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1782

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
  20      25      30
Leu Ser Leu Ser Leu Asn Leu Val Thr Val Leu Arg Asn Leu Leu Ser
  35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
  50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Leu Thr Ser Ala Thr
  65      70      75      80
Val Pro Lys Val Ile Leu Asp Met Gln Ser His Ser Arg Val Ile Ser
  85      90      95
His Val Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
  100     105     110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Gly Cys Phe Val Ala
  115     120     125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
  130     135     140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Asn Leu Leu Asp Ser Gln
  145     150     155     160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
  165     170     175
Ile Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys
  180     185     190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
  195     200     205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile

```

210	215	220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala		
225	230	235
Phe Ser Thr Tyr Gly Ser His Leu Gly Val Val Cys Trp Phe Tyr Gly		240
	245	250
Thr Val Ile Gly Met Tyr Leu Ala Ser Ala Val Ser Pro Pro Pro Arg		255
	260	265
Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu		270
	275	280
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu		285
	290	295
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser		300
305	310	315
Phe Phe Leu Cys		320

<210> 1783

<211> 339

<212> PRT

<213> Unknown (H38g701 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 1783

Pro Ile Glu Gln Gly Asn Tyr Thr Arg Val Lys Glu Phe Phe Phe Gln		
1	5	10
Gly Leu Thr Gln Ser Gln Glu Leu Ser Leu Val Leu Phe Leu Phe Leu		15
	20	25
Phe Phe Val Tyr Ser Ala Thr Val Leu Gly Asn Leu Leu Ile Met Val		30
	35	40
Val Val Thr Cys Glu Ser Arg Leu His Thr Pro Thr Tyr Phe Leu Leu		45
	50	55
Cys Asn Leu Ser Val Leu Val Ile Cys Phe Ser Ser Ile Thr Ala Arg		60
65	70	75
Lys Val Leu Ile Asp Leu Ser Ser Arg Lys Thr Ile Ser Phe Asn Gly		80
	85	90
Cys Met Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Thr Asp Val		95
	100	105
Phe Ser Leu Phe Val Met Ala Phe Asp Gln Tyr Met Ala Ile Phe Lys		110
	115	120
Pro Leu His Cys Val Thr Ile Val Ser Arg Gly Gln Cys Ile Pro Tyr		125
	130	135
Ile Val Ser Arg Gly Arg Glu Xaa Gly Ala Gly Leu Ile Met Ala Ser		140
145	150	155
Trp Val Gly Gly Phe Val His Ser Ile Val Gln Val Phe Leu Leu Leu		160
	165	170
Pro Leu Pro Phe Cys Gly His His Met Ile Asp Gly Phe Tyr Cys Asp		175
	180	185
Val Pro Gln Val Leu Lys Leu Ala Cys Thr His Thr Phe Ala Leu Glu		190
	195	200
Val Leu Met Ile Ser Asn Asn Gly Leu Ile Ser Met Leu Trp Phe Ile		205
	210	215
Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser His		220
225	230	235
Thr Glu Glu Gly Arg Arg Lys Ala Ile Ala Thr Cys Thr Ser His Ile		240
	245	250
		255

```

Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val His Ala Gln
      260      265      270
Pro Phe Thr Ala Leu Pro Thr Asp Arg Ala Val Ser Ile Thr Phe Thr
      275      280      285
Val Ile Ile Pro Val Leu Asn Pro Met Ile Tyr Thr Leu Arg Asn Gln
      290      295      300
Glu Met Lys Ser Ala Leu Arg Arg Arg Lys Lys Arg Pro Ser Gly Lys
305      310      315      320
Gly Xaa Met Leu Arg Ser Pro Asp Trp Lys Ile Arg Thr Glu Lys Tyr
      325      330      335
Phe Phe Ile

```

<210> 1784

<211> 335

<212> PRT

<213> Unknown (H38g702 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1784

```

Ser Thr Tyr Pro Gln Asn Leu Thr Asp Val Ser Leu Phe Leu Leu Leu
 1      5      10      15
Gly Ser Ser Glu Asp Pro Glu Gln Gln Pro Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ser Met Val Pro
      65      70      75      80
Lys Met Ile Val Asp Ile Xaa Ser His Ser Arg Leu Ile Ser Xaa Ala
      85      90      95
Gly Cys Leu Thr Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln
145      150      155      160
Val His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
      165      170      175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
      180      185      190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile
      195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
      210      215      220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225      230      235      240
Cys Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
      245      250      255
Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Gly
      260      265      270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Pro

```

275	280	285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu		
290	295	300
Arg Arg Pro His Gly Ser Thr Val Xaa Cys Gln Tyr Leu Leu Ile Cys		
305	310	315
Ser Met Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys		
325	330	335

<210> 1785

<211> 315

<212> PRT

<213> Unknown (H38g703 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1785

Met Lys Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly Leu Thr		
1	5	10
Gln Asn Gly Asp Thr Arg Leu Val Leu Phe Leu Phe Leu Leu Val		
20	25	30
Tyr Met Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr Val Thr		
35	40	45
Cys Glu Ser Cys Leu His Met Pro Met Tyr Phe Leu Leu His Asn Leu		
50	55	60
Ser Ile Ala Asp Ile Cys Phe Tyr Ser Ile Thr Glu Pro Lys Val Leu		
65	70	75
Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn Gly Cys Phe		
85	90	95
Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Ala Phe Ser		
100	105	110
Leu Ser Val Met Ala Leu Asp Gln Tyr Val Ala Ile Ser Lys Ser Leu		
115	120	125
His Tyr Ala Thr Ile Met Ser Arg Asp Arg Cys Ile Gly Leu Thr Val		
130	135	140
Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile Thr Leu		
145	150	155
Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr		
165	170	175
Cys Asp Val Pro Gln Val Leu Lys Leu Ala His Thr Asp Ile Phe Ile		
180	185	190
Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr Leu Trp		
195	200	205
Phe Phe Leu Leu Leu Val Ser Tyr Met Val Ile Leu Ser Leu Leu Lys		
210	215	220
Ser Gln Ala Gly Xaa Gly Arg Arg Lys Val Ile Ser Thr Cys Thr Ser		
225	230	235
His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr		
245	250	255
Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Lys Ala Ile Ser Val Thr		
260	265	270
Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg		
275	280	285
Asn His Glu Met Lys Ser Thr Met Lys Arg Arg Arg Leu Xaa Pro Ser		
290	295	300
Asp Arg Lys Xaa Thr Ser Ala Ser Leu Leu Leu		
305	310	315

<210> 1786
 <211> 321
 <212> PRT
 <213> Unknown (H38g704 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1786
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Lys Val Leu Leu Gly
 1 5 10 15
 Ser Leu Xaa Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Val Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Ser Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Val
 85 90 95
 Ser Cys Leu Thr Gln Ile Ser Phe Leu Val Leu Phe Ala Cys Met Glu
 100 105 110
 Asp Met Leu Thr Val Met Ala Tyr Asp Arg Val Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Arg Val Phe Leu
 130 135 140
 Val Leu Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145 150 155 160
 Trp Ile Val Leu Gln Phe Thr Leu Phe Lys Asn Val Glu Asn Ser Ser
 165 170 175
 Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Met Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Tyr Gly Ser Gln Leu Ala Ala Leu Cys Xaa Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ala Leu Pro Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu Asn Phe Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu
 290 295 300
 Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305 310 315 320
 Cys

<210> 1787
 <211> 318
 <212> PRT
 <213> Unknown (H38g705 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1787

```

Lys Gln Gln Glu Asn Gly Thr Cys Leu Val Thr Glu Phe Leu Met Met
 1          5          10          15
Gly Phe Ser Asn Leu Pro His Leu Arg Asn Thr Leu Phe Thr Leu Phe
          20          25          30
Phe Leu Thr Tyr Leu Val Thr Leu Gly Gly Asn Val Thr Ile Ile Thr
          35          40          45
Ile Thr His Ala Asp Arg Ser Arg His Thr Pro Met Tyr His Phe Leu
          50          55          60
Val Val Leu Ser Leu Ser Glu Thr Val Leu Tyr Thr Leu Val Thr Ile
65          70          75          80
Pro Ser Met Leu Ala His Leu Leu Met Glu Thr Arg Pro Ile Ser Ile
          85          90          95
Pro Gly Cys Gln Ala Gln Met Phe Phe Phe Leu Gly Leu Gly Cys Ser
          100          105          110
His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ser Met Val Met Arg Pro Thr Val Cys Leu
          130          135          140
Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe Ser Val Ala Leu Ile
145          150          155          160
Glu Thr Ser Met Ile Phe Ser Ser Pro Phe Cys Gly Gly Asp His Val
          165          170          175
Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ser Cys Ala
          180          185          190
Lys Ser Ala Ser Lys Ala Leu Gly Ile Phe Phe Leu Ser Val Leu Val
          195          200          205
Val Leu Met Ser Phe Val Pro Ile Leu Phe Ser Tyr Ala Phe Ile Val
          210          215          220
Ala Ala Ile Val Arg Ile Ser Leu Ala Ala Gly Arg Arg Lys Ala Phe
225          230          235          240
Ser Thr Cys Val Ala His Val Thr Val Val Val Val His Phe Asp Cys
          245          250          255
Ala Ser Ile Ile Tyr Leu Arg Pro Glu Ser Gly Ala Asn Pro Asp Gln
          260          265          270
Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val Met Pro Leu Leu Asn
          275          280          285
Pro Val Val Cys Thr Leu Trp Asn Lys Glu Val Arg Val Ala Leu Arg
          290          295          300
Arg Thr Leu Ala Trp Ser Arg Gly Val Phe Lys Xaa Glu Ser
305          310          315

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<210> 1788

<211> 112

<212> PRT

<213> Unknown (H38g706 protein)

<220>

<223> Synthetic construct

<400> 1788

```

Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu Lys Leu Ala
 1          5          10          15

```


Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg
 20 25 30
 Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser Tyr Gly
 35 40 45
 Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly Arg Arg
 50 55 60
 Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe
 65 70 75 80
 Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg Tyr Asn
 85 90 95
 Gln His Gly Asn Arg Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro
 100 105 110

<210> 1789

<211> 313

<212> PRT

<213> Unknown (H38g707 protein)

<220>

<223> Synthetic construct

<400> 1789

Met Asp Gln Arg Asn Tyr Thr Arg Val Lys Glu Phe Thr Phe Leu Gly
 1 5 10 15
 Ile Thr Gln Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe
 20 25 30
 Leu Val Tyr Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr
 35 40 45
 Val Thr Cys Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ser Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys
 65 70 75 80
 Val Leu Ile Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Val Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val
 100 105 110
 Phe Ser Leu Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys
 115 120 125
 Pro Leu His Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu
 130 135 140
 Ile Val Gly Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile
 145 150 155 160
 Ser Leu Leu Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr
 180 185 190
 Phe Thr Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp
 195 200 205
 Phe Val Phe Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met
 210 215 220
 Leu Arg Ser His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys
 225 230 235 240
 Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr
 245 250 255
 Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser
 260 265 270
 Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Met Lys Leu Ala Met Arg Lys Leu Lys Arg Arg
 290 295 300
 Leu Gly Gln Ser Glu Arg Ile Leu Ile

305

310

<210> 1790

<211> 162

<212> PRT

<213> Unknown (H38g708 protein)

<220>

<223> Synthetic construct

<400> 1790

Val	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Pro	Val	Met	Met	Ser	Asn	Lys
1				5					10					15	
Leu	Ser	Ala	Gln	Leu	Leu	Ser	Ile	Ser	Tyr	Val	Ile	Gly	Phe	Leu	His
		20						25					30		
Pro	Leu	Val	His	Val	Ser	Leu	Leu	Leu	Arg	Leu	Thr	Phe	Cys	Arg	Phe
		35					40					45			
Asn	Ile	Ile	His	Tyr	Phe	Tyr	Cys	Glu	Ile	Leu	Gln	Leu	Phe	Lys	Ile
	50					55				60					
Ser	Cys	Asn	Gly	Pro	Ser	Ile	Asn	Ala	Leu	Ile	Ile	Phe	Ile	Phe	Gly
65				70				75							80
Ala	Phe	Ile	Gln	Ile	Pro	Thr	Leu	Met	Thr	Ile	Ile	Ile	Ser	Tyr	Thr
			85					90						95	
Arg	Val	Leu	Phe	Asp	Ile	Leu	Lys	Lys	Lys	Ser	Glu	Lys	Gly	Arg	Ser
		100					105						110		
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ala	His	Leu	Leu	Ser	Val	Ser	Leu	Tyr
		115				120						125			
Tyr	Gly	Thr	Leu	Ile	Phe	Met	Tyr	Val	Arg	Pro	Ala	Ser	Gly	Leu	Ala
	130					135				140					
Glu	Asp	Gln	Asp	Lys	Val	Tyr	Ser	Leu	Phe	Tyr	Thr	Ile	Ile	Ile	Pro
145				150						155					160
Leu	Leu														

<210> 1791

<211> 258

<212> PRT

<213> Unknown (H38g709 protein)

<220>

<223> Synthetic construct

<400> 1791

Met	Tyr	Tyr	Phe	Leu	Cys	His	Leu	Ala	Leu	Val	Asp	Ala	Gly	Phe	Thr
1				5					10					15	
Thr	Ser	Val	Val	Pro	Pro	Leu	Leu	Ala	Asn	Leu	Arg	Gly	Pro	Ala	Leu
		20						25					30		
Trp	Leu	Pro	Arg	Ser	His	Cys	Thr	Ala	Gln	Leu	Cys	Ala	Ser	Leu	Ala
		35				40					45				
Leu	Gly	Ser	Ala	Glu	Cys	Val	Leu	Leu	Ala	Val	Met	Ala	Leu	Asp	Arg
	50				55					60					
Ala	Ala	Ala	Val	Cys	Arg	Pro	Leu	Arg	Tyr	Ala	Gly	Leu	Val	Ser	Pro
65				70					75						80
Arg	Leu	Cys	Arg	Thr	Leu	Ala	Ser	Ala	Ser	Trp	Leu	Ser	Gly	Leu	Thr
			85				90						95		
Asn	Ser	Val	Ala	Gln	Thr	Ala	Leu	Leu	Ala	Glu	Arg	Pro	Leu	Cys	Ala
		100					105						110		
Pro	Arg	Leu	Leu	Asp	His	Phe	Ile	Cys	Glu	Leu	Pro	Ala	Leu	Leu	Lys
		115				120						125			
Leu	Ala	Cys	Gly	Gly	Asp	Gly	Asp	Thr	Thr	Glu	Asn	Gln	Met	Phe	Ala
	130					135					140				

Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser
 145 150 155 160
 Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly
 165 170 175
 Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys
 180 185 190
 Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg
 195 200 205
 Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val
 210 215 220
 Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys Val
 225 230 235 240
 Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln Ala
 245 250 255
 Gly Gln

<210> 1792

<211> 316

<212> PRT

<213> Unknown (H38g710 protein)

<220>

<223> Synthetic construct

<400> 1792

Met Gln Arg Ala Asn His Ser Thr Val Thr Gln Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Val Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
 20 25 30
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
 35 40 45
 Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys
 50 55 60
 Ala Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
 85 90 95
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu
 130 135 140
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr
 145 150 155 160
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His
 165 170 175
 Phe Ala Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp
 180 185 190
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu
 195 200 205
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
 210 215 220
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Phe Ala
 245 250 255
 Ser Val Ile Tyr Leu Lys Pro Lys Ser Pro Gln Ser Leu Glu Gly Asp
 260 265 270
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro

275 280 285
 Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys
 290 295 300
 Thr Phe Phe Ser Lys Leu Tyr Pro Glu Lys Asn Val
 305 310 315

<210> 1793
 <211> 225
 <212> PRT
 <213> Unknown (H38g711 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(225)
 <223> Xaa = Any Amino Acid

<400> 1793
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Leu Ser Tyr Ala Gly Cys Leu Ile
 20 25 30
 Arg Cys Leu Ser Leu Pro Leu Leu Glu Ala Trp Lys Arg Gly Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Xaa Phe Cys Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Leu Phe Val Cys Phe Val Phe Leu Ser Leu Leu
 85 90 95
 Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Ser Lys
 100 105 110
 Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His
 115 120 125
 Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn Met Tyr Phe Pro
 130 135 140
 Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Phe Tyr Ser Tyr
 145 150 155 160
 Cys Lys Ile Leu Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys
 165 170 175
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa
 180 185 190
 Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser
 195 200 205
 Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr Thr Val Val Thr
 210 215 220
 Pro
 225

<210> 1794
 <211> 218
 <212> PRT
 <213> Unknown (H38g712 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1794

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
          35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Cys His Ser Ala Ile Thr Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
          65           70           75           80
Leu Ser Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln Leu His Asn Leu
          85           90           95
Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
          100          105          110
Phe Cys Asp Pro Ser Gln Phe Pro Arg Leu Ala Cys Cys Gly Thr Phe
          115          120          125
Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
          130          135          140
Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser Ile
          145          150          155          160
Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr Arg
          165          170          175
Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly
          180          185          190
Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val
          195          200          205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 1795

<211> 216

<212> PRT

<213> Unknown (H38g713 protein)

<220>

<223> Synthetic construct

<400> 1795

```

Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met Ala
 1           5           10           15
Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala Ala
          20           25           30
Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu Leu
          35           40           45
Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu His
          50           55           60
Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile Gly
          65           70           75           80
Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp Thr
          85           90           95
Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe Cys
          100          105          110
Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile Ser
          115          120          125
Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala Leu
          130          135          140
Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu Lys
          145          150          155          160
Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala Ser

```

165 170 175
 His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr
 180 185 190
 Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala Pro
 195 200 205
 Val Phe Tyr Thr Met Val Ile Pro
 210 215

<210> 1796

<211> 215

<212> PRT

<213> Unknown (H38g714 protein)

<220>

<223> Synthetic construct

<400> 1796

Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met Leu Thr
 1 5 10 15
 Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys Ile Met
 20 25 30
 Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu Ile Leu
 35 40 45
 Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala Val Ala
 65 70 75 80
 Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Leu Val Leu Ile
 85 90 95
 Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Cys Glu
 100 105 110
 Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln
 115 120 125
 Val Val Ile Phe Ala Ala Cys Val Phe Ile Leu Val Gly Pro Leu Cys
 130 135 140
 Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile
 145 150 155 160
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His
 165 170 175
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met
 180 185 190
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu
 195 200 205
 Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 1797

<211> 162

<212> PRT

<213> Unknown (H38g715 protein)

<220>

<223> Synthetic construct

<400> 1797

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
 1 5 10 15
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
 20 25 30
 Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
 35 40 45

```

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50          55          60
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65          70          75          80
Val Phe Ala Leu Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
      85          90          95
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
      100          105          110
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
      115          120          125
Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
      130          135          140
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Ser Val Ala Pro
145          150          155          160
Leu Leu

```

<210> 1798

<211> 224

<212> PRT

<213> Unknown (H38g716 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400> 1798

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1          5          10          15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
      20          25          30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
      35          40          45
Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro
      50          55          60
Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Gln Asp Leu
65          70          75          80
Leu Ser Leu Tyr Phe Phe Leu Phe Phe Ser Phe Phe Leu Arg Leu Leu
      85          90          95
Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys
      100          105          110
Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser Gln Leu Ser His
      115          120          125
Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala
      130          135          140
Ala Ile Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Tyr Cys
145          150          155          160
Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Gly Gly Lys Tyr
      165          170          175
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
      180          185          190
Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser
      195          200          205
Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys Met Val Thr Pro
210          215          220

```

<210> 1799

<211> 218

<212> PRT
 <213> Unknown (H38g717 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1799
 Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Cys Phe Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu
 85 90 95
 Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe
 100 105 110
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
 115 120 125
 Thr Ile Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
 130 135 140
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile
 145 150 155 160
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys
 165 170 175
 Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly
 180 185 190
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val
 195 200 205
 Ala Ser Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 1800
 <211> 295
 <212> PRT
 <213> Unknown (H38g718 protein)

<220>
 <223> Synthetic construct

<400> 1800
 Leu Ile Phe Phe Leu Ile Tyr Pro Leu Ile Leu Val Gly Asn Asp Gln
 1 5 10 15
 Ile Leu Val Val Val Met Ala Glu Ala Ser Leu His Lys Pro Val Tyr
 20 25 30
 Phe Phe Leu Ile Asn Leu Ser Ala Leu Asp Ile Leu Ser Thr Thr Val
 35 40 45
 Thr Val Pro Lys Thr Leu Pro Leu Phe Leu Leu Gly Asp His Phe Leu
 50 55 60
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Leu Phe His Ser Phe Ser
 65 70 75 80
 Cys Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val
 85 90 95

Ala Ile Cys His Pro Leu Gln Tyr Pro Val Leu Met Asn Pro Gln Thr
 100 105 110
 Asn Ala Val Leu Ala Thr Gly Ala Trp Leu Thr Ala Leu Leu Leu Pro
 115 120 125
 Ile Pro Ala Val Val Gln Thr Ser Gln Met Ala Phe Asp Ser Ile Ala
 130 135 140
 Asp Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser
 145 150 155 160
 Cys Ser Asp Thr Ser Pro Gln Thr Phe Met Gly Phe Cys Ile Ala Met
 165 170 175
 Val Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Ala His
 180 185 190
 Ile Leu Thr Ser Val Leu Arg Ile Asn Ser Gln Glu Gly Arg Ser Lys
 195 200 205
 Ala Phe Ser Thr Cys Ser Ser His Leu Pro Val Val Gly Thr Tyr Tyr
 210 215 220
 Ser Ser Ile Ala Ile Ala Tyr Val Ala Tyr Ser Ala Asp Leu Pro Leu
 225 230 235 240
 Asp Phe His Val Met Gly Asn Val Val His Ala Leu Leu Leu Pro Leu
 245 250 255
 Leu Leu Leu Leu Pro Leu Pro Leu Leu Pro Leu Pro Leu Arg Leu Pro
 260 265 270
 Leu Leu Leu Leu Leu Arg Ser Pro Ser Ser Ser Ser Ser Ser Pro Ser
 275 280 285
 Pro Ser Ser Ser Phe Phe Phe
 290 295

<210> 1801

<211> 311

<212> PRT

<213> Unknown (H38g719 protein)

<220>

<223> Synthetic construct

<400> 1801

Met Glu Met Glu Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly
 1 5 10 15
 Leu Thr Gln Asn Arg Glu Val Ser Leu Val Leu Phe Leu Phe Leu Leu
 20 25 30
 Leu Val Tyr Val Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr
 35 40 45
 Val Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu His
 50 55 60
 Asn Leu Ser Ile Ala Asp Ile Cys Phe Ser Ser Ile Thr Val Pro Lys
 65 70 75 80
 Val Leu Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn His
 85 90 95
 Cys Phe Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Val
 100 105 110
 Phe Ser Leu Ser Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser Lys
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Ser Arg Asp Gln Cys Ile Gly Leu
 130 135 140
 Thr Val Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile
 145 150 155 160
 Ser Leu Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr
 165 170 175
 Phe Tyr Cys Asp Val His Arg Val Leu Lys Leu Ala His Thr Asp Ile
 180 185 190
 Phe Ile Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr

```

      195              200              205
Leu Trp Phe Phe Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Ser Leu
  210              215              220
Pro Lys Ser Gln Ala Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys
  225              230              235              240
Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr
      245              250              255
Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Met Asp Lys Ala Ile Ser
      260              265              270
Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr
      275              280              285
Leu Arg Asn His Glu Met Lys Ser Ala Met Arg Arg Leu Lys Arg Arg
      290              295              300
Leu Val Pro Ser Asp Arg Lys
  305              310

```

<210> 1802

<211> 299

<212> PRT

<213> Unknown (H38g720 protein)

<220>

<223> Synthetic construct

<400> 1802

```

Thr Met Gln Gln Asn Asn Ser Val Pro Glu Phe Ile Leu Leu Gly Leu
  1              5              10              15
Thr Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile
      20              25              30
Phe Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile
      35              40              45
Lys Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr
      50              55              60
Leu Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu
      65              70              75              80
Ile Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys
      85              90              95
Met Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe
      100              105              110
Val Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro
      115              120              125
Leu Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile
      130              135              140
Val Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile
      145              150              155              160
Leu Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr
      165              170              175
Cys Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr
      180              185              190
Met Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser
      195              200              205
Ser Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu
      210              215              220
Arg Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr
      225              230              235              240
Ser His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile
      245              250              255
Tyr Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val
      260              265              270
Phe Tyr Thr Ile Gly Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275              280              285

```

Arg Asn Ala Glu Val Lys Asn Ala Met Arg Lys
290 295

<210> 1803

<211> 314

<212> PRT

<213> Unknown (H38g721 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1803

```

Met Glu Leu Gly Asn Val Thr Arg Val Lys Glu Phe Ile Phe Leu Gly
 1           5           10          15
Leu Thr Gln Ser Gln Asp Gln Ser Leu Val Leu Phe Leu Phe Leu Cys
           20          25          30
Leu Val Tyr Met Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr
 35          40          45
Val Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50          55          60
Asn Leu Ala Ile Leu Asp Ile Cys Phe Ser Ser Thr Thr Ala Pro Lys
 65          70          75          80
Val Leu Leu Asp Leu Leu Ser Lys Lys Lys Thr Ile Ser Tyr Thr Ser
           85          90          95
Cys Met Thr Gln Ile Phe Leu Phe His Leu Leu Gly Gly Ala Asp Ile
           100         105         110
Phe Ser Leu Ser Val Met Ala Phe Asp Cys Tyr Met Ala Ile Ser Lys
           115         120         125
Pro Leu His Tyr Val Thr Ile Met Ser Arg Gly Gln Cys Thr Ala Leu
           130         135         140
Ile Ser Ala Ser Trp Met Gly Gly Phe Val His Ser Ile Val Gln Ile
           145         150         155         160
Ser Leu Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr
           165         170         175
Phe Tyr Cys Asp Val Pro Gln Val Leu Lys Leu Thr Cys Thr Asp Thr
           180         185         190
Phe Ala Leu Glu Phe Leu Met Ile Ser Asn Asn Gly Leu Val Thr Thr
           195         200         205
Leu Trp Phe Ile Phe Leu Leu Val Ser Tyr Thr Val Ile Leu Met Thr
           210         215         220
Leu Arg Ser Gln Ala Gly Gly Arg Arg Lys Ala Ile Ser Thr Cys
           225         230         235         240
Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr
           245         250         255
Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Thr Glu Lys Ala Ile Ser
           260         265         270
Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr
           275         280         285
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Arg Arg Leu Lys Arg Arg
           290         295         300
Leu Val Pro Ser Glu Arg Glu Xaa Lys Thr
           305         310

```

<210> 1804

<211> 314

<212> PRT

<213> Unknown (H38g722 protein)

<220>

<223> Synthetic construct

<400> 1804

```

Met Leu Gly Leu Asn His Thr Ser Met Ser Glu Phe Ile Leu Val Gly
 1           5           10           15
Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Phe Leu
      20           25           30
Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
      35           40           45
Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys
      50           55           60
Val Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
      65           70           75           80
Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
      85           90           95
Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
      100          105          110
Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu
      130          135          140
Val Gly Cys Ser Trp Ala Gly Gly Ser Val Met Gly Met Val Val Thr
      145          150          155          160
Ser Ala Ile Phe Gln Leu Thr Phe Cys Gly Ser His Glu Ile Gln His
      165          170          175
Phe Leu Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asn Asn
      180          185          190
Val Pro Ala Val Ala Leu Gly Val Gly Leu Val Cys Ile Met Ala Leu
      195          200          205
Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
      210          215          220
Asp Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
      225          230          235          240
Thr Cys Ala Ser His Leu Ile Val Val Ile Val His Tyr Gly Phe Ala
      245          250          255
Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro His Ser Gln Glu Gly Asp
      260          265          270
Thr Leu Met Ala Thr Thr Tyr Ala Val Leu Thr Pro Phe Leu Ser Pro
      275          280          285
Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Arg
      290          295          300
Thr Phe Leu Ser Thr Leu Tyr Ser Ser Gly
      305          310

```

<210> 1805

<211> 316

<212> PRT

<213> Unknown (H38g723 protein)

<220>

<223> Synthetic construct

<400> 1805

```

Met Pro Gly Gln Asn Tyr Arg Thr Ile Ser Glu Phe Ile Leu Ser Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln Gln Leu Leu Pro Val Leu Phe Leu Leu Tyr
      20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
      35           40           45

```

```

Thr Val Trp Ile Glu Arg Arg Leu His Thr Pr Met Tyr Leu Phe Leu
 50          55          60
Cys Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65          70          75          80
Arg Met Leu Ala Asp Leu Leu Phe Thr His Arg Ser Ile Thr Phe Val
          85          90          95
Ala Cys Ala Ile Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
          100          105          110
Ser Phe Leu Leu Met Val Met Gly Tyr Asp His Tyr Val Thr Ile Cys
          115          120          125
His Pro Leu His Tyr Asn Met Leu Met Ser Pro Arg Gly Cys Ala His
          130          135          140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145          150          155          160
Thr Met Met Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
          165          170          175
His Phe Leu Cys His Val Leu Ser Leu Lys Leu Ala Cys Gly Ser
          180          185          190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
          195          200          205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Phe Val Phe Ile Val
          210          215          220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225          230          235          240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Met His Tyr Ser Phe
          245          250          255
Ala Ser Leu Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
          260          265          270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
          275          280          285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
          290          295          300
Lys Asn Phe Cys Arg Arg Phe Cys Pro Leu Ser Ser
305          310          315

```

<210> 1806

<211> 161

<212> PRT

<213> Unknown (H38g724 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(161)

<223> Xaa = Any Amino Acid

<400> 1806

```

Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu
 1          5          10          15
Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro
          20          25          30
Leu Val Phe Leu Phe Val Thr Ile Ser Ala Asn Ala Leu Val Ile
          35          40          45
His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu
          50          55          60
Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met
65          70          75          80
Pro Lys Met Leu Glu Gly Phe Val Tyr Tyr Ala Asn Pro Ile Ser Leu
          85          90          95
His Gly Arg Leu Ala Xaa Val Phe Phe Ile Tyr Phe Thr Leu Leu Leu

```

	100		105		110
Asp	Tyr	Asn	Phe	Leu	Trp
	115		120		125
Cys	His	Pro	Leu	Cys	Phe
	130		135		140
Leu	Leu	Ala	Ile	Leu	Ala
145		150		155	
Pro					160

<210> 1807
 <211> 198
 <212> PRT
 <213> Unknown (H38g725 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(198)
 <223> Xaa = Any Amino Acid

<400> 1807

Val	Ala	Ile	Cys	His	Pro	Leu	Cys	Phe	Gln	Thr	Glu	Xaa	Leu	Pro	Ser
1			5					10					15		
Trp	Leu	Gly	Leu	Leu	Ala	Ile	Leu	Ala	Leu	Thr	Gln	Ser	Trp	Gly	Val
		20					25					30			
Thr	Val	Pro	Leu	Val	Val	Leu	Thr	Ala	Lys	Ala	Asp	Phe	Cys	Arg	Thr
		35				40					45				
Ala	Val	Ile	Arg	His	Phe	Thr	Cys	Glu	Cys	Ile	Ala	Leu	Leu	Ser	Ile
	50			55				60							
Ala	Cys	Gly	Asp	Leu	Thr	Phe	Asn	Asn	Trp	Leu	Gly	Leu	Ala	Met	Cys
65			70				75					80			
Leu	Val	Thr	Val	Ile	Ser	Asp	Met	Ala	Leu	Gly	Thr	Ser	Tyr	Thr	
		85					90					95			
His	Ile	Ile	Tyr	Ala	Ala	Phe	Arg	Ile	Ser	Ser	Trp	Gly	Ala	Gln	Ala
		100					105					110			
Lys	Ala	Leu	His	Thr	Cys	Gly	Ser	His	Leu	Leu	Val	Ile	Leu	Ser	Ile
	115					120					125				
Tyr	Val	Ser	Gly	Leu	Ser	Thr	Ser	Ile	Thr	Phe	Xaa	Val	Ala	Lys	Thr
	130				135				140						
Val	Ser	Gln	Asn	Val	Gln	Asn	Leu	Leu	Ser	Ala	Ile	Tyr	Leu	Leu	Leu
145			150				155						160		
Pro	Gly	Ala	Leu	Asn	Pro	Val	Ile	Tyr	Gly	Val	Arg	Thr	Arg	Glu	Ile
		165					170						175		
Gln	Gln	His	Val	Glu	Lys	Met	Leu	Cys	Glu	Lys	Glu	Thr	Ala	Gln	Lys
		180					185						190		
Ala	Gly	Glu	Lys	Pro	Lys										
	195														

<210> 1808
 <211> 315
 <212> PRT
 <213> Unknown (H38g726 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1808

```

Phe Ser Gln Asn Leu Leu Ile Ser Gly Ser Gly Ser Phe Val Leu Leu
 1          5          10          15
Gly Met Pro Gly Leu Glu Ala Leu His Ala Trp Leu Ser Val Pro Val
          20          25          30
Cys Leu Leu Tyr Met Ala Ala Leu Val Gly Asn Ala Leu Leu Val Gly
          35          40          45
Leu Val Val Ala Asp Lys Ala Leu Trp Ala Pro Met Tyr Gln Leu Leu
          50          55          60
Trp Leu Leu Ala Ala Ala Asp Phe Val Leu Ala Thr Ser Thr Val Pro
65          70          75          80
Lys Ala Leu Ala Val Leu Trp Gly Leu Ser Ser Glu Ile Ser Phe Gly
          85          90          95
Gly Cys Leu Ala Gln Leu Phe Val Ala His Ser Val Asn His Cys His
          100          105          110
Ile Ala Glu Ser Ser Val Leu Leu Ser Thr Ala Val Asp Cys Gln Pro
          115          120          125
Leu Arg Tyr Gly Ala Leu Leu Ala Gln Phe Val Val Gly Leu Val Ala
          130          135          140
Leu Thr Thr Met Thr Arg Asp Val Cys Val Met Tyr Thr Leu Xaa Phe
          145          150          155          160
Leu Phe Lys Lys Leu Pro Tyr Cys Gly Gln Trp Ala Leu Pro His Thr
          165          170          175
Tyr Cys Glu His Met Gly Val Ala Cys Leu Ala Cys Gly Asp Thr Cys
          180          185          190
Pro Ile Ile Arg Tyr Gly Leu Ala Thr Thr Leu Leu Ser Pro Ala Leu
          195          200          205
Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val
          210          215          220
Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys
          225          230          235          240
Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe
          245          250          255
Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile
          260          265          270
His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn
          275          280          285
Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu
          290          295          300
Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu
          305          310          315

```

<210> 1809

<211> 313

<212> PRT

<213> Unknown (H38g727 protein)

<220>

<223> Synthetic construct

<400> 1809

```

Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu
          20          25          30
Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
          35          40          45
Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60
Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro His

```

```

65          70          75          80
Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
      85          90          95
Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
      100          105          110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
      115          120          125
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
      130          135          140
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
      145          150          155          160
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180          185          190
Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile Leu Leu
      195          200          205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
      210          215          220
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
      225          230          235          240
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245          250          255
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
      260          265          270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn Ser Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys Arg Leu
      290          295          300
Met Pro Arg Ile Phe Phe Cys Lys Lys
      305          310

```

<210> 1810

<211> 323

<212> PRT

<213> Unknown (H38g728 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1810

```

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Phe Ile Leu Leu
1          5          10          15
Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser
      20          25          30
Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr
      35          40          45
Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu
      50          55          60
Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro
      65          70          75          80
Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro
      85          90          95
Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe
      100          105          110
Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met
      115          120          125

```



```

Thr 11 Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr
130 135 140
Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu
145 150 155 160
Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile
165 170 175
Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr
180 185 190
Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met
195 200 205
Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr
210 215 220
Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala
225 230 235 240
Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr
245 250 255
Pro Thr Met Leu Ser Ala Leu Thr His His Phe Gly Gln Ser Ile Ser
260 265 270
Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro
275 280 285
Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn
290 295 300
Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp
305 310 315 320
Glu Asn Met

```

<210> 1811

<211> 337

<212> PRT

<213> Unknown (H38g729 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 1811

```

Met Lys Lys Asn Ala Ser Phe Glu Asp Phe Phe Ile Leu Leu Gly Phe
1 5 10 15
Ser Asn Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile
20 25 30
Phe Tyr Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser
35 40 45
Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
50 55 60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu
65 70 75 80
Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys
85 90 95
Thr Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val
100 105 110
Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro
115 120 125
Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala
130 135 140
Ala Ala Ser Trp Val Ser Gly Phe Thr Thr Ser Ala Leu His Ser Ser
145 150 155 160
Phe Thr Phe Trp Ile Pro Leu Cys Arg His Arg Leu Val Asp His Phe

```

<400>	1812															
Met	Ala	Met	Tyr	Asn	Met	Ser	Asp	His	Gly	Thr	Gly	Leu	Phe	Ile	Leu	
1				5					10					15		
Leu	Gly	Ile	Pro	Gly	Leu	Glu	Gln	Tyr	His	Val	Trp	Ile	Ser	Ile	Pro	
			20					25					30			
Phe	Cys	Leu	Ile	Tyr	Leu	Met	Ala	Val	Val	Ala	Lys	Ser	Ile	Leu	Leu	
		35					40					45				
Tyr	Leu	Ile	Val	Val	Glu	His	Ser	Leu	His	Ala	Pro	Met	Phe	Phe	Phe	
	50					55					60					
Leu	Ser	Met	Leu	Ala	Ile	Thr	Asp	Leu	Ile	Leu	Ser	Thr	Thr	Cys	Val	
65					70					75				80		
Pro	Lys	Thr	Leu	Ser	Ile	Phe	Trp	Phe	Gly	Pro	Gln	Ile	Ser	Phe	Pro	
				85					90					95		
Gly	Cys	Leu	Thr	Gln	Leu	Phe	Phe	Leu	His	Tyr	Ser	Phe	Val	Leu	Asp	
			100					105					110			
Ser	Ala	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys	
		115					120					125				
Ser	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Pro	Lys	Thr	Ile	Val	Lys	
		130				135					140					
Ile	Ala	Val	Gly	Ile	Cys	Phe	Arg	Ser	Phe	Cys	Val	Phe	Val	Pro	Cys	
145					150					155				160		
Val	Phe	Leu	Val	Asn	Arg	Leu	Pro	Phe	Cys	Arg	Thr	His	Ile	Ile	Ser	
				165					170					175		
His	Thr	Tyr	Cys	Glu	His	Ile	Gly	Val	Ala	Gln	Leu	Ala	Cys	Ala	Asp	
			180					185					190			

Ile Ser Ile Asn Ile Trp Cys Gly Phe Cys Val Pro Ile Met Thr Val
 195 200 205
 Met Thr Asp Val Ile Leu Ile Ala Val Ser Tyr Thr Leu Met Leu Cys
 210 215 220
 Gly Val Phe Cys Leu Pro Ser Gln Asp Ala Arg Gln Lys Ala Leu Cys
 225 230 235 240
 Ser Cys Gly Ser His Val Cys Val Ile Leu Ile Phe Tyr Thr Pro Ala
 245 250 255
 Phe Phe Ser Ile Leu Ala His Arg Phe Gly His Asn Val Pro His Thr
 260 265 270
 Phe His Ile Met Phe Ala Asn Leu Tyr Val Ile Ile Pro Pro Ala Leu
 275 280 285
 Asn Pro Ile Val Tyr Arg Ile Lys Thr Lys Gln Ile Gln Asn Arg Ile
 290 295 300
 Leu Leu Leu Phe Pro Lys Gly Ser Gln Xaa Xaa Val Pro Glu Leu
 305 310 315

<210> 1813

<211> 311

<212> PRT

<213> Unknown (H38g731 protein)

<220>

<223> Synthetic construct

<400> 1813

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
 1 5 10 15
 Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
 20 25 30
 Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
 35 40 45
 Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser
 65 70 75 80
 Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser
 85 90 95
 Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr
 100 105 110
 Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala
 115 120 125
 Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys
 130 135 140
 His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala
 145 150 155 160
 Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln
 165 170 175
 Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys
 180 185 190
 Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile
 195 200 205
 Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile
 210 215 220
 Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val
 225 230 235 240
 Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile
 245 250 255
 Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp
 260 265 270
 Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu

275 280 285
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val
 290 295 300
 Lys Arg Leu Met Gly Trp Glu
 305 310

<210> 1814
 <211> 88
 <212> PRT
 <213> Unknown (H38g732 protein)

<220>
 <223> Synthetic construct

<400> 1814
 Phe Ile His Ala Leu Ser Val Ile Glu Ser Ile Ile Val Leu Ala Met
 1 5 10 15
 Ala Phe Glu Arg Tyr Val Ala Ile Cys His Pro Leu Cys His Ala Glu
 20 25 30
 Val Leu Asn Ser Thr Val Thr Ala His Ile Gly Ile Val Ala Gly Val
 35 40 45
 Arg Gly Ser Leu Phe Phe Ser Pro Leu Ala Leu Leu Ile Lys Thr Leu
 50 55 60
 Gly Leu Cys His Ser Tyr Val Leu Ser His Ser Tyr Ser Leu His Gln
 65 70 75 80
 Asp Val Ala Asn Leu Ser Tyr Ala
 85

<210> 1815
 <211> 159
 <212> PRT
 <213> Unknown (H38g733 protein)

<220>
 <223> Synthetic construct

<400> 1815
 Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln
 1 5 10 15
 Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His
 20 25 30
 Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
 35 40 45
 Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu
 50 55 60
 Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser
 65 70 75 80
 Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala
 85 90 95
 Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys
 100 105 110
 Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe
 115 120 125
 Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
 130 135 140
 Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu
 145 150 155

<210> 1816
 <211> 316
 <212> PRT

<213> Unknown (H38g734 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1816

```

Met Ser Ala Pro Asn His Ser Thr Ala Asn His Asp Met Phe Val Leu
 1           5           10           15
Ile Gly Val Pro Gly Leu Lys Glu Leu His Val Trp Ile Ser Ile Pro
          20           25           30
Phe Cys Leu Met Tyr Leu Val Ala Val Ser Gly Asn Gly Leu Leu Val
          35           40           45
Cys Val Val Ala Val Glu His Ser Leu His Glu Pro Met Tyr Leu Phe
          50           55           60
Leu Ser Met Leu Ala Phe Trp Asp Leu Ile Leu Ser Thr Ser Ala Val
          65           70           75           80
Pro Lys Ala Leu Ser Ile Phe Trp Phe Asp Asp Val Asp Ile Ser Phe
          85           90           95
Gly Gly Cys Val Thr Gln Leu Phe Phe Met His Phe Ala Phe Val Ala
          100          105          110
Glu Ser Gly Ile Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Ser His Ser Val Ile Gly
          130          135          140
Lys Ile Gly Gly Val Val Phe Arg Ser Phe Ala Thr Val Phe Ser
          145          150          155          160
Ile Val Phe Leu Val Lys Arg Leu Pro Phe Cys Arg Thr Asn Ile Ile
          165          170          175
Ala His Thr Phe Cys Glu His Met Gly Leu Ala Lys Leu Gly Cys Ser
          180          185          190
Glu Ile Thr Ile Asn Ile Trp Tyr Gly Ile Ser Val Pro Leu Leu Ser
          195          200          205
Val Thr Leu Asp Met Val Thr Ile Val Ile Ser Xaa Gly Leu Ile Val
          210          215          220
Gln Ala Val Phe Arg Leu Pro Ser Leu Gly Ala Trp Met Lys Ala Leu
          225          230          235          240
Ser Thr Cys Gly Ser His Gly Ser Val Ile Leu Met Phe Cys Leu Pro
          245          250          255
Gly Ile Phe Thr Val Ile Val Gln Arg Phe Ala Xaa Lys Phe Pro Lys
          260          265          270
Tyr Val His Ile Leu Leu Ala Asn Leu Tyr Val Leu Val Pro Pro Met
          275          280          285
Met Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln Lys Gly
          290          295          300
Val Ala Leu Val Phe Ser Pro Lys Gly Lys Cys Cys
          305          310          315

```

<210> 1817

<211> 364

<212> PRT

<213> Unknown (H38g735 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(364)

<223> Xaa = Any Amino Acid

<400> 1817

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
          20           25           30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
          35           40           45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
          50           55           60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
65           70           75           80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
          85           90           95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
          100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
          130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
          165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
          180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
          195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
          210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
          245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
          260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
          290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp Val Asp Ile Thr Met
305          310          315          320
Lys Leu Leu Asn Ser Xaa Ser Arg Leu Leu Trp Phe Tyr Leu Thr Asn
          325          330          335
Ser Cys Leu Ile Ile Lys Tyr Arg Phe Thr Cys Ser Cys Lys Ile Cys
          340          345          350
Tyr Val Ser Glu Thr Leu Cys Lys His Val Gln Gln
          355          360

```

<210> 1818

<211> 166

<212> PRT

<213> Unknown (H38g736 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(166)

<223> Xaa = Any Amino Acid

<400> 1818

```

Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met
 1           5           10           15
Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala
      20           25           30
Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val
      35           40           45
Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu Ile Lys Arg Leu
      50           55           60
Ala Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln
      65           70           75           80
Asp Val Leu Lys Leu Ala Tyr Ala Asp Thr Leu Pro Asn Val Val Tyr
      85           90           95
Gly Leu Thr Ala Ile Leu Leu Ala Met Gly Val Asp Ala Met Phe Ile
      100           105           110
Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val Leu Gln Leu Pro Ser
      115           120           125
Lys Ser Xaa Arg Ala Lys Ala Phe Gly Thr Cys Val Val His Ile Gly
      130           135           140
Val Val Leu Gly Leu Tyr Val Pro Leu Ile Gly Thr Ser Ser Gly His
      145           150           155           160
Arg Phe Gly Asn Lys Leu
      165

```

<210> 1819

<211> 312

<212> PRT

<213> Unknown (H38g737 protein)

<220>

<223> Synthetic construct

<400> 1819

```

Met Met Ile Lys Lys Asn Ala Ser Ser Glu Asp Phe Phe Ile Leu Leu
 1           5           10           15
Gly Phe Ser Asn Trp Pro Gln Leu Glu Val Val Leu Phe Val Val Ile
      20           25           30
Leu Ile Phe Tyr Leu Met Thr Leu Thr Gly Asn Leu Phe Ile Ile Ile
      35           40           45
Leu Ser Tyr Val Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Asn Leu Ser Phe Leu Asp Leu Cys His Thr Ser Ser Ile Pro
      65           70           75           80
Gln Leu Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Ala
      85           90           95
Gly Cys Met Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Ile Ala Glu
      100           105           110
Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys
      115           120           125
Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys His Leu
      130           135           140
Leu Ala Ala Ala Ser Trp Val Ile Gly Phe Thr Ile Ser Ala Leu His
      145           150           155           160
Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Leu Val Asp
      165           170           175
His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys Val Asp
      180           185           190
Thr His Ala Asn Glu Leu Thr Leu Met Val Met Ser Ser Ile Phe Val
      195           200           205
Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala Tyr Gly Ala Ile Ala Arg

```

```

      210              215              220
Ala Val Leu Ser Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Arg
225              230              235              240
Thr Cys Gly Ala His Leu Met Val Val Ser Leu Phe Phe Ile Pro Val
      245              250              255
Met Cys Met Tyr Leu Gln Pro Pro Ser Glu Asn Ser Pro Asp Gln Gly
      260              265              270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro
      275              280              285
Leu Ile Tyr Thr Leu Arg Asn Lys His Val Lys Gly Ala Ala Lys Arg
      290              295              300
Leu Leu Gly Trp Glu Trp Gly Lys
305              310

```

<210> 1820
 <211> 151
 <212> PRT
 <213> Unknown (H38g738 protein)

<220>
 <223> Synthetic construct

```

<400> 1820
Arg Pro Leu Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu
 1              5              10              15
Pro Ala Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu
      20              25              30
Asn Gln Met Phe Ala Ala Arg Val Ile Leu Leu Arg Gly Val Ala
      35              40              45
Val Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met
      50              55              60
Arg Phe Asn Gly Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His
      65              70              75              80
Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu
      85              90              95
Gln Pro Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu
      100             105             110
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu
      115             120             125
Arg Asn Lys Lys Met Lys Gly Ala Pro Arg Arg Leu Leu Arg Ser Leu
      130             135             140
Gly Arg Gly Gln Ala Gly Gln
145             150

```

<210> 1821
 <211> 341
 <212> PRT
 <213> Unknown (H38g739 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(341)
 <223> Xaa = Any Amino Acid

```

<400> 1821
Met Met Glu Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile Leu Val
 1              5              10              15
Gly Phe Ser Asn Trp Pro Tyr Leu Glu Val Val Leu Phe Val Val Ile
      20              25              30

```



```

Leu Ile Phe Cys Leu Met Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile
    35              40              45
Leu Thr Tyr Leu Asp Ser His Leu His Thr Pro Leu Tyr Phe Phe Leu
    50              55              60
Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pr
    65              70              75              80
Gln Leu Leu Val Ser Leu Trp Gly Val Glu Lys Thr Ile Ser Tyr Ala
    85              90              95
Gly Cys Met Val Gln Leu Tyr Phe Phe Leu Thr Leu Gly Thr Thr Glu
    100             105             110
Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys
    115             120             125
Arg Pro Leu His Tyr Thr Val Leu Met His Ser Arg Phe Cys His Leu
    130             135             140
Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Pro Ala Leu His
    145             150             155             160
Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln Ile Asp
    165             170             175
His Phe Phe Cys Glu Val Pro Ala Leu Leu Xaa Leu Ser Phe Val Asn
    180             185             190
Thr Arg Glu Asn Lys Leu Thr Leu Met Ile Thr Ser Ser Ile Phe Val
    195             200             205
Leu Leu Leu Leu Thr Leu Ile Phe Thr Ser Tyr Gly Ala Ile Ala Gln
    210             215             220
Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Gly
    225             230             235             240
Thr Cys Gly Ala His His Met Val Val Ser Leu Phe Phe Ile Pro Ala
    245             250             255
Met Cys Met Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp Gln Gly
    260             265             270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro
    275             280             285
Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Gly Val Val Lys Arg
    290             295             300
Leu Arg Gly Trp Glu Xaa Ala Cys Val Cys Val Ile Leu Thr Ile Xaa
    305             310             315             320
Trp Ser Leu Ser Ser Gln Xaa Phe Ile His Leu Phe Ile Tyr Gln Pro
    325             330             335
Phe Phe Tyr Ser Leu
    340

```

<210> 1822

<211> 219

<212> PRT

<213> Unknown (H38g740 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1822

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
    1              5              10              15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
    20             25             30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Ile Leu
    35             40             45
Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys Cys His Pro Leu

```

```

      50      55      60
Tyr His Ser Ala Ile Met Asn Pro Cys Leu Cys Gly Phe Leu Leu Leu
65      70      75      80
Leu Ser Ile Phe Phe Ser Leu Ser Leu Leu Asp Ala Gln Leu Tyr Asn
      85      90      95
Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn
      100      105      110
Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr
      115      120      125
Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala Ile Phe Gly Phe
      130      135      140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser
145      150      155      160
Ile Leu Arg Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Leu Ser Thr
      165      170      175
Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val
      180      185      190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro Arg Lys Gly Ala
      195      200      205
Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
      210      215

```

<210> 1823

<211> 324

<212> PRT

<213> Unknown (H38g741 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1823

```

Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu Leu Gly
1      5      10      15
Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile Ile Phe
      20      25      30
Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val Leu Val
      35      40      45
Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val Pro Gln
65      70      75      80
Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ile Gly
      85      90      95
Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Tyr
      100      105      110
Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val Cys His
      115      120      125
Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu Gln Leu
      130      135      140
Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile Gln Ser
145      150      155      160
Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val Asp Asp
      165      170      175
Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr Asp Thr
      180      185      190
Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu Leu Val
      195      200      205

```

```

Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala Lys Ala
  210                215                220
Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe Gly Thr
  225                230                235                240
Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr Val Thr
                245                250                255
Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp Gly Lys
  260                265                270
Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu
  275                280                285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile Arg Leu
  290                295                300
Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn Xaa Gln Gly Xaa His Met
  305                310                315                320
Phe Thr Phe Ala

```

<210> 1824

<211> 218

<212> PRT

<213> Unknown (H38g742 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1824

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Met Val
  1          5          10          15
Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr
  20          25          30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
  35          40          45
Thr Val Met Ala Tyr Asn Xaa Phe Val Ala Ile Cys His Pro Leu His
  50          55          60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Val
  65          70          75          80
Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val
  85          90          95
Leu Gln Gln Leu Thr Phe Phe Lys Asn Val Glu Ile Ser Xaa Phe Phe
  100         105         110
Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Ile
  115         120         125
Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro Ile Phe Gly Phe Leu
  130         135         140
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile
  145         150         155         160
Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
  165         170         175
Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu Val
  180         185         190
Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser Met Val
  195         200         205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
  210         215

```

<210> 1825

<211> 124

<212> PRT
 <213> Unknown (H38g743 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(124)
 <223> Xaa = Any Amino Acid

<400> 1825
 Phe Leu Leu Xaa Ala Asn Tyr Ser Ala Glu Glu Arg Phe Leu Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val
 20 25 30
 Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ser Ala Leu Val Leu
 35 40 45
 Leu Ala Glu Lys Asp Pro Arg Leu Gln Thr Pro Arg Cys Met Asn Tyr
 50 55 60
 Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe Thr Thr Ser Val
 65 70 75 80
 Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu Leu Xaa Pro
 85 90 95
 Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala Leu Gly Ser
 100 105 110
 Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Glu
 115 120

<210> 1826
 <211> 216
 <212> PRT
 <213> Unknown (H38g744 protein)

<220>
 <223> Synthetic construct

<400> 1826
 Ile Leu Glu Ile Ser Phe Thr Thr Val Ser Ile Pro Lys Phe Leu Gly
 1 5 10 15
 Asn Ile Ile Ser Gly Asp Lys Thr Ile Ser Phe Asn Asn Cys Ile Val
 20 25 30
 Gln Leu Phe Phe Phe Ile Leu Leu Gly Val Thr Glu Phe Tyr Leu Leu
 35 40 45
 Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
 50 55 60
 Tyr Leu Ser Ile Met Asn Arg Arg Val Cys Thr Leu Leu Val Phe Thr
 65 70 75 80
 Ser Trp Leu Val Ser Phe Leu Ile Ile Phe Pro Ala Leu Met Leu Leu
 85 90 95
 Leu Lys Leu Asp Tyr Cys Arg Ser Asn Ile Ile Asp His Phe Thr Cys
 100 105 110
 Asp Tyr Phe Pro Leu Leu Gln Leu Ala Cys Ser Asp Thr Lys Phe Leu
 115 120 125
 Glu Val Met Gly Phe Ser Cys Ala Ala Phe Thr Leu Met Phe Thr Leu
 130 135 140
 Ala Leu Ile Phe Leu Ser Tyr Ile Tyr Ile Ile Arg Thr Ile Leu Arg
 145 150 155 160
 Ile Pro Ser Thr Ser Gln Arg Thr Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Met Val Val Ile Ser Ile Ser Tyr Gly Ser Cys Ile Phe Met Tyr
 180 185 190

Ile Lys Pro Ser Ala Lys Asp Arg Val Ser Leu Ser Lys Gly Val Ala
 195 200 205
 Ile Leu Asn Thr Ser Val Ala Pro
 210 215

<210> 1827
 <211> 219
 <212> PRT
 <213> Unknown (H38g745 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(219)
 <223> Xaa = Any Amino Acid

<400> 1827
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Ser Leu Ser Leu Leu Asp Ser Gln Leu His Asn
 85 90 95
 Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn
 100 105 110
 Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr
 115 120 125
 Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
 130 135 140
 Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser
 145 150 155 160
 Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Phe Ser Thr
 165 170 175
 Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val
 180 185 190
 Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala
 195 200 205
 Val Ala Ser Val Met Tyr Met Val Val Thr Pro
 210 215

<210> 1828
 <211> 268
 <212> PRT
 <213> Unknown (H38g746 protein)

<220>
 <223> Synthetic construct

<400> 1828
 Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr
 1 5 10 15
 Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val
 20 25 30
 Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile

```

      35              40              45
Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val
 50              55              60
Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu
65              70              75              80
Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr
      85              90              95
Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser
      100              105              110
Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn
      115              120              125
Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala
      130              135              140
Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala
145              150              155              160
Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu
      165              170              175
Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys
      180              185              190
Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr
      195              200              205
Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn
      210              215              220
Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met
225              230              235              240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
      245              250              255
Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly
      260              265

```

<210> 1829

<211> 316

<212> PRT

<213> Unknown (H38g747 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1829

```

Met Asp Leu Gly Asn Gln Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
 1              5              10              15
Phe Ser Gln Asp Leu Glu Asp Gln Gln Leu Leu Phe Ala Leu Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Arg Tyr Phe Phe Leu Ser
      50              55              60
Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Ala Val Pro Lys
65              70              75              80
Met Leu Val Asn Ile Gln Val Gln Ser Asn Ala Ile Ser Tyr Ala Asp
      85              90              95
Cys Ile Ala Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr
      100              105              110
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu Tyr Tyr Cys Val Thr Arg Asn Pro Cys Leu Cys Gly Leu Leu
      130              135              140

```

Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser
 145 150 155 160
 Leu Leu Val Leu Arg Val Ser Phe Cys Thr Ser Xaa Val Ile Gln His
 165 170 175
 Ph Tyr Cys Glu Leu Ala Gln Val Leu Arg Leu Thr Cys Ser Asp Thr
 180 185 190
 His Val Asn Tyr Ile Leu Leu Tyr Val Val Ala Gly Leu Leu Asp Phe
 195 200 205
 Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Tyr
 210 215 220
 Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Phe Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
 245 250 255
 Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser Trp Trp Gly Met
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Cys Leu Arg Asn Arg Asp Ile Lys Arg Thr Leu Glu Thr Leu
 290 295 300
 Leu Gly Arg Met Leu Tyr Ala Gln Xaa Arg Gly His
 305 310 315

<210> 1830

<211> 309

<212> PRT

<213> Unknown (H38g748 protein)

<220>

<223> Synthetic construct

<400> 1830

Met Glu Asn Cys Thr Glu Val Thr Lys Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Ser Val Pro Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Thr Phe Ile
 20 25 30
 Tyr Leu Leu Thr Leu Cys Gly Asn Leu Gly Met Met Leu Leu Ile Leu
 35 40 45
 Met Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met
 65 70 75 80
 Ala Gly Phe Leu Arg Gly Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala
 85 90 95
 Val Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Ala Ser Val Gly Ala Cys Leu Ala Leu
 130 135 140
 Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Phe His Ile Gly Gly
 145 150 155 160
 Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Phe Phe
 165 170 175
 Cys Asp Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Lys His Thr
 180 185 190
 Ser Glu Val Ile Leu Val Phe Thr Ser Ser Phe Asn Ile Phe Phe Val
 195 200 205
 Leu Leu Val Ile Phe Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu
 210 215 220
 Lys Met His Ser Ala Lys Gly His Gln Lys Ala Leu Ser Thr Cys Ala

225 230 235 240
 Ser His Phe Thr Ala Val Ser Val Phe Tyr Gly Thr Val Ile Phe Il
 245 250 255
 Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala
 260 265 270
 Ser Val Phe Tyr Ala Met Ile Ile Pro Met Leu Asn Pro Val Val Tyr
 275 280 285
 Ser Leu Arg Asn Arg Glu Val Gln Asn Ala Phe Lys Lys Val Leu Arg
 290 295 300
 Arg Gln Lys Phe Leu
 305

<210> 1831

<211> 313

<212> PRT

<213> Unknown (H38g749 protein)

<220>

<223> Synthetic construct

<400> 1831

Met His Thr Met Val Glu Asn His Thr Gln Val Thr Trp Phe Arg Leu
 1 5 10 15
 Leu Gly Leu Thr Glu Gln Glu Glu Leu Arg Gly Ile Leu Phe Val Leu
 20 25 30
 Phe Leu Leu Met His Ser Val Thr Val Met Gly Asn Leu Gly Met Ile
 35 40 45
 Thr Leu Ile His Ala Asp Pro Gln Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Val Leu Ser Phe Ile Asp Ser Ser Phe Ser Thr Val Asp Thr
 65 70 75 80
 Pro Arg Leu Leu Glu Ser Phe Leu Ile Ser Ser Gln Ser Ile Ser Phe
 85 90 95
 Ala Gly Cys Met Val Gln Met Ala Leu Met Ile Leu His Gly Thr Ala
 100 105 110
 Glu Cys Leu Leu Leu Ala Ile Met Ala Tyr Asp Arg Phe Thr Ala Ile
 115 120 125
 Cys His Pro Leu Leu Tyr His Thr Ile Ile Ser Gln Cys Leu Cys Ala
 130 135 140
 Leu Leu Val Val Thr Cys Tyr Thr Val Ser Val Ala Asn Ser Ala Leu
 145 150 155 160
 Leu Thr Gly Cys Ile Phe Lys Leu Pro Tyr Cys Gly Pro Asn Val Ile
 165 170 175
 Asn His Tyr Phe Cys Asp Ile Pro Pro Val Leu Gln Leu Ala Gly Ala
 180 185 190
 Asp Thr Tyr Glu Val Glu Thr Ile Ile Phe Ser Leu Cys Ala Leu Leu
 195 200 205
 Ile Leu Phe Thr Ile Thr Ile Ile Pro Val Ser Tyr Ala Tyr Ile Leu
 210 215 220
 Val Thr Ile Cys Arg Met Arg Ser Leu Gln Ala Gln Ser Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ile Ile Cys Leu Phe Tyr Ser Thr
 245 250 255
 Ile Thr Phe Met Tyr Ala Gln Pro Ser Ser His Asn Ser Met Glu His
 260 265 270
 Asn Lys Val Met Ser Val Phe Tyr Thr Val Val Ile Arg Arg Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Lys
 290 295 300
 Arg Arg Cys Leu Cys Lys Leu Ser S r
 305 310

<210> 1832
 <211> 314
 <212> PRT
 <213> Unknown (H38g750 prot in)

<220>
 <223> Synthetic construct

<400> 1832

```

Met Glu Asn Lys Thr Glu Val Thr Gln Phe Ile Leu Leu Gly Leu Thr
 1           5           10           15
Asn Asp Ser Glu Leu Gln Val Pro Leu Phe Ile Thr Phe Pro Phe Ile
 20           25           30
Tyr Ile Ile Thr Leu Val Gly Asn Leu Gly Ile Ile Val Leu Ile Phe
 35           40           45
Trp Asp Ser Cys Leu His Asn Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50           55           60
Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Ile Val Met
 65           70           75           80
Ala Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala
 85           90           95
Ala Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu
100           105           110
Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
115           120           125
His Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile
130           135           140
Gly Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp
145           150           155           160
Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe
165           170           175
Cys Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile
180           185           190
Ser Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala
195           200           205
Leu Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu
210           215           220
Lys Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala
225           230           235           240
Ser His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met
245           250           255
Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala
260           265           270
Pro Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr
275           280           285
Ser Leu Arg Asn Lys Glu Val Lys Ser Ala Phe Lys Lys Val Val Glu
290           295           300
Lys Ala Lys Leu Ser Val Gly Trp Ser Val
305           310

```

<210> 1833
 <211> 312
 <212> PRT
 <213> Unknown (H38g751 protein)

<220>
 <223> Synthetic construct

<400> 1833

Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile

```

1           5           10           15
Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
20           25           30
Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
35           40           45
Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
50           55           60
Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
65           70           75           80
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys
85           90           95
Leu Thr Gln Lys Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val
100          105          110
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
115          120          125
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr
130          135          140
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu
145          150          155          160
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe
165          170          175
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile
180          185          190
Asn Val Trp Tyr Gly Leu Ala Ala Ala Leu Leu Ser Thr Gly Leu Asp
195          200          205
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe
210          215          220
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly
225          230          235          240
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser
245          250          255
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His
260          265          270
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro
275          280          285
Val Ile Tyr Gly Val Arg Thr Lys Pro Ile Leu Glu Gly Ala Lys Gln
290          295          300
Met Phe Ser Asn Leu Ala Lys Gly
305          310

```

<210> 1834

<211> 332

<212> PRT

<213> Unknown (H38g752 protein)

<220>

<223> Synthetic construct

<400> 1834

```

Ser Ile Leu Phe Leu Tyr Phe Ser Leu Leu Gln Ala Ser Ser Asp Phe
1           5           10           15
Leu Ile Thr Leu Met Lys Asn Cys Thr Glu Val Thr Glu Phe Ile Leu
20           25           30
Leu Gly Leu Thr Asn Ala Pro Glu Leu Gln Val Pro Leu Leu Ile Met
35           40           45
Phe Thr Leu Ile Tyr Leu Val Asn Val Val Gly Asn Leu Gly Met Ile
50           55           60
Val Leu Ile Val Trp Asp Ile His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Ser His Leu Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr
85           90           95

```

Pro Thr Val Ile Ala Gly Leu Val Ile Gly Asp Lys Val Ile Ser Tyr
 100 105 110
 Asn Ala Cys Ala Ala Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val
 115 120 125
 Glu Asn Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val
 130 135 140
 Cys Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala
 145 150 155 160
 Cys Leu Ala Ile Ile Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile
 165 170 175
 His Ile Gly Glu Thr Phe Ser Leu Ser Phe Cys Met Ser Asn Glu Val
 180 185 190
 His Cys Phe Phe Cys Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys
 195 200 205
 Asp Arg His Val Asn Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn
 210 215 220
 Ile Phe Ser Ala Ile Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe
 225 230 235 240
 Ile Thr Ile Leu Lys Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu
 245 250 255
 Ser Thr Cys Ala Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr
 260 265 270
 Ile Ile Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr
 275 280 285
 Asp Lys Leu Ala Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Asn
 290 295 300
 Pro Leu Val Tyr Ser Leu Arg Asn Asn Glu Val Lys Ser Ala Phe Lys
 305 310 315 320
 Lys Val Ile Glu Lys Ala Lys Leu Ser Leu Leu Leu
 325 330

<210> 1835

<211> 318

<212> PRT

<213> Unknown (H38g753 protein)

<220>

<223> Synthetic construct

<400> 1835

Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
 1 5 10 15
 Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile
 20 25 30
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
 35 40 45
 Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
 50 55 60
 Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
 65 70 75 80
 Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
 85 90 95
 Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
 100 105 110
 Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
 130 135 140
 Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
 145 150 155 160
 Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val

				165						170						175
Met	Thr	His	Thr	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg	Leu	Ala	Cys	
			180						185					190		
Ala	Asn	Ile	Thr	Val	Asn	Ile	Val	Tyr	Gly	Leu	Thr	Val	Ala	Leu	Leu	
		195					200						205			
Ala	Met	Gly	Leu	Asp	Ser	Ile	Leu	Ile	Ala	Ile	Ser	Tyr	Gly	Phe	Ile	
	210					215					220					
Leu	His	Ala	Val	Phe	His	Leu	Pro	Ser	His	Asp	Ala	Gln	His	Lys	Ala	
225					230					235				240		
Leu	Ser	Thr	Cys	Gly	Ser	His	Ile	Gly	Ile	Ile	Leu	Val	Phe	Tyr	Ile	
			245					250						255		
Pro	Ala	Phe	Phe	Ser	Phe	Leu	Thr	His	Arg	Phe	Gly	His	His	Glu	Val	
		260						265					270			
Pro	Lys	His	Val	His	Ile	Phe	Leu	Ala	Asn	Leu	Tyr	Val	Leu	Val	Pro	
	275						280					285				
Pro	Val	Leu	Asn	Pro	Ile	Leu	Tyr	Gly	Ala	Arg	Thr	Lys	Glu	Ile	Arg	
	290					295					300					
Ser	Arg	Leu	Leu	Lys	Leu	Leu	His	Leu	Gly	Lys	Thr	Ser	Ile			
305					310						315					

<210> 1836

<211> 330

<212> PRT

<213> Unknown (H38g754 protein)

<220>

<223> Synthetic construct

<400> 1836

His	Ile	Glu	Pro	Gly	Asn	Asp	Thr	Gln	Ile	Ser	Glu	Phe	Leu	Leu	Leu	
1				5				10					15			
Gly	Leu	Ser	Asp	Lys	Pro	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	
		20						25				30				
Phe	Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	
		35				40						45				
Ala	Thr	Ile	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu	
	50					55				60						
Ser	Asn	Leu	Ser	Phe	Ala	Asp	Ile	Cys	Phe	Ile	Ser	Thr	Thr	Ile	Pro	
65					70				75					80		
Lys	Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Ser	Arg	Val	Ile	Thr	Tyr	Ala	
			85					90					95			
Gly	Cys	Ile	Thr	Gln	Met	Cys	Phe	Phe	Val	Leu	Leu	Glu	Ala	Leu	Asp	
		100						105					110			
Ser	Leu	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Gln	Phe	Val	Ala	Ile	Cys	
	115					120						125				
His	Pro	Leu	His	Tyr	Met	Val	Ile	Met	Ser	Pro	Trp	Phe	Cys	Gly	Leu	
	130					135					140					
Leu	Val	Leu	Ala	Ser	Trp	Ile	Ile	Met	Ser	Pro	Trp	Leu	Cys	Gly	Leu	
145					150					155				160		
Leu	Val	Leu	Ala	Ser	Trp	Ile	Ile	Ser	Asp	Leu	Asp	Ser	Ser	Leu	His	
			165					170					175			
Ser	Leu	Met	Val	Leu	Ser	Leu	Pro	Phe	Cys	Thr	Asp	Phe	Gln	Ile	Pro	
		180						185					190			
His	Phe	Val	Tyr	Glu	Leu	Asn	Gln	Val	Ile	Arg	Leu	Ala	Gly	Ser	Asp	
	195					200						205				
Thr	Phe	Leu	Asn	Asp	Met	Ala	Met	Tyr	Phe	Ala	Val	Gly	Pro	Leu	Gly	
	210					215					220					
Gly	Val	Pro	Leu	Ala	Gly	Ile	Leu	Tyr	Leu	Tyr	Cys	Lys	Ile	Val	Phe	
225					230					235				240		
Ser	Ile	Arg	Ala	Ile	Ser	Ser	Ala	Gln	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	
			245						250					255		

Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Arg Ser
 260 265 270
 Leu Gly Val Tyr Phe Ser Ser Ala Pro Thr Gln Asn S r His Ser Gly
 275 280 285
 Ala Ala Ala S r Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 290 295 300
 Phe Ile Cys Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Asn Gln
 305 310 315 320
 Phe Ile Arg Val Val Pro Phe Phe Arg Lys
 325 330

<210> 1837

<211> 312

<212> PRT

<213> Unknown (H38g755 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1837

Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu
 1 5 10 15
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe
 20 25 30
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu
 35 40 45
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro
 65 70 75 80
 Lys Met Met Ala Gly Leu Leu Ile Ala His Lys Val Ile Ser Tyr Asn
 85 90 95
 Val Cys Ala Ala Gln Met Phe Phe Phe Ala Val Phe Ala Thr Val Glu
 100 105 110
 Ser Tyr Phe Leu Thr Ser Val Ala Tyr Asp Cys Tyr Arg Val Met Cys
 115 120 125
 Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Ser
 130 135 140
 Leu Ala Ile Ala Cys Tyr Val Leu Gly Leu Leu Thr Ala Ala Val Asp
 145 150 155 160
 Ile Gly Asp Ile Cys Met Ser Asn Glu Ile His His Phe Phe Cys Asp
 165 170 175
 Ile Leu Ala Val Met Thr Leu Thr Cys Ser Asn Lys His Ile Asn Glu
 180 185 190
 Leu Ile Leu Val Leu Leu Gln Ala Ile Phe Phe Thr Leu Leu Val Ile
 195 200 205
 Leu Ile Ser Cys Leu Phe Val Phe Val Phe Val Thr Ile Leu Lys Met
 210 215 220
 His Leu Phe Lys Ser Tyr Lys Lys Val Leu Ser Thr Tyr Gly Ser His
 225 230 235 240
 Leu Thr Ala Val Pro Leu Phe Tyr Glu Thr Val Leu Ile Thr Tyr Val
 245 250 255
 Gln Pro Ser Ser Ser His Phe Met Asn Thr Glu Lys Ile Val Ser Val
 260 265 270
 Phe His Ile Met Val Ile Pro Met Leu Ile Pro Val Val Tyr Ser Leu
 275 280 285
 Arg Asn Asn Glu Val Lys Ser Ala Phe Lys Thr Val Val Glu Glu Thr

290 295 300
 Lys Tyr Phe Leu Gly Leu Val Phe
 305 310

<210> 1838
 <211> 315
 <212> PRT
 <213> Unknown (H38g756 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1838
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu
 1 5 10 15
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu
 20 25 30
 Leu Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu
 35 40 45
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe
 85 90 95
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr
 100 105 110
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala
 130 135 140
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val
 165 170 175
 Leu Ala His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys
 180 185 190
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser
 195 200 205
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile
 210 215 220
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr
 225 230 235 240
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val
 245 250 255
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro
 260 265 270
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His
 290 295 300
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys
 305 310 315

<210> 1839
 <211> 329
 <212> PRT

<213> Unknown (H38g757 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1839

```

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly
 1          5          10          15
Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val
          20          25          30
Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile
          35          40          45
Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe
          50          55          60
Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val
65          70          75          80
Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser
          85          90          95
Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu
          100          105          110
Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly
          130          135          140
Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu
          145          150          155          160
His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile
          165          170          175
Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser
          180          185          190
Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu
          195          200          205
Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Thr Val
          210          215          220
Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe
          225          230          235          240
Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr
          245          250          255
Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser
          260          265          270
Gly Ala Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
          275          280          285
Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys
          290          295          300
Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Leu Gly Leu
          305          310          315          320
Lys Leu Tyr Pro Xaa Leu Gln Gly Ser
          325

```

<210> 1840

<211> 320

<212> PRT

<213> Unknown (H38g758 protein)

<220>

<223> Synthetic construct

<400> 1840

```

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly
 1           5           10           15
Phe Ala Glu Asp Ser Asp Met Gln Leu Leu Leu His Gly Leu Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr
          35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65           70           75           80
Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly
          85           90           95
Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn
          100          105          110
Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr
          115          120          125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
          130          135          140
Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
145          150          155          160
Leu Thr Ile Leu Arg Leu Ser Ser Cys Thr Asn Met Glu Ile Pro His
          165          170          175
Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Phe Ile Asn Asn Ile Val Met Cys Phe Val Thr Ile Val Leu Gly Val
          195          200          205
Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser
          210          215          220
Val Leu Arg Val Ser Ser Ala Arg Gly Gln His Lys Ala Phe Thr Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
          245          250          255
Gly Val Tyr Leu Ser Ser Ala Val Thr Pro Pro Ser Arg Thr Ser Leu
          260          265          270
Ala Ala Ser Val Met His Thr Met Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu
          290          295          300
Leu Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser
305          310          315          320

```

<210> 1841

<211> 328

<212> PRT

<213> Unknown (H38g759 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1841

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
          20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
          35           40           45

```



```

Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
 50          55          60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Il Val Asp Ile Gln Ser His S r Arg Val Ile Ser Tyr Ala Gly
      85          90          95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
      100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys
      115          120          125
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
      130          135          140
Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu
145          150          155          160
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile
      165          170          175
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
      180          185          190
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
      195          200          205
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
      210          215          220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
225          230          235          240
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
      245          250          255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
      260          265          270
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275          280          285
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
      290          295          300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
305          310          315          320
Leu Phe His Ser Phe Cys Arg Met
      325

```

<210> 1842

<211> 210

<212> PRT

<213> Unknown (H38g760 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 1842

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1          5          10          15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
      20          25          30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
      35          40          45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
      50          55          60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65          70          75          80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile

```

<400> 1843																
Met	Glu	Pro	Glu	Lys	Gln	Thr	Glu	Ile	Ser	Glu	Phe	Phe	Leu	Gln	Gly	
1				5					10					15		
Leu	Ser	Glu	Lys	Pro	Glu	His	Gln	Thr	Leu	Leu	Phe	Thr	Met	Phe	Leu	
			20					25					30			
Ser	Thr	Tyr	Leu	Val	Thr	Ile	Ile	Gly	Asn	Ala	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Ile	Ile	Thr	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	
	50					55					60					
Asn	Leu	Ser	Leu	Val	Asp	Thr	Leu	Leu	Ser	Ser	Thr	Thr	Val	Pro	Lys	
65					70					75					80	
Met	Leu	Ala	Asn	Ile	Gln	Ala	Gln	Ser	Arg	Ala	Ile	Pro	Phe	Val	Gly	
			85						90					95		
Cys	Leu	Thr	Gln	Met	Tyr	Ala	Phe	His	Leu	Phe	Gly	Thr	Met	Asp	Ser	
			100					105					110			
Phe	Leu	Leu	Ala	Val	Met	Ala	Ile	Asp	Arg	Phe	Val	Ala	Ile	Val	His	
		115					120					125				
Pro	Gln	Arg	Tyr	Leu	Val	Leu	Met	Cys	Ser	Pro	Val	Cys	Gly	Leu	Leu	
	130					135					140					
Leu	Gly	Ala	Ser	Trp	Met	Ile	Thr	Asn	Leu	Gln	Ser	Leu	Ile	His	Thr	
145					150					155					160	
Cys	Leu	Met	Ala	Gln	Leu	Thr	Phe	Cys	Ala	Gly	Ser	Glu	Ile	Ser	His	
			165						170					175		
Phe	Phe	Cys	Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu	Ser	Gly	Ser	Asp	Thr	
			180					185					190			
His	Thr	Asn	Glu	Leu	Val	Ile	Phe	Ala	Phe	Gly	Ile	Val	Val	Gly	Thr	
		195					200					205				
Ser	Pro	Phe	Ser	Cys	Ile	Leu	Leu	Ser	Tyr	Ile	Arg	Ile	Phe	Trp	Thr	
	210					215					220					
Val	Phe	Lys	Ile	Pro	Ser	Thr	Arg	Gly	Lys	Trp	Lys	Ala	Phe	Ser	Thr	
225					230					235					240	
Cys	Gly	Leu	His	Leu	Thr	Val	Val	Ser	Leu	Ser	Tyr	Gly	Thr	Ile	Phe	
			245						250					255		
Ala	Val	Tyr	Leu	Gln	Pro	Thr	Ser	Pro	Ser	Ser	Ser	Gln	Lys	Asp	Lys	
			260					265					270			

Ala Ala Ala Leu Met Cys Gly Val Ph Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pr Cys Pro Arg Pr
 305 310 315

<210> 1844

<211> 316

<212> PRT

<213> Unknown (H38g762 protein)

<220>

<223> Synthetic construct

<400> 1844

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu
 20 25 30
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu
 35 40 45
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly
 50 55 60
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg
 65 70 75 80
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala
 85 90 95
 Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys Arg
 115 120 125
 Pro Leu Arg Tyr Gly Ala Leu Val Thr Pro Trp Ala Cys Ala Ser Leu
 130 135 140
 Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr
 145 150 155 160
 Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro
 165 170 175
 Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr
 180 185 190
 Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu
 195 200 205
 Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Val Leu Gly Leu Pro Arg Pro Arg Ala Phe Ser Tyr Cys Gly Ala
 225 230 235 240
 His Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser
 245 250 255
 Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu
 260 265 270
 Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile
 275 280 285
 Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu
 290 295 300
 Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
 305 310 315

<210> 1845

<211> 312

<212> PRT

<213> Unknown (H38g763 protein)

<220>

<223> Synthetic construct

<400> 1845

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1      5      10      15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
 20      25      30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35      40      45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50      55      60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65      70      75      80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85      90      95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100     105     110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
 115     120     125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130     135     140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145     150     155     160
Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
 165     170     175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180     185     190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195     200     205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
 210     215     220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225     230     235     240
Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245     250     255
Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260     265     270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275     280     285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290     295     300
Leu Val Ile Tyr Lys Arg Ile Ser
 305     310

```

<210> 1846

<211> 318

<212> PRT

<213> Unknown (H38g764 protein)

<220>

<223> Synthetic construct

<400> 1846

```

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1      5      10      15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
 20      25      30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
 35      40      45

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Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50          55          60
Gln Leu S r Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
65          70          75          80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
          85          90          95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
          130          135          140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
145          150          155          160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
          165          170          175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
          180          185          190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu Leu
          195          200          205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
          210          215          220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
          245          250          255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
          260          265          270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
          290          295          300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305          310          315

```

<210> 1847

<211> 105

<212> PRT

<213> Unknown (H38g765 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(105)

<223> Xaa = Any Amino Acid

<400> 1847

```

Thr Leu Cys Ala Thr Ala Xaa Leu Asp His Phe Ile Cys Glu Leu Pro
 1          5          10          15
Ala Leu Leu Lys Leu Ala Arg Gly Gly Ile Gly Asp Thr Thr Glu Asn
          20          25          30
Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val
          35          40          45
Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg
          50          55          60
Phe Ser Gly Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu
65          70          75          80
Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln
          85          90          95
Pro Ala Gln Arg Arg Asn Gln Ala Arg

```

100

105

<210> 1848
 <211> 104
 <212> PRT
 <213> Unknown (H38g766 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(104)
 <223> Xaa = Any Amino Acid

<400> 1848
 Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met Ala
 1 5 10 15
 Phe Asn Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala Val
 20 25 30
 Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val Arg
 35 40 45
 Gly Ser Leu Phe Phe Phe Pro Leu Leu Ile Lys Arg Leu Ala
 50 55 60
 Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln Asp
 65 70 75 80
 Val Met Lys Leu Ala Tyr Ala Asp Asn Leu Pro Asn Val Val Tyr Gly
 85 90 95
 Leu Asn Xaa Pro Phe Trp Leu Val
 100

<210> 1849
 <211> 320
 <212> PRT
 <213> Unknown (H38g767 protein)

<220>
 <223> Synthetic construct

<400> 1849
 Met Glu Thr Gly Asn Gln Thr His Ala Gln Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Ala Thr Ser Glu Ile Gln Phe Ile Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Phe Thr Gly Asn Leu Leu Ile Leu Ala
 35 40 45
 Ile Cys Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn
 100 105 110
 Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Gly Ser Trp Cys Il Ser Val Met Gly Ser Leu Leu Glu Thr
 145 150 155 160
 Leu Thr Val Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His
 165 170 175

Phe Phe Cys Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Ile Asn Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val
 195 200 205
 Ile Ser Phe Thr Gly Ile Phe Phe S r Tyr Tyr Lys Ile Val Phe Ser
 210 215 220
 Ile Leu Arg Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe
 245 250 255
 Gly Val Tyr Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu
 260 265 270
 Val Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Thr Asp Met Lys Arg Ala Leu Gly Arg Leu
 290 295 300
 Leu Ser Arg Ala Thr Phe Phe Asn Gly Asp Ile Thr Ala Gly Leu Ser
 305 310 315 320

<210> 1850

<211> 312

<212> PRT

<213> Unknown (H38g768 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1850

Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1 5 10 15
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
 20 25 30
 Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35 40 45
 Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
 65 70 75 80
 Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
 85 90 95
 Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
 100 105 110
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
 130 135 140
 Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
 145 150 155 160
 Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
 165 170 175
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
 180 185 190
 Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
 195 200 205
 Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
 210 215 220
 Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys

225 230 235 240
 Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val
 245 250 255
 Val Tyr Leu Val Pr Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile
 260 265 270
 Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu
 290 295 300
 Gln Lys Lys Arg Thr Met Xaa Met
 305 310

<210> 1851

<211> 319

<212> PRT

<213> Unknown (H38g769 protein)

<220>

<223> Synthetic construct

<400> 1851

Met Glu Pro Gly Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Gln Glu Pro Gly Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys
 65 70 75 80
 Met Leu Met Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ile Ala
 85 90 95
 Cys Leu Met Gln Met Tyr Phe Phe Ile Leu Phe Ala Gly Phe Glu Asn
 100 105 110
 Phe Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Met Val Ile Met Asn Pro His Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Ala Ser Trp Thr Met Ser Ala Leu Tyr Ser Leu Leu Gln Ile
 145 150 155 160
 Leu Met Val Val Arg Leu Ser Phe Cys Thr Ala Leu Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Asn Gln Val Ile Gln Leu Ala Cys Ser Asp Ser
 180 185 190
 Phe Leu Asn His Met Val Ile Tyr Phe Thr Val Ala Leu Leu Gly Gly
 195 200 205
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ile Ser Ser
 210 215 220
 Ile His Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Leu
 245 250 255
 Gly Val Tyr Leu Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala
 260 265 270
 Thr Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Gly Ile His
 290 295 300
 Leu Leu Trp Gly Thr M t Lys Gly Gln Phe Phe Lys Lys Cys Pro
 305 310 315

<210> 1852
 <211> 74
 <212> PRT
 <213> Unknown (H38g770 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(74)
 <223> Xaa = Any Amino Acid

<400> 1852
 Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg Val Val Ile Leu
 1 5 10 15
 Leu Leu Pro Tyr Asp Val Ile Leu Ala Ser Xaa Gly Ala Val Ala Arg
 20 25 30
 Ala Val Cys Cys Met Arg Phe Ser Gly Gly Pro Arg Arg Ala Leu Gly
 35 40 45
 Thr Cys Gly Ser His Pro Thr Ala Val Trp Leu Phe Xaa Gly Ser Gly
 50 55 60
 Lys Xaa Thr Tyr Leu Gln Ala Ala Gln Leu
 65 70

<210> 1853
 <211> 309
 <212> PRT
 <213> Unknown (H38g771 protein)

<220>
 <223> Synthetic construct

<400> 1853
 Met Lys Ser Trp Asn Asn Thr Ile Ile Leu Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Gly Ile Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn
 100 105 110
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser
 145 150 155 160
 Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly
 195 200 205
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser

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      210              215              220
Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu
      245              250              255
Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala
      260              265              270
Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe
      290              295              300
Phe Arg Gly Lys Gln
305

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<210> 1854
 <211> 82
 <212> PRT
 <213> Unknown (H38g772 protein)

<220>
 <223> Synthetic construct

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<400> 1854
Met Val Thr Glu Phe Leu Pro Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1              5              10              15
Gln Met Leu Leu Leu Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Pro
      20              25              30
Leu Gly Asn Gly Thr Ile Pro Gly Leu Ile Ser Leu Asp Ser Arg Leu
      35              40              45
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
      50              55              60
Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
      65              70              75              80
Pro Ala

```

<210> 1855
 <211> 216
 <212> PRT
 <213> Unknown (H38g773 protein)

<220>
 <223> Synthetic construct

```

<400> 1855
Leu Met Asp Leu Lys Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe
 1              5              10              15
Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Val Thr
      20              25              30
Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys Phe Leu Leu
      35              40              45
Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
      50              55              60
Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met Ala Thr Phe
      65              70              75              80
Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala Val Ala Thr
      85              90              95
Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
      100              105              110
Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
      115              120              125

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Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val Phe Pro Val
 130 135 140
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
 145 150 155 160
 Met Gly Ser Gly Glu Gly Arg Cys Lys Ala Phe Thr Thr Cys Ser Ser
 165 170 175
 His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr
 180 185 190
 Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys Met Val Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1856

<211> 305

<212> PRT

<213> Unknown (H38g774 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(305)

<223> Xaa = Any Amino Acid

<400> 1856

Met Lys Pro Gly Asn Asp Thr Arg Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Ala Glu Pro Glu Leu Gln Pro Phe Phe Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Ile Ser Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Ala Val Leu Asp Ser
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Tyr Tyr Thr Ile Ile Met Asn Pro Gln Phe Tyr Ser Trp Ile
 130 135 140
 Leu Ser Val Leu Asn Ser Leu Leu Gln Ser Leu Met Val Leu Pro Leu
 145 150 155 160
 Pro Phe Tyr Thr Asp Ile Ala Ile Pro His Phe Phe Cys Glu Leu Asn
 165 170 175
 Gln Ile Ile Cys Ile Ala Cys Ser Asp Thr Phe Leu Asn Asp Ile Met
 180 185 190
 Ile Tyr Cys Ala Thr Val Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile
 195 200 205
 Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser
 210 215 220
 Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser
 225 230 235 240
 Val Val Ser Leu Phe Tyr Gly Thr Ser Leu Gly Met Tyr Leu Ser Ser
 245 250 255
 Ala Ala Thr His Asn Ser Pro Ser Ser Ala Thr Ala Ser Val Met Tyr
 260 265 270
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn

275 280 285
 Lys Asp Leu Lys Asp Ala Leu Lys Arg Phe Phe Arg Arg Lys Gln Xaa
 290 295 300

Lys
305

<210> 1857
 <211> 120
 <212> PRT
 <213> Unknown (H38g775 protein)

<220>
 <223> Synthetic construct

<400> 1857
 Phe Ser Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
 1 5 10 15
 Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
 20 25 30
 Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
 35 40 45
 Val Thr Glu Cys Phe Leu Leu Val Val Lys Ser Asn Asp Leu Tyr Val
 50 55 60
 Ala Ile Cys His Pro Ser Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
 65 70 75 80
 Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
 85 90 95
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
 100 105 110
 Lys Ile Tyr His Phe Phe Cys Glu
 115 120

<210> 1858
 <211> 214
 <212> PRT
 <213> Unknown (H38g776 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(214)
 <223> Xaa = Any Amino Acid

<400> 1858
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
 35 40 45
 Pro Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu
 85 90 95
 Gln Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn Phe Leu Cys Asp
 100 105 110
 Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr Phe Thr Asn His
 115 120 125

Ile Ile Met Tyr Phe Pr Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
 130 135 140
 Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser Ile Leu Arg Val
 145 150 155 160
 Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr Gly Ser His
 165 170 175
 Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu
 180 185 190
 Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala Ser Val
 195 200 205
 Met Tyr Ala Val Val Thr
 210

<210> 1859
 <211> 166
 <212> PRT
 <213> Unknown (H38g777 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(166)
 <223> Xaa = Any Amino Acid

<400> 1859
 Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Phe
 1 5 10 15
 Leu Ser Pro Arg Ile His Met Leu Leu Phe Gly Leu Phe Tyr Leu Phe
 20 25 30
 Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser
 35 40 45
 Leu Asp Ser Ile Leu His Thr Pro Met Tyr Phe Phe Leu Xaa His Leu
 50 55 60
 Ser Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu
 65 70 75 80
 Val Asn Leu Leu His Ser Ala Lys Pro Ile Tyr Phe Ala Gly Cys Met
 85 90 95
 Thr Tyr Thr Phe Leu Phe Leu Arg Phe Ala His Thr Glu Cys Leu Leu
 100 105 110
 Leu Val Leu Met Ser Tyr Asp Trp Tyr Val Ala Ile Leu Thr Pro Leu
 115 120 125
 Arg Tyr Ile Ile Ile Met Thr Trp Lys Val Phe Ile Ile Ser Ala Ile
 130 135 140
 Thr Ser Trp Thr Cys Gly Ser Phe Leu Ser Met Val His Val Ser Leu
 145 150 155 160
 Ile Leu Arg Leu Pro Phe
 165

<210> 1860
 <211> 93
 <212> PRT
 <213> Unknown (H38g778 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(93)
 <223> Xaa = Any Amino Acid

<400> 1860

Gln Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Leu Phe
 1 5 10 15
 Lys Leu Ala Leu Ala Tyr Arg Pro Xaa Cys Tyr Cys His Leu Cys Thr
 20 25 30
 His Pro Phe Tyr His Ile Asp His Val Xaa Glu Ala Ile Ile Phe Phe
 35 40 45
 Leu Val Ala Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val
 50 55 60
 Thr Thr Ser Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val His Leu
 65 70 75 80
 His Phe Phe Cys Asp Ile Pro Ser Phe Cys Ser Tyr Ser
 85 90

<210> 1861

<211> 215

<212> PRT

<213> Unknown (H38g779 protein)

<220>

<223> Synthetic construct

<400> 1861

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
 35 40 45
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu
 65 70 75 80
 Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys
 100 105 110
 Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn
 115 120 125
 Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe
 130 135 140
 Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala
 195 200 205
 Met Met Tyr Thr Val Val Ala
 210 215

<210> 1862

<211> 219

<212> PRT

<213> Unknown (H38g780 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amin Acid

<400> 1862

```

Ser Asn Leu Ser Phe Thr Asp L u Xaa Phe S r Ser Val Thr Met Pr
 1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
 20           25           30
Gly Cys Leu Thr Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu
 35           40           45
Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 50           55           60
Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser
 65           70           75           80
Leu Val Leu Leu Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His
 85           90           95
Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro
100           105           110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
115           120           125
Ile His Ile Asn Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val
130           135           140
Ile Leu Pro Phe Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser
145           150           155           160
Ser Ile Leu Lys Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser
165           170           175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
180           185           190
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp
195           200           205
Thr Val Met Ser Met Met Tyr Thr Val Val Thr
210           215

```

<210> 1863

<211> 314

<212> PRT

<213> Unknown (H38g781 protein)

<220>

<223> Synthetic construct

<400> 1863

```

Met Glu Asn Asn Thr Glu Val Thr Glu Phe Ile Leu Val Gly Leu Thr
 1           5           10           15
Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Ile Val Phe Leu Phe Ile
 20           25           30
Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Glu Leu Ile Leu
 35           40           45
Leu Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50           55           60
Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met
 65           70           75           80
Val Gly Phe Leu Thr Gly Asp Lys Phe Ile Leu Tyr Asn Ala Cys Ala
 85           90           95
Thr Gln Phe Phe Phe Phe Val Ala Phe Ile Thr Ala Glu Ser Phe Leu
100           105           110
Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Leu Cys Lys Pro Leu
115           120           125
His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Cys Leu Ala Ile
130           135           140
Gly Ser Tyr Ile Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asn

```

145		150		155		160									
Thr	Phe	Arg	Leu	Ser	Phe	Cys	Arg	Ser	Asn	Val	Val	Glu	His	Phe	Phe
				165					170					175	
Cys	Asp	Ala	Pro	Pro	Leu	Leu	Thr	Leu	Ser	Cys	Ser	Asp	Asn	Tyr	Ile
			180					185					190		
Ser	Glu	Met	Val	Ile	Phe	Phe	Val	Val	Gly	Phe	Asn	Asp	Leu	Phe	Ser
		195					200					205			
Ile	Leu	Val	Ile	Leu	Ile	Ser	Tyr	Leu	Phe	Ile	Phe	Ile	Thr	Ile	Met
		210				215						220			
Lys	Met	Arg	Ser	Pro	Glu	Gly	Arg	Gln	Lys	Ala	Phe	Ser	Thr	Cys	Ala
225				230						235				240	
Ser	His	Leu	Thr	Ala	Val	Ser	Ile	Phe	Tyr	Gly	Thr	Gly	Ile	Phe	Met
				245					250				255		
Tyr	Leu	Arg	Pro	Asn	Ser	Ser	His	Phe	Met	Gly	Thr	Asp	Lys	Met	Ala
			260					265					270		
Ser	Val	Phe	Tyr	Ala	Ile	Val	Ile	Pro	Met	Leu	Asn	Pro	Leu	Val	Tyr
		275				280						285			
Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Ser	Ala	Phe	Lys	Lys	Thr	Val	Gly
		290				295					300				
Lys	Ala	Lys	Ala	Ser	Ile	Gly	Phe	Ile	Phe						
305				310											

<210> 1864

<211> 189

<212> PRT

<213> Unknown (H38g782 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(189)

<223> Xaa = Any Amino Acid

<400> 1864

Ala	Thr	Lys	Glu	Leu	Cys	Phe	Leu	Gly	Val	Tyr	Ile	Pro	Lys	Gly	Asp
1				5				10						15	
Ala	Cys	Trp	Lys	Xaa	Leu	Xaa	Leu	Gly	Leu	His	Leu	Leu	Leu	Leu	Gly
		20						25					30		
Xaa	Gln	Val	Val	Ser	Met	Val	Gly	Asn	Leu	Ala	Leu	Ile	Ala	Leu	Ile
		35					40					45			
Gly	Xaa	Asn	Ser	Tyr	Leu	His	His	Pro	Gln	Ala	Leu	Phe	Ser	Phe	Thr
		50				55					60				
Gln	Ser	Phe	Pro	Asp	Leu	Tyr	Cys	Pro	Val	Cys	Thr	Pro	Arg	Met	Leu
65				70					75					80	
Met	Thr	Phe	Val	Ser	Lys	Lys	Asn	Ile	Phe	Tyr	Val	Arg	Cys	Met	Thr
				85				90					95		
Gln	Leu	Ser	Gln	Leu	Phe	Phe	Leu	Phe	Ile	Val	Leu	Ser	Ile	Lys	Tyr
		100						105					110		
His	Val	Leu	Met	Phe	Ile	Ala	Cys	Gly	Cys	Leu	Val	Ala	Ile	Tyr	Asn
		115				120						125			
Pro	Ser	Leu	His	Glu	Val	Thr	Met	Ser	Pro	Gln	Val	Arg	Glu	Met	Arg
		130				135					140				
Glu	Ser	Gly	Phe	Ala	Gly	Thr	Thr	Ala	His	Thr	Gly	His	Ile	Leu	Arg
145				150					155					160	
Pro	Asn	Leu	Cys	Asn	Ile	Asp	Val	Ile	Asn	His	His	Leu	Thr	Asp	Ser
				165					170					175	
Leu	Leu	Val	Leu	Xaa	Val	Ser	Cys	Thr	Ser	Thr	Cys	Ala			
		180						185							

<210> 1865

<211> 311
 <212> PRT
 <213> Unknown (H38g783 protein)

<220>
 <223> Synthetic construct

<400> 1865

```

Met Thr Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu
 1           5           10           15
Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
          20           25           30
Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
          35           40           45
Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
65           70           75           80
Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Thr Ile Thr Phe Val
          85           90           95
Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
          100          105          110
Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
          115          120          125
Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp
          130          135          140
Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln
145          150          155          160
Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg
          165          170          175
His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp
          180          185          190
Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly
          195          200          205
Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile
          210          215          220
Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Pro Lys Ala Phe Asn
225          230          235          240
Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly
          245          250          255
Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp
          260          265          270
Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg
          290          295          300
Leu Gln Lys Arg Lys Cys Cys
305          310

```

<210> 1866
 <211> 312
 <212> PRT
 <213> Unknown (H38g784 protein)

<220>
 <223> Synthetic construct

<400> 1866

```

Met Thr Gly Glu Arg Asn Ser Thr Arg Ile Thr Lys Phe Ile Leu Leu
 1           5           10           15
Gly Phe Ser Glu Phe Pro Lys Asn Pro Ile Phe Leu Phe Ser Ile Phe

```

```

      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Val Ser Trp Asn Ile Asn Leu Ile Thr
  35      40      45
Leu Ile Arg Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50      55      60
Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Thr Ile Ala Pro
  65      70      75      80
Lys Met Leu Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
      85      90      95
Gly Cys Ser Met Gln Tyr Phe Phe Phe Ser Ser Leu Gly Leu Thr Glu
      100      105      110
Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
      115      120      125
Asn Pro Leu Leu Tyr Arg Ala Ile Met Phe Pro Thr Leu Cys Val Gln
      130      135      140
Met Val Ala Gly Ser Cys Ile Thr Gly Phe Leu Gly Ser Phe Ile Gln
      145      150      155      160
Leu Cys Ala Leu Leu Gln Leu His Phe Cys Gly Pro Asn Val Ile Asn
      165      170      175
His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser Asp
      180      185      190
Thr Phe Phe Phe Gln Val Met Thr Ser Val Leu Thr Val Ile Phe Gly
      195      200      205
Leu Thr Ser Val Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Ile Ala
      210      215      220
Thr Ile Leu Lys Ile Thr Ser Ala Glu Gly Arg Ala Lys Ser Phe Asn
      225      230      235      240
Thr Cys Ala Ser His Leu Thr Ala Val Ile Leu Phe Phe Gly Ser Gly
      245      250      255
Ile Phe Val Tyr Met Tyr Pro Asn Ala Gly Asp Ser Leu Ser Gln Asn
      260      265      270
Lys Leu Ala Ser Val Leu Tyr Thr Val Thr Ile Pro Met Leu Asn Pro
      275      280      285
Val Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Asn Arg
      290      295      300
Trp Lys Lys Arg Ile Phe Ser Trp
305      310

```

<210> 1867

<211> 444

<212> PRT

<213> Unknown (H38g785 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 1867

```

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu
  1      5      10      15
Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe
      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala
      35      40      45
Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu
      50      55      60
Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro
      65      70      75      80

```

Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
 85 90 95
 Gly Cys Thr Met Gln Tyr Phe Ser S r Leu Asn Val Thr Glu Cys Cys
 100 105 110
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pr
 115 120 125
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val
 130 135 140
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys
 145 150 155 160
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe
 165 170 175
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe
 180 185 190
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His
 195 200 205
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His
 210 215 220
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp
 225 230 235 240
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met
 245 250 255
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr
 260 265 270
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Leu Ser Leu Ala
 275 280 285
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln
 290 295 300
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser
 305 310 315 320
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val
 325 330 335
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr
 340 345 350
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys
 355 360 365
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr
 370 375 380
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu
 385 390 395 400
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg
 405 410 415
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala
 420 425 430
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro
 435 440

<210> 1868

<211> 310

<212> PRT

<213> Unknown (H38g786 protein)

<220>

<223> Synthetic construct

<400> 1868

Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 Leu Leu Gly Pro Arg Il Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu Ile

35	40	45
Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His		
50	55	60
Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln Met		
65	70	75
Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys		
85	90	95
Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys Leu		
100	105	110
Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro		
115	120	125
Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala		
130	135	140
Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val Val		
145	150	155
Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His Phe		
165	170	175
Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp		
180	185	190
Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val Gly		
195	200	205
Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile		
210	215	220
Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys		
225	230	235
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Ile		
245	250	255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val		
260	265	270
Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu Ile		
275	280	285
Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala Leu		
290	295	300
Gly Lys Glu Ser His Ser		
305	310	

<210> 1869

<211> 314

<212> PRT

<213> Unknown (H38g787 protein)

<220>

<223> Synthetic construct

<400> 1869

Met Glu Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly	
1	5
Phe Ser Asn Tyr Pro Glu Leu Gln Gly Gln Leu Phe Val Ala Phe Leu	
20	25
Val Ile Tyr Leu Val Thr Leu Ile Gly Asn Ala Ile Ile Ile Val Ile	
35	40
Val Ser Leu Asp Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu	
50	55
Asn Leu Ser Val Val Asp Leu Ser Phe Ser Ala Val Ile Met Pro Glu	
65	70
Met Leu Val Val Leu Ser Thr Glu Lys Thr Thr Ile Ser Phe Gly Gly	
85	90
Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Ala Glu Cys	
100	105
Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His	
115	120
	125

```

Pro Leu Asn Tyr Gln Met Ile Met Asn Lys Gly Val Phe Met Lys Leu
 130                      135                      140
Ile Ile Phe Ser Trp Ala Leu Gly Phe Met Leu Gly Thr Val Gln Thr
145                      150                      155                      160
Ser Trp Val Ser Ser Phe Pro Phe Cys Gly Leu Asn Glu Ile Asn His
                      165                      170                      175
Ile Ser Cys Glu Thr Pro Ala Val Leu Glu Leu Ala Cys Ala Asp Thr
                      180                      185                      190
Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Phe Leu Ile Ile Leu
                      195                      200                      205
Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala
                      210                      215                      220
Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr
225                      230                      235                      240
Cys Ala Ala His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Ser
                      245                      250                      255
Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys
                      260                      265                      270
Val Met Ser Leu Ser Tyr Ser Leu Leu Thr Pro Leu Leu Asn Leu Leu
                      275                      280                      285
Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Ala Leu Met Lys Leu
                      290                      295                      300
Trp Arg Arg Arg Val Val Leu His Thr Ile
305                      310

```

<210> 1870

<211> 331

<212> PRT

<213> Unknown (H38g788 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1870

```

Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1      5      10      15
Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu
      20      25      30
Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu
      35      40      45
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
      50      55      60
Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
      65      70      75      80
Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met Thr Xaa Thr Phe Leu
      85      90      95
Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu Leu Val Leu Met Ser
      100     105     110
Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile
      115     120     125
Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys
      130     135     140
Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro
      145     150     155     160
Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe Cys Glu Ile Leu Ser
      165     170     175
Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile

```

<400> 1871															
Met	Gly	Asp	Asn	Ile	Thr	Ser	Ile	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Phe
1				5					10					15	
Pro	Val	Gly	Pro	Arg	Ile	Gln	Met	Leu	Leu	Phe	Gly	Leu	Phe	Ser	Leu
			20					25					30		
Phe	Tyr	Val	Phe	Thr	Leu	Leu	Gly	Asn	Gly	Thr	Ile	Leu	Gly	Leu	Ile
		35					40					45			
Ser	Leu	Asp	Ser	Arg	Leu	His	Ala	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His
		50				55					60				
Leu	Ala	Val	Val	Asp	Ile	Ala	Tyr	Ala	Cys	Asn	Thr	Val	Pro	Arg	Met
65				70						75					80
Leu	Val	Asn	Leu	Leu	His	Pro	Ala	Lys	Pro	Ile	Ser	Phe	Ala	Gly	Arg
				85					90					95	
Met	Met	Gln	Thr	Phe	Leu	Phe	Ser	Thr	Phe	Ala	Val	Thr	Glu	Cys	Leu
			100					105					110		
Leu	Leu	Val	Val	Met	Ser	Tyr	Asp	Leu	Tyr	Val	Ala	Ile	Cys	His	Pro
		115					120					125			
Leu	Arg	Tyr	Leu	Ala	Ile	Met	Thr	Trp	Arg	Val	Cys	Ile	Thr	Leu	Ala
		130				135					140				
Val	Thr	Ser	Trp	Thr	Thr	Gly	Val	Leu	Leu	Ser	Leu	Ile	His	Leu	Val
145					150					155					160
Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Arg	Pro	Gln	Lys	Ile	Tyr	His	Phe
				165					170					175	
Phe	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	His
			180					185					190		
Ile	Asn	Glu	Asn	Met	Val	Leu	Ala	Gly	Ala	Ile	Ser	Gly	Leu	Val	Gly
		195					200					205			
Pro	Leu	Ser	Thr	Ile	Val	Val	Ser	Tyr	Met	Cys	Ile	Leu	Cys	Ala	Ile
		210				215					220				
Leu	Gln	Ile	Gln	Ser	Arg	Glu	Val	Gln	Arg	Lys	Ala	Phe	Cys	Thr	Cys
225					230					235					240
Phe	Ser	His	Leu	Cys	Val	Ile	Gly	Leu	Phe	Tyr	Gly	Thr	Ala	Ile	Ile
				245					250					255	

Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
 260 265 270
 Leu Pro Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
 290 295 300
 Gly Val Glu Arg Ala Leu
 305 310

<210> 1872

<211> 314

<212> PRT

<213> Unknown (H38g790 protein)

<220>

<223> Synthetic construct

<400> 1872

Met Lys Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn Phe Pro Glu Leu Gln Val Gln Leu Phe Gly Val Phe Leu
 20 25 30
 Val Ile Tyr Val Val Thr Leu Met Gly Asn Ala Ile Ile Thr Val Ile
 35 40 45
 Ile Ser Leu Asn Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu
 50 55 60
 Asn Leu Ser Val Val Glu Val Ser Phe Ser Ala Val Ile Thr Pro Glu
 65 70 75 80
 Met Leu Val Val Leu Ser Thr Glu Lys Thr Met Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Pro Val Ile Met Asn Arg Gly Val Phe Met Lys Leu
 130 135 140
 Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr Val Gln Thr
 145 150 155 160
 Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu Ile Asn His
 165 170 175
 Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys Ala Asp Thr
 180 185 190
 Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu Ile Val Met
 195 200 205
 Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala
 210 215 220
 Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Asn
 245 250 255
 Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys
 260 265 270
 Leu Ile Ser Leu Ala Tyr Thr Leu Leu Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Thr Leu Ile Lys Leu
 290 295 300
 Trp Arg Arg Lys Val Ile Leu His Thr Phe
 305 310

<210> 1873

<211> 312

<212> PRT

<213> Unknown (H38g791 protein)

<220>

<223> Synthetic construct

<400> 1873

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
 20           25           30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
 35           40           45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
 50           55           60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
 65           70           75           80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
 85           90           95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
 100          105          110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
 115          120          125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
 130          135          140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
 145          150          155          160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
 165          170          175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
 180          185          190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
 195          200          205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
 210          215          220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225          230          235          240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
 245          250          255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
 260          265          270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
 275          280          285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
 290          295          300
Gln Lys Thr Val Pro Met Glu Ile
 305          310

```

<210> 1874

<211> 276

<212> PRT

<213> Unknown (H38g792 protein)

<220>

<223> Synthetic construct

<400> 1874

```

Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ala
 1           5           10           15
Ile Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20           25           30

```



```

Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Met Val Pro Lys Met
   35                               40                               45
Leu Val Asn Ile Gln Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys
   50                               55                               60
Ile Thr Gln Met Cys Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu
   65                               70                               75                               80
Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro
   85                               90                               95
Leu His Tyr Thr Val Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Val
  100                               105                               110
Leu Val Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser Leu
  115                               120                               125
Val Thr Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe
  130                               135                               140
Phe Cys Glu Leu Asn Glu Met Ile His Leu Ala Cys Ser Asp Thr Phe
  145                               150                               155                               160
Val Asn Asn Met Val Met His Phe Ala Ala Val Leu Leu Asp Gly Gly
  165                               170                               175
Pro Leu Val Gly Ile Leu Tyr Ser Tyr Cys Arg Ile Val Ser Ser Ile
  180                               185                               190
Arg Ala Ile Ser Ser Thr Gln Gly Lys Tyr Lys Ala Leu Ser Thr Cys
  195                               200                               205
Ala Ser His Leu Ser Val Val Ser Ile Phe Tyr Gly Thr Gly Leu Gly
  210                               215                               220
Val Tyr Leu Ser Ser Thr Met Thr Gln Asn Leu His Ser Thr Ala Val
  225                               230                               235                               240
Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
  245                               250                               255
Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Thr Gln Phe Phe
  260                               265                               270
Arg Gly Lys Gln
  275

```

<210> 1875

<211> 317

<212> PRT

<213> Unknown (H38g793 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1875

```

Ser Ile Thr Trp Glu Asn His Ser Val Leu Met Glu Phe Val Phe Leu
   1           5           10           15
Ala Tyr Pro Ser Cys Pro Glu Leu His Ile Leu Ser Phe Leu Gly Val
  20           25           30
Ser Leu Val Tyr Gly Leu Ile Ile Thr Gly Asn Ile Leu Ile Val Val
  35           40           45
Ser Ile His Thr Glu Thr Cys Leu Cys Thr Ser Met Tyr Tyr Phe Leu
  50           55           60
Gly Ser Leu Ser Gly Ile Glu Ile Cys Tyr Thr Ala Val Val Val Pro
  65           70           75           80
His Ile Leu Ala Asn Thr Leu Gln Ser Glu Lys Thr Ser Leu Ser Val
  85           90           95
Gly Cys Ala Thr Gln Met Ala Phe Phe Ile Ala Leu Gly Ser Ala Asp
  100          105          110
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys

```

115	120	125
His Pro Leu Gln Tyr Pro Leu Met Thr Leu Thr Leu Cys Val His		
130	135	140
Leu Val Val Ala Ser Val Ile Ser Gly Leu Phe Leu Ser Leu Gln Leu		
145	150	155
Val Ala Phe Ile Phe Ser Leu Pro Phe Cys Gln Ala Gln Gly Ile Glu		
165	170	175
His Phe Phe Cys Asp Val Pro Pro Val Met His Val Val Cys Ala Gln		
180	185	190
Ser His Ile His Glu Gln Ser Val Leu Val Ala Ala Ile Leu Ala Ile		
195	200	205
Ala Val Pro Phe Phe Leu Ile Thr Thr Ser Tyr Thr Phe Ile Val Ala		
210	215	220
Ala Leu Leu Lys Ile His Ser Ala Ala Gly Arg His Arg Ala Phe Ser		
225	230	235
Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys Cys		
245	250	255
Ala Phe Met Tyr Leu Cys Pro Ser Ser Ser Tyr Asn Pro Lys Gln Asp		
260	265	270
Arg Phe Ile Ser Leu Val Tyr Thr Leu Gly Thr Pro Leu Leu Asn Pro		
275	280	285
Leu Ile Tyr Ala Leu Arg Asn Ser Glu Met Lys Gly Ala Val Gly Arg		
290	295	300
Val Leu Thr Arg Asn Cys Leu Ser Gln Asn Ser Xaa Glu		
305	310	315

<210> 1876

<211> 309

<212> PRT

<213> Unknown (H38g794 protein)

<220>

<223> Synthetic construct

<400> 1876

Met Glu Pro Glu Asn Asp Thr Gly Ile Ser Glu Phe Val Leu Leu Gly	
1	5
Leu Ser Glu Glu Pro Glu Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu	
20	25
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala	
35	40
Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser	
50	55
Asn Leu Ser Phe Ala Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys	
65	70
Met Leu Ile Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly	
85	90
Cys Ile Thr Gln Met Cys Phe Phe Val Leu Phe Gly Gly Leu Asp Ser	
100	105
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His	
115	120
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu	
130	135
Val Leu Ala Ser Trp Met Ile Ala Ala Leu Asn Ser Leu Ser Gln Ser	
145	150
Leu Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His	
165	170
Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr	
180	185
Phe Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly	
195	200
	205

Gly Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Il Val Ser Ser
 210 215 220
 Ile Arg Ala Il Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu
 245 250 255
 Gly Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala
 260 265 270
 Thr Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser
 290 295 300
 Phe Arg Gly Lys Gln
 305

<210> 1877

<211> 314

<212> PRT

<213> Unknown (H38g795 protein)

<220>

<223> Synthetic construct

<400> 1877

Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile
 20 25 30
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
 35 40 45
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu
 65 70 75 80
 Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala
 85 90 95
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile
 130 135 140
 Gly Cys Tyr Val Ile Gly Phe Leu Asn Ala Ser Ile Gln Ile Gly Asp
 145 150 155 160
 Thr Phe Arg Leu Ser Phe Cys Met Ser Asn Val Ile His His Phe Phe
 165 170 175
 Cys Asp Lys Pro Ala Val Ile Thr Leu Thr Cys Ser Glu Lys His Ile
 180 185 190
 Ser Glu Leu Ile Leu Val Leu Ile Ser Ser Phe Asn Val Phe Phe Ala
 195 200 205
 Leu Leu Val Thr Leu Ile Ser Tyr Leu Phe Ile Leu Ile Thr Ile Leu
 210 215 220
 Lys Arg His Thr Gly Lys Gly Tyr Gln Lys Pro Leu Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ile Ala Ile Phe Leu Phe Tyr Ile Thr Val Ile Ile Met
 245 250 255
 Tyr Ile Arg Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Ile Ala
 260 265 270
 Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Ser Pro Ile Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Asp Val Lys Asn Ala Phe Met Lys Val Val Glu

290 295 300
 Lys Ala Lys Tyr Ser Leu Asp Ser Val Phe
 305 310

<210> 1878
 <211> 315
 <212> PRT
 <213> Unknown (H38g796 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1878
 Met Xaa Asn Asn Ser Lys Phe Thr Asp Phe Ile Leu Val Gly Leu Thr
 1 5 10 15
 Asn Ala Thr Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Ile Leu Ile
 20 25 30
 His Leu Leu Ile Leu Thr Arg Asn Leu Glu Ile Ile Leu Leu Ile Leu
 35 40 45
 Leu Asp Ser Cys Leu His Ile Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Leu Gly Tyr Leu Thr Val Thr Pro Arg Val Thr Ala Ser Arg
 65 70 75 80
 Ala Gly Tyr Leu Glu Gly Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys
 85 90 95
 Ala Ala Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Met
 100 105 110
 Leu Leu Thr Ser Met Ala Tyr Asp His Tyr Ile Ala Val Cys Lys Pro
 115 120 125
 Leu His Tyr Thr Thr Thr Thr Ile Ala Ser Val Cys Ala His Leu Val
 130 135 140
 Ile Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Leu Arg Ile Gly
 145 150 155 160
 Asp Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Leu
 165 170 175
 Phe Cys Asp Val Pro Pro Val Met Ala Val Ser Cys Ser Gly Lys His
 180 185 190
 Ile Ser Lys Lys Ile Leu Val Phe Met Ser Ser Phe Asn Val Phe Leu
 195 200 205
 Ala Leu Leu Val Ile Leu Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile
 210 215 220
 Leu Lys Met His Ser Ala Gln Gly His Leu Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Ile Ala Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe
 245 250 255
 Met His Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Glu Met
 260 265 270
 Ala Ser Leu Phe Tyr Ala Val Phe Ile Ser Met Leu Asn Leu Val Phe
 275 280 285
 Tyr Ser Leu Arg Ser Lys Glu Val Lys Asn Ala Phe Lys Lys Ala Val
 290 295 300
 Glu Lys Ala Lys Phe Phe Leu Glu Leu Xaa Phe
 305 310 315

<210> 1879
 <211> 314
 <212> PRT

<213> Unknown (H38g797 protein)

<220>

<223> Synthetic construct

<400> 1879

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
1      5      10      15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
20      25      30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
35      40      45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
50      55      60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65      70      75      80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
85      90      95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
100     105     110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
115     120     125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
130     135     140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
145     150     155     160
Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
165     170     175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr
180     185     190
Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser
195     200     205
Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val
210     215     220
Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr
225     230     235     240
Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser
245     250     255
Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg
260     265     270
Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
275     280     285
Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met Lys Trp
290     295     300
Met Ser Arg Met Gln Thr Phe Phe Phe Arg
305     310

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<210> 1880

<211> 316

<212> PRT

<213> Unknown (H38g798 protein)

<220>

<223> Synthetic construct

<400> 1880

```

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
1      5      10      15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
20      25      30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val

```

35	40	45
Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu		
50	55	60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu		
65	70	75
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser		
85	90	95
Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu		
100	105	110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu		
115	120	125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser		
130	135	140
Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser		
145	150	155
Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu		
165	170	175
Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr		
180	185	190
Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro		
195	200	205
Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu		
210	215	220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser		
225	230	235
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val		
245	250	255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe		
260	265	270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr		
275	280	285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly		
290	295	300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala		
305	310	315

<210> 1881

<211> 324

<212> PRT

<213> Unknown (H38g799 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1881

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu	
1	15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser	
20	30
Leu Ser Leu Ser Met Tyr Met Val Thr Val Leu Arg Asn Leu Leu Ser	
35	45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Cys Phe	
50	60
Phe Leu Ser Lys Leu Cys Xaa Ala Asp Ile Gly Phe Thr Leu Ala Met	
65	80
Val Pro Lys Met Ile Val Asn Met Gln Ser His Ser Arg Val Ile Ser	
85	95

Tyr Glu Gly Cys L u Thr Arg Met Ser Phe Phe Val Leu Ph Ala Cys
 100 105 110
 Met Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Pro Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Leu Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Thr Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Asn Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Gly
 225 230 235 240
 Phe Ser Thr Cys Gly Ser Tyr Leu Ala Val Val Cys Xaa Phe Asp Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Gly Lys Arg Asp Ile Gln Ser Val Leu
 290 295 300
 Arg Arg Leu Cys Ser Arg Thr Val Glu Ser Pro Xaa Tyr Val Pro Ser
 305 310 315 320
 Phe Phe Leu Cys

<210> 1882

<211> 158

<212> PRT

<213> Unknown (H38g800 protein)

<220>

<223> Synthetic construct

<400> 1882

Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
 100 105 110
 Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile
 145 150 155

<210> 1883
 <211> 318
 <212> PRT
 <213> Unknown (H38g801 protein)

<220>
 <223> Synthetic construct

<400> 1883
 Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1 5 10 15
 Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
 20 25 30
 Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
 35 40 45
 Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
 50 55 60
 Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
 65 70 75 80
 Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
 85 90 95
 Ala Arg Cys Leu Ala Gln Phe Phe Phe Tyr Ala Phe Gly Val Thr
 100 105 110
 Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
 130 135 140
 Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
 145 150 155 160
 Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
 165 170 175
 Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
 180 185 190
 Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
 195 200 205
 Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
 210 215 220
 Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
 225 230 235 240
 Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
 245 250 255
 Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
 260 265 270
 Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
 275 280 285
 Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
 290 295 300
 Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
 305 310 315

<210> 1884
 <211> 307
 <212> PRT
 <213> Unknown (H38g802 protein)

<220>
 <223> Synthetic construct

<400> 1884
 Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1 5 10 15

Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
 20 25 30
 Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala Val Leu Met Ile Val Ile
 35 40 45
 Ser Asp Pro Arg Leu His Ser Leu Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val Thr Leu Pro Lys Met Leu
 65 70 75 80
 Gln Asn Phe Leu Ser Thr His Lys Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ser Met Leu
 100 105 110
 Phe Ala Val Met Ala Phe Asp Leu Ser Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
 130 135 140
 Thr Ile Trp Val Ile Gly Phe Phe His Ala Leu Leu His Ser Val Met
 145 150 155 160
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe Leu
 165 170 175
 Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala Cys Gly Asn Thr Glu Leu
 180 185 190
 Asn Gln Trp Leu Leu Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro
 195 200 205
 Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr Ile Ile Thr Tyr Leu Phe
 210 215 220
 Phe Lys Thr Arg Ser Cys Ser Met Leu Cys Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Phe Met Val Val Ile Leu Phe Tyr Ala Pro Val Leu Phe
 245 250 255
 Thr Tyr Ile His Pro Ala Leu Glu Ser Phe Met Asp Gln Asp Arg Ile
 260 265 270
 Val Ala Ile Met Tyr Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Val Ile
 290 295 300
 Arg Arg Leu
 305

<210> 1885

<211> 320

<212> PRT

<213> Unknown (H38g803 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1885

Gln Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Met Gly Leu
 1 5 10 15
 Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser Leu Ser
 20 25 30
 Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
 35 40 45
 Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 50 55 60
 Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Ile

65					70					75				80
Ile	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Val	Gly Cys
				85					90					95
Leu	Thr	Arg	Met	Ser	Phe	Leu	Val	Leu	Phe	Ala	Cys	Ile	Glu	Asp Met
			100					105					110	
Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Ala	Ile	Cys	Arg Pro
			115				120					125		
Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Ala	His	Leu	Arg	Val	Phe	Leu Val
			130			135					140			
Leu	Val	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Ser Xaa
					150					155				160
Ile	Val	Leu	Gln	Phe	Thr	Phe	Phe	Lys	Asn	Val	Glu	Ile	Ser	Asn Phe
				165					170					175
Val	Cys	Glu	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ser Ile
			180					185					190	
Ile	Asn	Ser	Ile	Phe	Ile	Tyr	Phe	Asp	Ser	Thr	Met	Phe	Gly	Phe Leu
		195					200					205		
Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Cys	Lys	Ile	Val	Pro	Ser Ile
		210				215					220			
Leu	Arg	Ile	Ser	Thr	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr Cys
					230					235				240
Gly	Ser	His	Leu	Ala	Leu	Val	Cys	Leu	Phe	Tyr	Gly	Ala	Gly	Ile Gly
				245					250					255
Val	Tyr	Leu	Thr	Ser	Ala	Val	Ser	Pro	Pro	Pro	Arg	Asn	Gly	Val Val
			260					265					270	
Val	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe Ile
			275				280					285		
Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Thr	Leu	Arg	Arg	Leu Leu
		290				295					300			
Ser	Arg	Thr	Val	Glu	Ser	Pro	Xaa	Ser	Val	Pro	Ser	Phe	Phe	Leu Cys
		305			310					315				320

<210> 1886

<211> 328

<212> PRT

<213> Unknown (H38g804 protein).

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1886

Met	Ala	Pro	Gly	Asn	Gly	Ser	Phe	Val	Thr	Glu	Phe	Ile	Leu	Ala	Gly
1				5					10					15	
Leu	Thr	His	Gln	Pro	Asp	Leu	Gln	Ser	Pro	Leu	Phe	Phe	Leu	Phe	Leu
			20					25					30		
Val	Ile	Tyr	Val	Val	Thr	Leu	Leu	Gly	Asn	Leu	Gly	Leu	Val	Thr	Leu
			35				40					45			
Ile	Gly	Leu	Asn	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe
			50				55				60				
Asn	Leu	Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Ile	Pro	Lys
					70				75					80	
Met	Leu	Met	Asn	Phe	Ile	Ser	Glu	Lys	Asn	Ile	Met	Ser	Phe	Lys	Gly
				85					90					95	
Cys	Met	Thr	Gln	Leu	Ser	Phe	Tyr	Xaa	Phe	Phe	Val	Val	Ile	Ser	Glu
			100					105					110		
Gly	Tyr	Val	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Val	Ala	Ile	Cys	Thr
			115				120					125			

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Pro Leu Leu Tyr His Ile Ala Met Ser Pro Thr Val Cys Ser Ser Leu
 130          135          140
Met Phe Gly Ser Tyr Leu Met Pro Phe Ser Gly Ala Met Ala His Thr
145          150          155          160
Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp His
          165          170          175
Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
          180          185          190
Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile Ile
          195          200          205
Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser
          210          215          220
Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
          245          250          255
Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg Lys
          260          265          270
Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys Ala
          290          295          300
Leu Ser Ser Arg Lys Leu Xaa Xaa Val Ile Val Cys Val Cys Val Tyr
305          310          315          320
Ser His Lys Thr Gly Ile Phe Cys
          325

```

<210> 1887

<211> 310

<212> PRT

<213> Unknown (H38g805 protein)

<220>

<223> Synthetic construct

<400> 1887

```

Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu
          20          25          30
Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys
65          70          75          80
Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu
          85          90          95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser
          100          105          110
Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu
          130          135          140
Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile
145          150          155          160
Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His
          165          170          175
Phe Phe Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His
          180          185          190
Phe Val Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met

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195	200	205
Thr Pro Phe Ser Cys Ile Il	Ile Ser Tyr Leu Arg Ile Leu Ile Thr	
210	215	220
Val Leu Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser		240
245	250	255
Tyr Leu Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile		
260	265	270
Ala Thr Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile		
275	280	285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met		
290	295	300
His Arg Met Lys Cys Gln		
305	310	

<210> 1888

<211> 315

<212> PRT

<213> Unknown (H38g806 protein)

<220>

<223> Synthetic construct

<400> 1888

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu	
1	5
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val	
20	25
Phe Thr Ala Val Tyr Val Phe Ile Ile Ile Gly Asn Met Leu Ile Ile	
35	40
Val Ala Val Val Ser Ser Gln Arg Leu His Lys Pro Met Tyr Ile Phe	
50	55
Leu Ala Asn Leu Ser Phe Leu Asp Ile Leu Tyr Thr Ser Ala Val Met	
65	70
Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser Val Ala	
85	90
Gly Cys Leu Leu Gln Phe Phe Ile Phe Gly Ser Leu Ala Thr Ala Glu	
100	105
Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys	
115	120
Tyr Pro Leu His Tyr Pro Leu Met Gly Pro Arg Arg Tyr Met Gly	
130	135
Leu Val Val Thr Thr Trp Leu Ser Gly Phe Val Val Asp Gly Leu Val	
145	150
Val Ala Leu Val Ala Gln Leu Arg Phe Cys Gly Pro Asn His Ile Asp	
165	170
Gln Phe Tyr Cys Asp Phe Met Leu Phe Val Gly Leu Ala Cys Ser Asp	
180	185
Pro Arg Val Ala Gln Val Thr Thr Leu Ile Leu Ser Val Phe Cys Leu	
195	200
Thr Ile Pro Phe Gly Leu Ile Leu Thr Ser Tyr Ala Arg Ile Val Val	
210	215
Ala Val Leu Arg Val Pro Ala Gly Ala Ser Arg Arg Arg Ala Phe Ser	
225	230
Thr Cys Ser Ser His Leu Ala Val Val Thr Thr Phe Tyr Gly Thr Leu	
245	250
Met Ile Phe Tyr Val Ala Pro Ser Ala Val His Ser Gln Leu Leu Ser	
260	265
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Phe Asn Pro	
275	280
	285

Val Ile Tyr Thr Met Arg Asn Lys Glu Val His Gln Ala Leu Arg Lys
 290 295 300
 Ile Leu Cys Ile Lys Gln Thr Glu Thr Leu Asp
 305 310 315

<210> 1889
 <211> 188
 <212> PRT
 <213> Unknown (H38g807 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(188)
 <223> Xaa = Any Amino Acid

<400> 1889
 His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile
 1 5 10 15
 Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile
 20 25 30
 Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe
 35 40 45
 Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu
 50 55 60
 Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro
 65 70 75 80
 Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys
 85 90 95
 Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val
 100 105 110
 Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu
 115 120 125
 Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala
 130 135 140
 Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu
 145 150 155 160
 Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg
 165 170 175
 Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala
 180 185

<210> 1890
 <211> 313
 <212> PRT
 <213> Unknown (H38g808 protein)

<220>
 <223> Synthetic construct

<400> 1890
 Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu
 20 25 30
 Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr
 35 40 45
 Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln

65					70					75				80
Met	Val	Val	Asn	Ile	Leu	Thr	Gly	Thr	Lys	Thr	Ile	Ser	Phe	Ala
				85					90					95
Cys	Leu	Thr	Gln	Leu	Phe	Phe	Phe	Val	Ser	Phe	Val	Asn	Met	Asp
			100					105					110	
Leu	Leu	Leu	Cys	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
			115				120					125		
Pro	Leu	His	Tyr	Thr	Ala	Arg	Met	Asn	Leu	Cys	Leu	Cys	Val	Gln
	130					135					140			
Val	Ala	Gly	Leu	Trp	Leu	Val	Thr	Tyr	Leu	His	Ala	Leu	Leu	His
145					150					155				160
Val	Leu	Ile	Ala	Gln	Leu	Ser	Phe	Cys	Ala	Ser	Asn	Ile	Ile	His
			165					170						175
Phe	Leu	Cys	Asp	Leu	Asn	Pro	Leu	Leu	Gln	Leu	Ser	Cys	Ser	Asp
			180				185					190		
Ser	Phe	Asn	Val	Met	Ile	Ile	Phe	Ala	Val	Gly	Asp	Leu	Leu	Ala
	195					200					205			
Thr	Pro	Leu	Val	Cys	Ile	Leu	Val	Ser	Tyr	Gly	Leu	Ile	Phe	Ser
	210					215				220				
Val	Leu	Lys	Ile	Thr	Ser	Thr	Gln	Gly	Lys	Gln	Arg	Ala	Val	Ser
225					230					235				240
Cys	Ser	Cys	His	Leu	Ser	Val	Val	Val	Leu	Phe	Tyr	Gly	Thr	Ala
			245						250					255
Ala	Val	Tyr	Phe	Ser	Pro	Ser	Ser	Pro	His	Met	Pro	Glu	Ser	Asp
		260					265					270		
Leu	Ser	Thr	Ile	Met	Tyr	Ser	Met	Val	Ala	Pro	Met	Leu	Asn	Pro
	275					280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Arg	Asp	Met	Lys	Arg	Gly	Leu	Gln	Lys
	290				295						300			
Leu	Leu	Lys	Cys	Thr	Val	Phe	Gln	Gln						
305					310									

<210> 1891

<211> 312

<212> PRT

<213> Unknown (H38g809 protein)

<220>

<223> Synthetic construct

<400> 1891

Met	Asp	Gly	Gly	Asn	Gln	Ser	Glu	Gly	Ser	Glu	Phe	Leu	Leu	Leu	Gly
1				5				10						15	
Met	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Gln	Ile	Leu	Phe	Trp	Met	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Val	Thr	Val	Val	Gly	Asn	Val	Leu	Ile	Ile	Leu	Ala
		35				40					45				
Ile	Ser	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu	Ala
	50				55					60					
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro	Lys
65				70				75						80	
Met	Leu	Val	Asn	Leu	Gln	Ser	His	Asn	Lys	Ala	Ile	Ser	Tyr	Ala	Gly
			85					90					95		
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Ala	Leu	Asp	Asn
			100					105					110		
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Cys
	115					120						125			
Pro	Leu	His	Tyr	Thr	Thr	Ala	Met	Ser	Pro	Lys	Leu	Cys	Ile	Leu	Leu
	130				135						140				
Leu	Ser	Leu	Cys	Trp	Val	Leu	Ser	Val	Leu	Tyr	Gly	Leu	Ile	His	Thr
145					150					155					160

Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 1892

<211> 317

<212> PRT

<213> Unknown (H38g810 protein)

<220>

<223> Synthetic construct

<400> 1892

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu
 20 25 30
 Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val
 145 150 155 160
 Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr
 180 185 190
 Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met
 195 200 205
 Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala
 210 215 220
 Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser

<210> 1894

<211> 328
 <212> PRT
 <213> Unknown (H38g812 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(328)
 <223> Xaa = Any Amino Acid

<400> 1894

Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu	Leu
1			5						10					15	
Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe	Phe
			20					25					30		
Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val	Phe
		35				40					45				
Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu	Leu
	50					55				60					
Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val	Pro
65				70					75					80	
Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe	His
			85					90					95		
Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val	Glu
		100						105					110		
Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile	Cys
	115					120					125				
Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met	Phe
	130					135					140				
Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser	Gln
145				150					155					160	
Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val	Gly
			165					170					175		
Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met	Asp
		180					185					190			
Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile	Ser
	195					200						205			
Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu	Val
	210					215					220				
Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe	Thr
225				230					235					240	
Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys	Met
			245						250					255	
Phe	Leu	Tyr	Val	Trp	Pro	Phe	Pro	Thr	Lys	Ser	Leu	Asp	Lys	Phe	Phe
		260						265					270		
Ala	Ile	Met	Asn	Phe	Val	Val	Thr	Pro	Val	Leu	Asn	Pro	Ala	Ile	Tyr
	275						280					285			
Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Phe	Ala	Met	Arg	Arg	Leu	Asn	Gln
	290				295						300				
His	Ile	Leu	Asn	Ser	Met	Glu	Thr	Thr	Xaa	His	Ile	Trp	Leu	Met	Arg
305				310					315					320	
Ala	Gln	Asp	Lys	Cys	His	Gly	Pro								
				325											

<210> 1895
 <211> 272
 <212> PRT
 <213> Unknown (H38g813 protein)

<220>

<223> Synthetic construct

<400> 1895

```

Met Trp Ile Asn Asn Gln S r Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
 20           25           30
Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35           40           45
His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50           55           60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
 65           70           75           80
Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
 85           90           95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
 100          105          110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
 115          120          125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
 130          135          140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
 145          150          155          160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
 165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
 180          185          190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
 195          200          205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
 210          215          220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
 225          230          235          240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
 245          250          255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
 260          265          270

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<210> 1896

<211> 315

<212> PRT

<213> Unknown (H38g814 protein)

<220>

<223> Synthetic construct

<400> 1896

```

Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
 1           5           10           15
Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
 20           25           30
Ser Leu Phe Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala
 35           40           45
Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr
 50           55           60
Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser
 65           70           75           80
Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile
 85           90           95
Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
 100          105          110

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Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu
 130 135 140
 Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe
 145 150 155 160
 Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn
 165 170 175
 Ile Ile Asp His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp
 180 185 190
 Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser
 195 200 205
 Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu
 210 215 220
 Val Leu Lys Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr
 245 250 255
 Ser Ser Leu Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr
 260 265 270
 Gly Met Gln Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu
 275 280 285
 Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala
 290 295 300
 Leu Arg Lys Val Leu Gly Ser Ser Asn Ile Ile
 305 310 315

<210> 1897

<211> 305

<212> PRT

<213> Unknown (H38g815 protein)

<220>

<223> Synthetic construct

<400> 1897

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
 1 5 10 15
 Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
 20 25 30
 Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
 35 40 45
 His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Tyr Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu Asn Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile

195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1898

<211> 318

<212> PRT

<213> Unknown (H38g816 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1898

Met Thr Leu Pro Ser Asp Asp Ser Thr Val Pro Val Ser Glu Phe Leu
 1 5 10 15
 Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Leu Leu Ser Leu
 20 25 30
 Pro Leu Ser Leu Met Phe Leu Leu Ala Met Gly Thr Asn Thr Thr Pro
 35 40 45
 Pro Ile Thr Ile His Leu Glu Ala Ser Leu His Leu Pro Leu Tyr Tyr
 50 55 60
 Leu Pro Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
 65 70 75 80
 Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Gly
 85 90 95
 Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Pro
 100 105 110
 Met Glu Ser Cys Thr Phe Met Val Lys Asp Tyr Asp His Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu Gln Tyr Leu Ser Ile Ile Thr His Gln Phe Val
 130 135 140
 Ala Lys Ala Ser Val Phe Ile Val Val Gln Asn Ala Leu Leu Leu Ser
 145 150 155 160
 Pro Val Pro Ile Leu Ser Ala Gln Leu His Tyr Cys Arg Lys Asn Val
 165 170 175
 Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser Arg Leu Ser Cys
 180 185 190
 Asp Asn Phe Thr Leu Asn Arg Leu Tyr Gln Phe Val Ala Gly Trp Thr
 195 200 205
 Phe Leu Gly Ser Asp Phe Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile
 210 215 220
 Leu Arg Ala Val Leu Arg Phe Lys Val Glu Gly Val Ala Val Lys Ala
 225 230 235 240
 Leu Ser Thr Cys Gly Ser His Phe Ile Leu Il Leu Phe Phe Ser Ile
 245 250 255

L u Leu Val Val Val Leu Thr Asn Val Ala Arg Lys Lys Val Pro Met
 260 265 270
 Asp Ile Leu Ile Leu Phe Asn Val L u His Pro Phe Ser Pro Pro Ala
 275 280 285
 Leu Asn Pro Ile Ile Cys Gly Phe Gln Thr Lys Glu Leu Lys Lys Glu
 290 295 300
 Phe Xaa Lys Leu Leu Gln Arg Gly Leu Xaa Lys His Gly Arg
 305 310 315

<210> 1899

<211> 317

<212> PRT

<213> Unknown (H38g817 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1899

Lys His Asn His Thr Ala Val Thr Lys Val Thr Glu Phe Ile Leu Met
 1 5 10 15
 Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro Leu Phe Gly Leu Phe
 20 25 30
 Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn Leu Gly Met Val Ile
 35 40 45
 Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Lys His Leu Ala Ile Thr Asp Leu Gly Tyr Ser Thr Val Ile Gly Pro
 65 70 75 80
 Gln Met Met Phe Ser Glu Thr Ser Tyr Val His Lys Glu His Asn Phe
 85 90 95
 Phe Tyr Asn Trp Tyr Ala Asn His Arg Ala Arg Phe Glu Arg Asn Ile
 100 105 110
 Ile Ser His Arg Gly Ile Leu Ser Ala Thr Asn Asn Glu Pro Tyr Lys
 115 120 125
 Pro Ile Thr Lys Gln Leu Leu Asn Pro Ile Ile Met Pro Glu Lys Ile
 130 135 140
 Arg Glu Glu Gln Ile Thr Val Pro Glu Leu Asp Lys Thr Cys Ala Pro
 145 150 155 160
 Leu Phe Leu Lys Arg Lys Xaa Val Lys Thr Val Ser Thr Asn Pro Asp
 165 170 175
 Thr Thr Asn Asn Cys His Gly Glu Gly Thr Ala Lys Met Xaa Ile Leu
 180 185 190
 Arg Ser Glu Lys Lys Lys Ile Thr Ile Ile Lys Ala Met Thr Ala Gly
 195 200 205
 Thr Asn Met Leu Ile Ser Leu Ser Ile Val Leu Ile Ser Tyr Met Phe
 210 215 220
 Ile Leu Val Ala Asn Leu Arg Met Asn Ser Arg Lys Gly Arg Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met Phe Tyr
 245 250 255
 Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His Thr Leu
 260 265 270
 Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala
 290 295 300
 Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile

305

310

315

<210> 1900
 <211> 220
 <212> PRT
 <213> Unknown (H38g818 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(220)
 <223> Xaa = Any Amino Acid

<400> 1900
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
 1 5 10 15
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro Tyr Ala
 20 25 30
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 35 40 45
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 50 55 60
 Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
 65 70 75 80
 Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 85 90 95
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Ser Asn Val Glu Ile Ala
 100 105 110
 Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu Asp Cys Ser Asp
 115 120 125
 Thr Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Met Phe Gly Phe
 130 135 140
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val Pro Ser
 145 150 155 160
 Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ala Thr
 165 170 175
 Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly Ile
 180 185 190
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val
 195 200 205
 Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
 210 215 220

<210> 1901
 <211> 311
 <212> PRT
 <213> Unknown (H38g819 protein)

<220>
 <223> Synthetic construct

<400> 1901
 Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
 20 25 30
 Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
 35 40 45
 Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50 55 60

Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pr Lys Leu Met
 65 70 75 80
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
 85 90 95
 Ile Gln Leu Ph Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
 100 105 110
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile
 130 135 140
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu
 145 150 155 160
 Thr Ile Phe Val Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met
 180 185 190
 Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr
 195 200 205
 Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg
 210 215 220
 Ala Tyr Ser Ala Glu Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser
 225 230 235 240
 His Val Ile Val Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr
 245 250 255
 Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe
 260 265 270
 Tyr Thr Ile Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile
 290 295 300
 Leu Leu Lys Arg Asn Gln Leu
 305 310

<210> 1902

<211> 222

<212> PRT

<213> Unknown (H38g820 protein)

<220>

<223> Synthetic construct

<400> 1902

Arg Asn Phe Ser Phe Leu Glu Ile Ser Phe Thr Thr Val Cys Ile Pro
 1 5 10 15
 Arg Phe Leu Gly Ala Ile Ile Thr Arg Asn Lys Thr Ile Ser Tyr Asn
 20 25 30
 Asn Cys Ala Ala Gln Leu Phe Phe Phe Ile Phe Met Gly Val Thr Glu
 35 40 45
 Phe Tyr Ile Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
 50 55 60
 Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys Leu Cys Thr Leu
 65 70 75 80
 Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Pro Thr Ile Phe Pro Pro
 85 90 95
 Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser Asn Val Ile Asp
 100 105 110
 His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp
 115 120 125
 Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala Leu Val Thr Leu
 130 135 140
 Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met Tyr Ile Ile Arg

145		150		155		160									
Thr	Ile	Leu	Arg	Ile	Pro	Ser	Ala	Ser	Gln	Arg	Lys	Lys	Ala	Phe	Ser
		165		170		175									
Thr	Cys	Ser	Ser	His	Met	Ile	Val	Ile	Ser	Ile	Ser	Tyr	Gly	Ser	Cys
		180		185		190									
Ile	Phe	Met	Tyr	Ala	Asn	Pro	Ser	Ala	Lys	Glu	Lys	Ala	Ser	Leu	Thr
	195			200		205									
Lys	Gly	Ile	Ala	Ile	Leu	Asn	Thr	Ser	Val	Ala	Pro	Met	Leu		
210				215		220									

<210> 1903

<211> 267

<212> PRT

<213> Unknown (H38g821 protein)

<220>

<223> Synthetic construct

<400> 1903

Ile	Ile	Leu	Cys	Phe	Phe	Ile	Ile	Gly	Asn	Ser	Gln	Asp	Asn	Ser	Gln
1				5				10					15		
Met	Thr	Leu	Met	Asp	Asn	Ile	Ser	Glu	Val	Thr	Glu	Phe	Val	Leu	Val
		20						25					30		
Gly	Leu	Thr	Asp	Val	Leu	Glu	Leu	Gln	Val	Pro	Leu	Phe	Ile	Ile	Phe
	35					40						45			
Thr	Val	Ile	Tyr	Leu	Thr	Thr	Leu	Val	Gly	Asn	Phe	Gly	Met	Ile	Met
	50					55					60				
Leu	Ile	Leu	Leu	Asp	Ser	Arg	Leu	His	Ile	Pro	Met	Tyr	Phe	Phe	Leu
65				70						75					80
Gly	Lys	Leu	Ser	Leu	Val	Asp	Ser	Val	Cys	Ala	Cys	Leu	Val	Thr	Gly
		85							90					95	
Ser	Tyr	Ile	Cys	Gly	Leu	Phe	Gln	Ser	Ser	Ile	His	Val	Ala	Phe	Thr
		100						105						110	
Phe	His	Leu	Ser	Phe	Cys	His	Ser	Asn	Val	Val	Asn	His	Phe	Phe	Cys
	115							120					125		
Asp	Ile	Pro	Pro	Leu	Leu	Ala	Leu	Ser	Cys	Ser	Asp	Ile	Tyr	Ala	His
	130					135					140				
Glu	Ile	Val	Leu	Phe	Ile	Leu	Ala	Ala	Phe	Asn	Ile	Phe	Phe	Thr	Leu
145					150					155					160
Leu	Ile	Ile	Leu	Asn	Ser	Tyr	Val	Phe	Ile	Phe	Ile	Ala	Ile	Leu	Arg
		165						170						175	
Met	His	Ser	Ala	Glu	Gly	Gln	Lys	Lys	Val	Phe	Ser	Thr	Cys	Ala	Tyr
		180						185						190	
His	Leu	Thr	Thr	Val	Ser	Ile	Phe	Tyr	Gly	Thr	Ile	Thr	Phe	Met	Tyr
	195					200						205			
Leu	Gln	Pro	Ser	Ser	Gly	His	Ser	Met	Asp	Thr	Asp	Lys	Ile	Ser	Ser
	210					215					220				
Val	Phe	Tyr	Thr	Met	Val	Ile	Pro	Met	Leu	Asn	Pro	Leu	Val	Tyr	Ser
225				230						235					240
Leu	Arg	Asn	Lys	Glu	Val	Gln	Ser	Ala	Phe	Lys	Val	Val	Ile	Gly	Lys
		245							250					255	
Ala	Lys	Ser	Ser	Leu	Gly	Leu	Ala	Tyr	Tyr	Leu					
	260							265							

<210> 1904

<211> 316

<212> PRT

<213> Unknown (H38g822 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1904

```

Trp Xaa Pro Val Phe Asn Gln Ser Ala Pro Leu Gln Phe Val Phe Arg
 1          5          10          15
Val Phe Thr Thr Val Pro Glu Phe Gln Val Leu Leu Phe Leu Leu Phe
      20          25          30
Leu Leu Phe Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp
      35          40          45
Val Val Cys Thr Tyr Ser Val Leu Arg Thr Pro Met Tyr Phe Phe Leu
      50          55          60
Ser Asn Leu Ser Phe Val Glu Ile Cys Tyr Thr Val Val Val Pro
      65          70          75          80
Leu Met Leu Ser Asn Ile Phe Gly Ala Gln Lys Pro Ile Pro Leu Ala
      85          90          95
Gly Cys Gly Ala Gln Met Phe Phe Phe Leu Thr Leu Gly Gly Ala Asp
      100          105          110
Cys Phe Leu Leu Ala Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Arg Leu Ile Met Thr Cys Asn Leu Cys Val Gln
      130          135          140
Met Leu Gly Gly Ala Val Gly Leu Ala Leu Phe Leu Ser Leu Gln Leu
      145          150          155          160
Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly Tyr Arg Gln Glu Ile
      165          170          175
Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala
      180          185          190
Ala Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val
      195          200          205
Leu Thr Val Pro Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr
      210          215          220
Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg His Gln Ala Phe
      225          230          235          240
Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys
      245          250          255
Cys Ala Leu Ala Tyr Leu His Pro Gln Ser Ser Ser Ser Ala Asp Glu
      260          265          270
Asp Arg Gln Phe Ala Leu Val Tyr Thr Phe Ile Thr Pro Leu Leu Asn
      275          280          285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu
      290          295          300
Lys Ser Ala Gln Tyr Gln Arg Asp Thr Xaa Val Leu
      305          310          315

```

<210> 1905

<211> 312

<212> PRT

<213> Unknown (H38g823 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1905

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser

```

1           5           10           15
Asn Val Pro Glu Leu Gln Val Pro Phe Phe Ile Met Phe Val Leu Ile
20           25           30
Tyr Leu Il Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
35           40           45
Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu
50           55           60
Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met
65           70           75           80
Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala
85           90           95
Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu
100          105          110
Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu
115          120          125
His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile
130          135          140
Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu
145          150          155          160
Thr Phe Ser Leu Phe Cys Met Ser Ser Glu Val His His Phe Phe Cys
165          170          175
Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn
180          185          190
Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu
195          200          205
Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys
210          215          220
Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser
225          230          235          240
His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His
245          250          255
Ile Gln Pro Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala
260          265          270
Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg
275          280          285
Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val
290          295          300
Lys Leu Ser Leu Gly Leu Xaa Val
305          310

```

<210> 1906

<211> 318

<212> PRT

<213> Unknown (H38g824 protein)

<220>

<223> Synthetic construct

<400> 1906

```

Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
1           5           10           15
Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
20           25           30
Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
35           40           45
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
50           55           60
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
65           70           75           80
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
85           90           95

```

Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pr Arg Ala Cys Met Ala
 130 135 140
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220
 Ala Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255
 Ser Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp
 260 265 270
 Arg Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr
 290 295 300
 Leu Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly
 305 310 315

<210> 1907

<211> 311

<212> PRT

<213> Unknown (H38g825 protein)

<220>

<223> Synthetic construct

<400> 1907

Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala Ile Phe
 20 25 30
 Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile Ile Leu
 35 40 45
 Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val
 85 90 95
 Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
 100 105 110
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
 115 120 125
 Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu
 130 135 140
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
 145 150 155 160
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
 165 170 175
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp

```

      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser
225      230      235      240
Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Arg His Arg Ile Tyr Ser
305      310

```

<210> 1908

<211> 131

<212> PRT

<213> Unknown (H38g826 protein)

<220>

<223> Synthetic construct

<400> 1908

```

Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1      5      10      15
Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala
      20      25      30
Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu
      35      40      45
Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
50      55      60
Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu
65      70      75      80
Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe
      85      90      95
Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu
      100      105      110
Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met
      115      120      125
Thr Met His
      130

```

<210> 1909

<211> 311

<212> PRT

<213> Unknown (H38g827 protein)

<220>

<223> Synthetic construct

<400> 1909

```

Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1      5      10      15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
      20      25      30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
      35      40      45

```

Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pr Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
 85 90 95
 Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
 100 105 110
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
 115 120 125
 Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
 130 135 140
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
 145 150 155 160
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
 165 170 175
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
 180 185 190
 Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
 195 200 205
 Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
 210 215 220
 Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
 245 250 255
 Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
 260 265 270
 Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
 290 295 300
 Leu Gln Asp Arg Ile Tyr Arg
 305 310

<210> 1910

<211> 313

<212> PRT

<213> Unknown (H38g828 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1910

Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp
 1 5 10 15
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala
 20 25 30
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Ile Thr Met
 35 40 45
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln
 50 55 60
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly
 85 90 95
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe

<210> 1911
<211> 317
<212> PRT
<213> Unknown (H38g829 protein)

<220>
<223> Synthetic construct

Met 1	Asn	Ser	Glu	Asn 5	Leu	Thr	Arg	Ala	Ala 10	Val	Ala	Pro	Ala	Glu 15	Phe
Val	Leu	Leu	Gly 20	Ile	Thr	Asn	Arg	Trp 25	Asp	Leu	Arg	Val	Ala 30	Leu	Phe
Leu	Thr	Cys 35	Leu	Pro	Val	Tyr	Leu 40	Val	Ser	Leu	Leu	Gly 45	Asn	Met	Gly
Met	Ala 50	Leu	Leu	Ile	Arg	Met 55	Asp	Ala	Arg	Leu	His 60	Thr	Pro	Met	Tyr
Phe 65	Phe	Leu	Ala	Asn 70	Leu	Ser	Leu	Leu	Asp	Ala 75	Cys	Tyr	Ser	Ser	Ala 80
Ile	Gly	Pro	Lys	Met 85	Leu	Val	Asp	Leu 90	Leu	Leu	Pro	Arg	Ala 95	Thr	Ile
Pro	Tyr	Thr	Ala 100	Cys	Ala	Leu	Gln	Met 105	Phe	Val	Phe	Ala	Gly 110	Leu	Ala
Asp	Thr	Glu 115	Cys	Cys	Leu	Leu	Ala 120	Ala	Met	Ala	Tyr	Asp 125	Arg	Tyr	Val
Ala	Ile 130	Arg	Asn	Pro	Leu	Leu 135	Tyr	Thr	Thr	Ala 140	Met	Ser	Gln	Arg	Leu
Cys 145	Leu	Ala	Leu	Leu 150	Gly	Ala	Ser	Gly	Leu 155	Gly	Gly	Ala	Val	Ser	Ala 160
Phe	Val	His	Thr	Thr 165	Leu	Thr	Phe	Arg	Leu 170	Ser	Phe	Cys	Arg	Ser 175	Arg
Lys	Ile	Asn	Ser 180	Phe	Phe	Cys	Asp	Ile 185	Pro	Pro	Leu	Leu	Ala 190	Ile	Ser

Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly
 195 200 205
 Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe
 210 215 220
 Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg
 225 230 235 240
 Ala Ala Ser Thr Glu Gly Ser His Leu Thr Ala Val Ala Met Met Tyr
 245 250 255
 Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu
 260 265 270
 Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
 290 295 300
 Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln
 305 310 315

<210> 1912

<211> 316

<212> PRT

<213> Unknown (H38g830 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1912

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val
 1 5 10 15
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met
 20 25 30
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile
 35 40 45
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile
 65 70 75 80
 Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser
 85 90 95
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala
 100 105 110
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys
 130 135 140
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala
 145 150 155 160
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu
 165 170 175
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys
 180 185 190
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
 195 200 205
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly

<400> 1913															
Glu 1	Xaa	Met	Gly	Thr 5	Ser	Asn	Asn	Val 10	Thr	Glu	Phe	Val	Leu 15	Pro	Gly
Leu	Ser	Gln	Asp 20	Pro	Asp	Val	Gln 25	Lys	Ala	Leu	Phe	Val	Met 30	Phe	Leu
Leu	Thr	Tyr 35	Asn	Val	Thr	Met	Val 40	Gly	Asn	Leu	Leu	Ile 45	Val	Val	Thr
Ile	Ile 50	Ala	Ile	Ala	Ser	Leu 55	Asp	Ser	Pro	Val	Ser	Phe 60	Phe	Leu	Ala
Cys 65	Leu	Ser	Phe	Ile 70	Asp	Ala	Val	Tyr	Ser	Thr 75	Ser	Phe	Ser	Pro	Lys 80
Leu	Met	Ile	Asp 85	Leu	Cys	Asp	Lys 90	Lys	Thr	Val	Ser	Phe 95	Leu	Ala	
Cys	Met	Gly	Gln 100	Leu	Phe	Ile	Asn 105	Tyr	Pro	Phe	Gly	Gly 110	Ile	Glu	Val
Phe	Leu	Leu 115	Val	Gly	Met	Ala 120	Cys	Asp	His	Tyr	Val	Asp 125	Ile	Cys	Lys
Leu	Leu 130	His	Tyr	Leu	Thr	Ile 135	Met	Asn	Trp	Gln	Val 140	Cys	Ile	Leu	Leu
Phe 145	Met	Val	Ala	Val	Thr 150	Gly	Gly	Phe	Leu	His	Ser 155	Met	Phe	Gln	Ile 160
Val	Val	Val	Tyr 165	Ser	Leu	Pro	Phe	Cys	Gly 170	Pro	Asn	Val	Ile	Asp 175	His
Phe	Cys	Asp 180	Met	Tyr	Pro	Leu	Leu	Glu 185	Met	Val	Cys	Thr 190	Asp	Thr	Tyr
Phe	Ile 195	Gly	Leu	Thr	Val	Ile 200	Ala	Asn	Gly	Gly	Ala 205	Val	Cys	Met	Val
Ile 210	Phe	Ile	Leu	Leu	Leu	Ile 215	Ser	Tyr	Gly	Val	Ile 220	Leu	Asn	Ser	Leu
Lys 225	Thr	Tyr	Ser	Gln 230	Glu	Gly	Gly	His	Lys	Ala 235	Leu	Ser	Thr	Cys	Ser 240
Ser	Asn	Ile 245	Thr	Val	Ser	Leu	Phe	Phe 250	Asp	Pro	Cys	Ile 255	Phe	Ile	
Tyr	Val	Arg 260	Pro	Asp	Ser	Asn	Phe 265	Pro	Ile	Asp	Lys	Phe 270	Met	Thr	Val
Phe	Tyr 275	Thr	Ile	Ile	Thr	Pro 280	Met	Leu	Asn	Pro	Leu	Ile 285	Tyr	Thr	Leu
Arg	Asn 290	Leu	Glu	Val	Arg	Ile 295	Ala	Val	Lys	Asn	Leu 300	Trp	Cys	Lys	Asn

Xaa Thr Ile Val Arg
305

<210> 1914

<211> 318

<212> PRT

<213> Unknown (H38g832 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1914

Met	Asp	Arg	Val	Asn	Asn	Ser	Ala	Val	Ser	Lys	Phe	Val	Leu	Ile	Gly
1				5					10					15	
Leu	Ser	Ser	Ser	Trp	Glu	Met	His	Pro	Phe	Leu	Phe	Trp	Phe	Phe	Ser
			20					25					30		
Val	Phe	Tyr	Met	Gly	Ile	Ile	Leu	Glu	Asn	Leu	Phe	Ile	Val	Phe	Thr
		35					40					45			
Val	Ile	Ile	Asp	Ser	His	Leu	Asn	Ser	Pro	Val	Tyr	Cys	Leu	Leu	Ala
	50					55					60				
Asn	Ile	Tyr	Leu	Leu	Asp	Leu	Val	Phe	Ser	Tyr	Ser	Ser	Asp	Phe	Phe
65					70				75						80
Thr	Asn	Cys	Ser	Ile	Ile	Ser	Phe	Pro	Arg	Cys	Met	Ile	Gln	Ile	Phe
				85				90					95		
Phe	Ile	Cys	Val	Met	Arg	Lys	Ile	Glu	Met	Val	Leu	Leu	Ile	Thr	Met
			100					105					110		
Ala	Xaa	Ser	Arg	Tyr	Thr	Ala	Ile	Cys	Lys	Pro	Pro	His	Tyr	Leu	Thr
		115					120					125			
Thr	Met	Asn	Pro	Lys	Met	Cys	Val	Ser	Leu	Leu	Glu	Ala	Ser	Trp	Ile
	130					135					140				
Val	Arg	Ile	Ile	His	Ala	Val	Ser	Gln	Phe	Val	Phe	Ala	Ile	Asn	Leu
145					150				155						160
Pro	Phe	Cys	Gly	Pro	Asn	Arg	Val	Gly	Ser	Phe	His	Cys	Asp	Phe	Pro
			165					170					175		
Tyr	Val	Met	Lys	Leu	Ala	Cys	Val	Asp	Thr	Tyr	Lys	Leu	Glu	Val	Val
		180						185					190		
Val	Thr	Ala	Asn	Ser	Gly	Leu	Ile	Ser	Ile	Ala	Thr	Cys	Phe	Leu	Leu
		195					200					205			
Ile	Ile	Ser	Tyr	Ile	Phe	Ile	Ser	Val	Thr	Val	Xaa	Asn	Pro	Ser	Ser
	210					215					220				
Gly	Asp	Leu	Ser	Lys	Ala	Phe	Val	Ser	Cys	Ser	Asp	His	Ile	Thr	Val
225					230				235						240
Gly	Ile	Leu	Phe	Phe	Met	Pro	Cys	Ile	Phe	Leu	Tyr	Val	Xaa	Pro	Leu
				245					250					255	
Pro	Lys	Thr	Thr	His	Asp	Xaa	Tyr	Leu	Phe	Ile	Val	Pro	Leu	Leu	Ser
		260						265					270		
Pro	Leu	Ser	Arg	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Asn	Val	Ser
		275					280					285			
Met	Glu	Arg	Leu	Gly	Lys	Trp	Ile	Ala	Gly	Ser	Ser	Arg	Met	Ser	Xaa
	290					295					300				
Xaa	Met	Val	Leu	Ser	Arg	Val	Gln	Asp	Asp	Ser	Val	Ser	Pro		
305					310					315					

<210> 1915

<211> 309

<212> PRT

<213> Unknown (H38g833 protein)

<220>

<223> Synthetic construct

<400> 1915

```

Met Glu Gly Ile Asn Lys Thr Ala Lys Met Gln Phe Phe Phe Arg Pro
 1           5           10           15
Phe Ser Pro Asp Pro Glu Val Gln Met Leu Ile Phe Val Val Phe Leu
          20           25           30
Met Met Tyr Leu Thr Ser Leu Gly Asn Ala Thr Ile Ala Val Ile
      35           40           45
Val Gln Ile Asn His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ala Val Leu Glu Ile Phe Tyr Thr Ser Ser Ile Thr Pro Leu
65           70           75           80
Ala Leu Ala Asn Leu Leu Ser Met Gly Lys Thr Pro Val Ser Ile Thr
          85           90           95
Gly Cys Gly Thr Gln Met Phe Phe Phe Val Phe Leu Gly Gly Ala Asp
      100           105           110
Cys Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys
      115           120           125
His Pro Leu Arg Tyr Arg Leu Ile Met Ser Trp Ser Leu Cys Val Glu
      130           135           140
Leu Leu Val Gly Ser Leu Val Leu Gly Phe Leu Leu Ser Leu Pro Leu
145           150           155           160
Thr Ile Leu Ile Phe His Leu Pro Phe Cys His Asn Asp Glu Ile Tyr
          165           170           175
His Phe Tyr Cys Asp Met Pro Ala Val Met Arg Leu Ala Cys Ala Asp
          180           185           190
Thr Arg Val His Lys Thr Ala Leu Tyr Ile Ile Ser Phe Ile Val Leu
          195           200           205
Ser Ile Pro Leu Ser Leu Ile Ser Ile Ser Tyr Val Phe Ile Val Val
      210           215           220
Ala Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Gln Ala Tyr Ser
225           230           235           240
Thr Cys Ser Ser His Ile Leu Val Val Leu Leu Gln Tyr Gly Cys Thr
          245           250           255
Ser Phe Ile Tyr Leu Ser Pro Ser Ser Ser Tyr Ser Pro Glu Met Gly
          260           265           270
Arg Val Val Ser Val Ala Tyr Thr Phe Ile Thr Pro Ile Leu Asn Pro
          275           280           285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Leu Lys Asp Ala Leu Arg Lys
      290           295           300
Ala Leu Arg Lys Phe
305

```

<210> 1916

<211> 329

<212> PRT

<213> Unknown (H38g834 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1916

```

Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu
 1           5           10           15

```

Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe
 20 25 30
 Phe Ser L u Phe Tyr Val Gly Ile Ile Leu Gly Asn Leu Phe Ile Val
 35 40 45
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu
 50 55 60
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Thr Thr Val
 65 70 75 80
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe
 85 90 95
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val
 100 105 110
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met
 130 135 140
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser
 145 150 155 160
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val
 165 170 175
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met
 180 185 190
 Asp Thr Tyr Gly Leu Glu Phe Val Thr Ala Asn Ser Gly Phe Ile
 195 200 205
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu
 210 215 220
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe
 225 230 235 240
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys
 245 250 255
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1917

<211> 257

<212> PRT

<213> Unknown (H38g835 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 1917

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr
 1 5 10 15
 Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly
 20 25 30
 Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe
 35 40 45
 Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe

50	55	60
Asp Trp Phe Val Ala	Ile Cys Cys Pro Leu Cys Tyr Gly Leu Ile Met	
65	70	75
Ser Trp Arg Leu Cys	Val Gln Leu Thr Leu Gly Ser Leu Leu Leu Gly	80
85	90	95
Phe Phe Leu Ala Met	Gln Leu Thr Val Leu Ile Phe Gln Leu Pro Leu	
100	105	110
Cys Ser Ser Lys Glu	Ile Ser Thr Phe Tyr Cys Asp Val Leu Pro Val	
115	120	125
Met Arg Leu Ala Cys	Ala Asp Thr Trp Val His Glu Ala Thr Met Ser	
130	135	140
Met Val Ser Thr Thr	Phe Leu Thr Val Pro Phe Leu Leu Ile Thr Leu	
145	150	155
Ser Tyr Val Ser Ile	Met Ala Ala Ile Leu Lys Ile Cys Ser Ala Glu	
165	170	175
Gly Arg His Lys Ala	Phe Ser Thr Cys Ser Ser His Leu Thr Val Val	
180	185	190
Leu Leu Gln Asp Xaa	Cys Thr Arg Leu Ala Phe Leu Cys Pro Ser Ser	
195	200	205
Ser Tyr Tyr Pro Glu	Arg Gly Gln Ala Val Ser Val Val Tyr Thr Phe	
210	215	220
Ile Thr Pro Val Leu	Asn Pro Leu Ile Tyr Ser Met Arg Asn Thr Glu	
225	230	235
Leu Lys Asp Ala Leu	Lys Arg Ala Met Thr Arg Val Pro Leu Leu Xaa	
245	250	255
Thr		

<210> 1918

<211> 305

<212> PRT

<213> Unknown (H38g836 protein)

<220>

<223> Synthetic construct

<400> 1918

Met Val Thr Glu Phe	Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
1	5 10 15
Gln Thr Phe Leu Phe	Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
20	25 30
Phe Gly Asn Leu Leu	Ile Val Ile Thr Val Val Ser Asp Ser His Leu
35	40 45
His Ser Pro Met Tyr	Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
50	55 60
Ser Leu Ser Ser Val	Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
65	70 75 80
Gln Arg Lys Val Ile	Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
85	90 95
Leu His Phe Phe Gly	Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
100	105 110
Phe Asp Arg Tyr Ile	Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
115	120 125
Met Cys Gly Asn Ala	Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
130	135 140
Gly Phe Leu His Ser	Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
145	150 155 160
Phe Cys Gly Pro Asn	Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
165	170 175
Val Ile Lys Leu Ala	Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
180	185 190

Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile S r Tyr Thr Ile Ile Leu Met Thr Ile Gln His Cys Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Arg Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1919

<211> 318

<212> PRT

<213> Unknown (H38g837 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1919

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1 5 10 15
 Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
 20 25 30
 Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
 35 40 45
 Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
 50 55 60
 Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
 65 70 75 80
 Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
 85 90 95
 Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
 100 105 110
 Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
 115 120 125
 Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
 130 135 140
 Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
 145 150 155 160
 Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
 165 170 175
 Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
 180 185 190
 Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
 195 200 205
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
 210 215 220
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
 225 230 235 240
 Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu

<400> 1920															
Leu	Ser	Ile	Cys	Phe	Phe	Leu	Cys	Ile	Phe	Ser	Ala	Asp	Ile	Xaa	Ser
1				5					10					15	
Met	Leu	Ala	Met	Glu	Gln	Asn	Asn	Gly	Thr	Glu	Val	Thr	Glu	Phe	Ile
			20					25					30		
Leu	Leu	Gly	Phe	Ala	Gly	Gln	His	Lys	Ser	Trp	His	Ile	Leu	Ser	Ile
		35					40					45			
Ala	Phe	Leu	Ala	Ile	Tyr	Val	Val	Thr	Pro	Val	Gly	Asn	Ile	Gly	Met
	50					55					60				
Ile	Leu	Leu	Ile	Lys	Ile	Asp	Ala	Ser	Leu	His	Ile	Pro	Met	Xaa	Ile
65					70					75					80
Phe	Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Leu	Cys	Tyr	Thr	Ser	Ala	Ile
			85						90					95	
Thr	Pro	Lys	Met	Leu	Lys	Asn	Phe	Val	Glu	Thr	Lys	Lys	Ser	Ile	Ser
			100					105					110		
Cys	Ile	Gly	Cys	Met	Val	Gln	Leu	Leu	Val	Tyr	Gly	Thr	Phe	Ala	Thr
		115					120					125			
Ser	Asp	Cys	Tyr	Ile	Leu	Ala	Ala	Met	Ala	Val	Asp	Arg	Tyr	Val	Ala
	130					135					140				
Phe	Cys	Asn	Pro	Leu	His	Tyr	Pro	Gly	Val	Met	Ser	Gln	Arg	Leu	Cys
145					150					155					160
Ile	Lys	Leu	Leu	Val	Ser	Ser	Tyr	Val	Met	Gly	Phe	Leu	Asn	Ala	Ser
				165					170					175	
Ile	Asn	Ile	Ser	Phe	Thr	Phe	Ser	Leu	Asn	Phe	Cys	Lys	Ser	Lys	Thr
			180					185						190	
Ile	Asn	His	Phe	Phe	Cys	Asp	Glu	Pro	Pro	Ile	Ile	Ala	Leu	Pro	Cys
		195					200					205			
Ser	Asn	Ile	Asp	Leu	Asn	Ile	Met	Leu	Leu	Thr	Val	Phe	Val	Gly	Leu
	210					215					220				
Asn	Leu	Met	Cys	Thr	Val	Met	Val	Val	Ile	Ile	Ser	Cys	Ile	Tyr	Val
225					230					235					240
Leu	Val	Ala	Ile	Leu	Arg	Ile	Ser	Ser	Ala	Ala	Gly	Lys	Lys	Lys	Ser
				245					250					255	
Leu	Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Gly
			260					265					270		
Val	Leu	Ser	Tyr	Met	Tyr	Leu	Cys	His	Arg	Ile	Asn	Glu	Ser	Gln	Lys
		275					280					285			
Gln	Glu	Lys	Val	Ala	Ser	Val	Phe	Tyr	Gly	Ile	Ile	Ile	Pro	Met	Leu
	290					295					300				

Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Il
 305 310 315 320
 Lys Leu Thr Glu Lys Lys Tyr Phe
 325

<210> 1921

<211> 338

<212> PRT

<213> Unknown (H38g839 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1921

Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg
 1 5 10 15
 Gly Val Val His Phe His Phe His Phe Ser Thr Asp Leu Val Val
 20 25 30
 Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val
 35 40 45
 Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His
 50 55 60
 Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu
 65 70 75 80
 Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu
 85 90 95
 Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met
 100 105 110
 Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn
 130 135 140
 Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu
 145 150 155 160
 Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His
 165 170 175
 Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met
 180 185 190
 Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser
 195 200 205
 Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser
 210 215 220
 Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met
 225 230 235 240
 His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His
 245 250 255
 Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu
 260 265 270
 Cys Pro Ser Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu
 275 280 285
 Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val
 290 295 300
 Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met
 305 310 315 320
 Ser Leu Val Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro
 325 330 335
 Xaa Leu

<210> 1922
 <211> 329
 <212> PRT
 <213> Unknown (H38g840 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1922
 Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu
 1 5 10 15
 Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe
 20 25 30
 Phe Ser Leu Phe Tyr Val Gly Ile Leu Gly Asn Leu Phe Ile Val
 35 40 45
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu
 50 55 60
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Ser Thr Thr Val
 65 70 75 80
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe
 85 90 95
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val
 100 105 110
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met
 130 135 140
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser
 145 150 155 160
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val
 165 170 175
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met
 180 185 190
 Asp Thr Tyr Gly Leu Glu Phe Val Val Thr Ala Asn Ser Gly Phe Ile
 195 200 205
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu
 210 215 220
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe
 225 230 235 240
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys
 245 250 255
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1923
 <211> 245
 <212> PRT

<213> Unknown (H38g841 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 1923

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Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser
 1           5           10           15
Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser
          20           25           30
Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
          35           40           45
Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys
          50           55           60
Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met
65           70           75           80
Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
          85           90           95
Gly Ser Pro Ile Pro Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
          100          105          110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Arg Phe Xaa
          115          120          125
Phe Ser Tyr Leu Asn Leu Lys Met Xaa Thr Asn Tyr Ser Phe Val Xaa
          130          135          140
Ala Phe Gln Asn Asn Xaa Arg Gln Leu Cys Pro Phe Leu Asp Asn His
145          150          155          160
His Thr Phe Phe Thr Leu Ile Asp Thr Gln Leu Leu Ile Ser His Gly
          165          170          175
Phe Ser Thr Gln Thr Thr Phe Ile Leu Ser Ser Tyr Ala Ser Gly Tyr
          180          185          190
Ala Thr Val Asp Ser Gln Cys Phe Ile Tyr Phe Leu Asn Met Met Ile
          195          200          205
Thr Ile Asn Leu Phe Val Arg Phe Lys Asn Ile Phe Met His Ser Ser
          210          215          220
Ile Ser Ile Asn Tyr Asn Tyr Tyr Phe Lys Lys Xaa Asn Lys Gly Gly
225          230          235          240
Ile Tyr Glu Ile Tyr
          245

```

<210> 1924

<211> 305

<212> PRT

<213> Unknown (H38g842 protein)

<220>

<223> Synthetic construct

<400> 1924

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1           5           10           15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
          20           25           30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
          35           40           45
His Ser Pro Met Tyr Phe Leu Ala Asn Leu Ser Leu Ile Asp Leu
          50           55           60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser

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65          70          75          80
Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
      85          90          95
Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
      100         105         110
Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
      115         120         125
Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
      130         135         140
Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
145         150         155         160
Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
      165         170         175
Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
      180         185         190
Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
      195         200         205
Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
210         215         220
Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
225         230         235         240
Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
      245         250         255
Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
      260         265         270
Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
      275         280         285
Thr Ala Ile Arg Arg Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
290         295         300
Phe
305

```

<210> 1925

<211> 309

<212> PRT

<213> Unknown (H38g843 protein)

<220>

<223> Synthetic construct

<400> 1925

```

Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
1          5          10          15
Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20          25          30
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
      35          40          45
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
      50          55          60
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
65         70         75         80
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
      85         90         95
Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
      100        105        110
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115        120        125
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
130        135        140
Val Ala Val Val Tyr Ala Ile Gly L u Ile Gly Ser Thr Ile Glu Thr
145        150        155        160

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Gly Leu Met Leu Lys Leu Pr Tyr Cys Glu His Leu Ile Ser His Tyr
 165 170 175
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
 195 200 205
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
 210 215 220
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
 245 250 255
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
 260 265 270
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
 290 295 300
 Arg Gly Lys Leu Phe
 305

<210> 1926

<211> 310

<212> PRT

<213> Unknown (H38g844 protein)

<220>

<223> Synthetic construct

<400> 1926

Met Ala Ala Lys Asn Ser Ser Val Thr Glu Phe Ile Leu Glu Gly Leu
 1 5 10 15
 Thr His Gln Pro Gly Leu Arg Ile Pro Leu Phe Phe Leu Phe Leu Gly
 20 25 30
 Phe Tyr Thr Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu Ile
 35 40 45
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
 50 55 60
 Leu Ser Leu Ile Asp Phe Cys Phe Ser Thr Thr Ile Thr Pro Lys Met
 65 70 75 80
 Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly Cys
 85 90 95
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Val Ser Glu Ser Phe
 100 105 110
 Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Leu Tyr Thr Val Thr Met Ser Cys Gln Val Cys Leu Leu Leu Leu
 130 135 140
 Leu Gly Ala Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr Gly
 145 150 155 160
 Ser Ile Met Asn Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His Phe
 165 170 175
 Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
 180 185 190
 Met Asn Glu Leu Val Val Phe Ile Val Val Ala Val Asp Val Gly Met
 195 200 205
 Pro Ile Val Thr Val Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile
 210 215 220
 Leu His Asn Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe

245 250 255
 Met Tyr Leu Lys Pro Leu Ser Ile Leu Pro Leu Glu Gln Gly Lys Val
 260 265 270
 Ser Ser Leu Phe Tyr Thr Ile Ile Val Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Leu
 290 295 300
 Gly Arg Lys Ile Phe Ser
 305 310

<210> 1927

<211> 157

<212> PRT

<213> Unknown (H38g845 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1927

Met Gly Glu Ala Arg Asn Arg Thr Val Val Gln Glu Phe Ile Leu Glu
 1 5 10 15
 Gly Phe Pro Ala Val Gln His Leu Gly Asn Val Leu Phe Leu Val His
 20 25 30
 Leu Leu Ala Tyr Leu Ala Ser Ile Met Ala Asn Met Leu Ile Ile Thr
 35 40 45
 Ile Thr Trp Ala Asp His His Leu Gln Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Ser Phe Ser Phe Cys Glu Cys Cys Phe Ile Thr Thr Val Ile Pro
 65 70 75 80
 Lys Leu Leu Val Ile Leu Leu Ser Gly Arg Ala Lys Ile Pro Leu Ser
 85 90 95
 Thr Thr Leu Ser His Ala Val Pro Phe Ser Phe Leu Tyr Ser Trp Val
 100 105 110
 Asn Ser Phe Ser Ser Leu Asn Gly Cys Asp Val Pro Leu Asp Xaa Tyr
 115 120 125
 Leu Ala Ile Cys Lys Pro Leu His Tyr Ser Thr Ile Met Ser Leu Arg
 130 135 140
 Thr Ser Phe His Lys Val Thr Ala Trp Leu Cys Pro Gly
 145 150 155

<210> 1928

<211> 333

<212> PRT

<213> Unknown (H38g846 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1928

Thr Asp Pro Gln Asn Leu Thr Thr Asp Val Ser Ile Phe Leu Val Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30

```

Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Il  Ile Leu
   35                               40                               45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
   50                               55                               60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
  65                               70                               75                               80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Leu Ile Ser Tyr Ala
   85                               90                               95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
  100                               105                               110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
  115                               120                               125
Cys His Pro Leu Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
  130                               135                               140
Phe Leu Val Leu Leu Ser Cys Cys Leu Ser Leu Leu Asp Ser Gln Leu
  145                               150                               155                               160
His Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile
  165                               170                               175
Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His His Ala Cys Cys
  180                               185                               190
Asp Thr Phe Thr Asn Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe
  195                               200                               205
Gly Phe Leu Pro Thr Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val
  210                               215                               220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Leu
  225                               230                               235                               240
Ser Ala Cys Gly Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr
  245                               250                               255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys
  260                               265                               270
Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
  275                               280                               285
Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
  290                               295                               300
Arg Leu His Gly Arg Thr Val Xaa Ser Gln Tyr Leu Ile Ile Cys Ser
  305                               310                               315                               320
Ile Pro Phe Val Val Trp Val Xaa Lys Gly Ser Lys Val
   325                               330

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<210> 1929

<211> 222

<212> PRT

<213> Unknown (H38g847 protein)

<220>

<223> Synthetic construct

<400> 1929

```

Ser Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Leu Pro
  1                               5                               10                               15
Lys Met Ile Phe Ser Tyr Leu Ser Gly Lys Lys Ser Ile Ser Leu Ala
  20                               25                               30
Gly Cys Gly Thr Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ala Glu
  35                               40                               45
Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
  50                               55                               60
His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys Val Phe
  65                               70                               75                               80
Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile Ile Val
  85                               90                               95
Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu Ile His

```

	100		105		110										
His	Phe	Phe	Cys	Asp	Val	Ala	Ala	Leu	Leu	Pro	Leu	Ser	Cys	Thr	Glu
	115						120					125			
Thr	Ser	Ala	Phe	Glu	Arg	Leu	Leu	Val	Ile	Cys	Cys	Val	Val	Met	Leu
	130					135					140				
Ile	Phe	Pro	Val	Ser	Val	Ile	Ile	Leu	Ser	Tyr	Ser	His	Val	Leu	Arg
145				150					155					160	
Ala	Val	Ile	His	Met	Gly	Ser	Gly	Glu	Ser	Arg	Arg	Lys	Ala	Phe	Thr
			165					170						175	
Thr	Cys	Ser	Ser	His	Pro	Ser	Val	Val	Gly	Leu	Tyr	Tyr	Gly	Ala	Ala
		180					185						190		
Met	Phe	Met	Tyr	Met	Arg	Pro	Ala	Ser	Lys	His	Thr	Pro	Asp	Gln	Asp
	195					200						205			
Lys	Met	Val	Ser	Ala	Phe	Tyr	Thr	Asn	Leu	Thr	Pro	Met	Leu		
	210					215					220				

<210> 1930

<211> 114

<212> PRT

<213> Unknown (H38g848 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(114)

<223> Xaa = Any Amino Acid

<400> 1930

Leu	Ala	Cys	Ile	Val	Gly	Xaa	Lys	Phe	Ala	Phe	Ile	Ile	Ser	Pro	Asn
1			5					10					15		
His	His	Phe	Met	Ile	Met	Val	Thr	Phe	Ile	Leu	Val	Asn	Ile	Xaa	Lys
		20					25					30			
His	Ser	Ser	Gly	Asn	Leu	Ser	Ser	Ala	Leu	Ile	Ile	Leu	Phe	Ile	Phe
	35					40					45				
Ile	Pro	Val	Val	Ser	Leu	Phe	Phe	Thr	Pro	Cys	Val	Val	Leu	Tyr	Val
	50				55					60					
Trp	Pro	Thr	Leu	Pro	Pro	Ser	Leu	Asp	Lys	Asn	Met	Phe	Ile	Val	Asp
65				70					75					80	
Phe	Val	Val	Asn	Pro	Val	Leu	Lys	Pro	Ala	Thr	Tyr	Ile	Leu	Gln	Asn
			85				90						95		
Lys	Asp	Ile	Lys	Val	Ala	Leu	Xaa	Asn	Leu	His	Glu	Lys	Arg	Thr	Tyr
		100					105						110		
Ser	Ser														

<210> 1931

<211> 305

<212> PRT

<213> Unknown (H38g849 protein)

<220>

<223> Synthetic construct

<400> 1931

Met	Val	Thr	Glu	Phe	Ile	Phe	Leu	Gly	Leu	Ser	Asp	Ser	Gln	Gly	Leu
1			5					10					15		
Gln	Thr	Phe	Leu	Phe	Met	Leu	Phe	Phe	Val	Phe	Tyr	Gly	Gly	Ile	Val
		20					25					30			
Phe	Gly	Asn	Leu	Leu	Ile	Val	Ile	Thr	Val	Val	Ser	Asp	Ser	His	Leu
		35				40						45			

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp L u
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1932

<211> 223

<212> PRT

<213> Unknown (H38g850 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1932

Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro
 1 5 10 15
 Lys Met Val Val Asp Ile Gln Ser His Ser Arg Ser Phe Ser Tyr Ala
 20 25 30
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 35 40 45
 Glu Thr Leu Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile
 50 55 60
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 65 70 75 80
 Phe Leu Leu Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
 85 90 95
 Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu

	100		105		110										
Ile	Pro	Asn	Phe	Leu	Cys	Asp	Pro	Ser	Pro	Leu	Pro	His	Leu	Ala	Cys
	115						120					125			
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
	130						135					140			
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	Ile
	145						150				155				160
Val	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala
			165							170					175
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly
			180						185					190	
Thr	Gly	Val	Gly	Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg
		195					200					205			
Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	
	210					215					220				

<210> 1933

<211> 329

<212> PRT

<213> Unknown (H38g851 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1933

Asp	Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu
1			5					10						15	
Leu	Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe
		20					25					30			
Phe	Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val
	35					40					45				
Phe	Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu
	50				55					60					
Leu	Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val
	65				70				75					80	
Pro	Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe
			85					90					95		
His	Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val
		100					105						110		
Glu	Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile
	115					120					125				
Cys	Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met
	130					135				140					
Phe	Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser
	145				150				155					160	
Gln	Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val
			165					170						175	
Gly	Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met
		180					185						190		
Asp	Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile
	195					200					205				
Ser	Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu
	210					215					220				
Val	Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe
	225				230				235					240	
Thr	Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys
			245					250						255	

Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Thr Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1934

<211> 220

<212> PRT

<213> Unknown (H38g852 protein)

<220>

<223> Synthetic construct

<400> 1934

Ser Val Leu Ser Ile Ser Glu Thr Tyr Tyr Thr Val Ala Ile Asn Pro
 1 5 10 15
 Gln Met Leu Ser Gly Leu Leu Ser Pro Gln Gln Thr Ile Ser Ile Pro
 20 25 30
 Gly Cys Ala Ala Gln Leu Phe Phe Tyr Leu Thr Phe Gly Val Asn Lys
 35 40 45
 Cys Phe Leu Leu Thr Ala Met Gly Tyr Asp His Tyr Val Ala Ile Cys
 50 55 60
 Asn Pro Leu Gln Tyr Ser Val Ile Met Gly Lys Lys Ala Cys Ile Gln
 65 70 75 80
 Leu Val Ser Gly Ser Trp Asn Ile Gly Leu Ser Thr Ala Ile Ile Gln
 85 90 95
 Val Ser Ser Val Phe Ser Leu Pro Phe Cys Asp Ala Asn Leu Ile Ser
 100 105 110
 His Phe Phe Cys Asp Ile Arg Pro Ile Met Lys Leu Ala Cys Ala Asp
 115 120 125
 Thr Thr Ile Lys Glu Phe Ile Thr Leu Leu Ile Ser Leu Cys Val Leu
 130 135 140
 Val Leu Pro Met Val Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Thr
 145 150 155 160
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
 165 170 175
 Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Arg Thr
 180 185 190
 Ser Phe Ile Tyr Leu Lys Pro Lys Ser Gln Asn Ser Leu Gln Asp Arg
 195 200 205
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu
 210 215 220

<210> 1935

<211> 313

<212> PRT

<213> Unknown (H38g853 protein)

<220>

<223> Synthetic construct

<400> 1935

Met Ser Thr Ser Asn His Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Val Pro

20 25 30
 Phe Phe Phe Val Tyr Leu Val Ala Leu Leu Gly Asn Thr Ala Leu Leu
 35 40 45
 Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ala Met Leu Asp Ser Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
 65 70 75 80
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Thr Lys Glu Ile Ser Phe
 85 90 95
 Gly Gly Cys Leu Ser His Met Phe Phe Ile His Phe Phe Thr Ala Met
 100 105 110
 Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
 115 120 125
 Cys Lys Pro Leu Arg Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
 130 135 140
 Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Val Pro
 145 150 155 160
 Leu Val Phe Leu Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
 165 170 175
 Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
 180 185 190
 Ser Ile Lys Val Asn Ile Arg Phe Gly Leu Gly Asn Ile Ser Leu Leu
 195 200 205
 Leu Leu Asp Val Ile Leu Ile Ile Leu Ser Tyr Val Arg Ile Leu Tyr
 210 215 220
 Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Phe Thr Pro Ala
 245 250 255
 Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Gln Tyr
 260 265 270
 Ile His Ile Ile Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
 275 280 285
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
 290 295 300
 Leu Arg Ile Phe Leu Lys Thr Asn His
 305 310

<210> 1936

<211> 295

<212> PRT

<213> Unknown (H38g854 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 1936

Tyr Met Ile Thr Ile Leu Trp Glu Ile Ser Lys Pro Val Asn Asn Ile
 1 5 10 15
 Phe Leu Thr Leu Ser Val Arg Tyr Gln Met Leu Ile Thr Thr Val Ser
 20 25 30
 Xaa Leu Xaa Met Lys Ser Ile Ile Xaa Ile Tyr Xaa Ser Phe Ser Glu
 35 40 45
 Tyr Leu Met Ser Xaa Lys Ile Trp Glu His Met Xaa Tyr Cys Ala Cys
 50 55 60
 Ile Asn Met Asp Lys Val Ser Glu Val Phe Ser Glu His Leu Phe Gly
 65 70 75 80

Ala Ala Glu Ile Ile Pro Leu Met Gly Met Val His Gly Cys Tyr Val
 85 90 95
 Thr Ile Cys Thr Ala Xaa Asn Ile Met Thr Gln Tyr Arg Cys Gly His
 100 105 110
 Leu Ala Gly Met Ala Cys Thr Gly Arg Phe Ile His Gly Thr Val Xaa
 115 120 125
 Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asn Ser Asn Val Thr Ile
 130 135 140
 Xaa Ile Ala His Phe Ile Cys Asp Leu Asn Thr Leu Leu Lys Leu Leu
 145 150 155 160
 Cys Ile Gly Ser His Asp Thr Leu Gly Leu Phe Val Ala Ala Asn Asp
 165 170 175
 Gly Phe Asn Cys Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa Val
 180 185 190
 Ala Ile Leu Tyr Thr Leu Lys Ser His Ser Leu Glu Glu Arg Tyr Lys
 195 200 205
 Ala Leu Ser Thr Cys Val Ser His Thr Thr Val Ala Ile Xaa Phe Phe
 210 215 220
 Val Phe Cys Ile Leu Val Tyr Leu Cys Pro Val Thr Leu Leu Pro Val
 225 230 235 240
 Ser Lys Ala Val Ala Val Leu Tyr Thr Met Ile Thr Pro Thr Leu Asn
 245 250 255
 Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Val Glu Lys
 260 265 270
 Leu Leu Gly Gln Lys Met Thr Xaa Arg Glu Lys Xaa Ser Lys His Lys
 275 280 285
 Met Ile Leu Leu Phe Gln Trp
 290 295

<210> 1937

<211> 309

<212> PRT

<213> Unknown (H38g855 protein)

<220>

<223> Synthetic construct

<400> 1937

Met Glu Lys Lys Lys Asn Val Thr Glu Phe Ile Leu Ile Gly Leu Thr
 1 5 10 15
 Gln Asn Pro Ile Met Glu Lys Val Thr Phe Val Val Phe Leu Val Leu
 20 25 30
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Ile Val Val Thr Ile Thr
 35 40 45
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Thr His Leu
 50 55 60
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
 65 70 75 80
 Val Asp Ser Phe Gln Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Ala Gln Ala Tyr Ala Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
 100 105 110
 Leu Thr Val Met Ala Cys Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Asn Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Ala
 130 135 140
 Val Ala Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
 145 150 155 160
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Gly His Phe Met
 165 170 175
 Cys Asp Leu Tyr Pro Leu Leu Lys Leu Val Cys Ile Asp Thr His Thr

```

      180      185      190
Leu Gly Leu Phe Val Ala Val Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195      200      205
Phe Leu Il Leu Val Val Ser Tyr Val Ile Ile Leu Arg Ser Leu Lys
      210      215      220
Asn Asn Ser Leu Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ile Ser
225      230      235      240
His Ile Ile Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
      245      250      255
Leu Arg Ser Val Thr Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
      260      265      270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Val Val Tyr Thr Leu Arg
      275      280      285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
      290      295      300
Thr Ser Asp Asn Asp
305

```

<210> 1938

<211> 246

<212> PRT

<213> Unknown (H38g856 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(246)

<223> Xaa = Any Amino Acid

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<400> 1938
Cys Ile Gln Gln His Xaa Ser Pro Leu Cys Leu Cys Met Phe Ser Phe
 1      5      10      15
Tyr Phe Asn Leu Tyr His Phe Phe Pro Lys Xaa Lys Tyr Leu His Ser
      20      25      30
Leu Arg Asp Ala Glu Ile Asn Xaa Leu Val Xaa Ser Lys Val Leu Ile
      35      40      45
Asn Gln Ile Tyr Thr Lys Ala Asn Trp Pro Phe His Gly Leu Xaa His
      50      55      60
Tyr Ala Gln Pro Leu His Thr Gln Thr Cys Ile Ser Phe Ser Asn Val
65      70      75      80
Ile Xaa Cys Ser Thr Xaa Leu Phe Thr Gly His Phe Phe Leu Gly Gly
      85      90      95
Ser Gln Ile Phe Leu Leu Leu Val Met Ala Tyr Gly His Tyr Arg Ala
      100      105      110
Ile Cys Lys Ser Leu Gln Tyr Leu Val Val Met Lys Gln Trp Leu Cys
      115      120      125
Val Val Leu Leu Val Val Ser Trp Ala Gly Gly Phe Leu His Ile Val
      130      135      140
Ile Gln Leu Gly Leu Ile Tyr Gly Leu Pro Ser Tyr Asp Pro Asn Val
145      150      155      160
Ile Gly His Phe Ile Cys Asp Met Asp Pro Leu Met Lys Leu Val Cys
      165      170      175
Asp Tyr Thr Leu Asn Arg Phe Ala Tyr Phe Ala Gly His Asp Xaa Ile
      180      185      190
Leu Gly Phe Met Tyr Phe Thr Tyr Ala Gln Thr Gly Leu Phe Pro Phe
      195      200      205
Gly Asp Ser Thr Ser Leu Phe Phe Cys His Phe Phe Pro Arg Gly Leu
      210      215      220
Gly Ser Ile Asn Leu Ala Ile His Ser Tyr Tyr Pro Cys Gly Ile Ser
225      230      235      240

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Arg Asp Thr Glu Pro Thr
245

<210> 1939
<211> 262
<212> PRT
<213> Unknown (H38g857 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(262)
<223> Xaa = Any Amino Acid

<400> 1939
Leu Ile Val Val Thr Val Thr Val Ser Glu Thr Leu Gly Ser Pro Met
1 5 10 15
Tyr Phe Phe Leu Ala Gly Leu Ser Phe Ile Asp Ile Ile Tyr Ser Ser
20 25 30
Ser Ile Ser His Arg Leu Ile Ser Asp Leu Phe Phe Gly Asn Asn Ser
35 40 45
Ile Ser Phe Pro Ser Cys Leu Ala Gln Leu Phe Thr Glu His Leu Phe
50 55 60
Gly Gly Ser Glu Val Phe Leu Leu Leu Val Met Ala Tyr Asp Leu His
65 70 75 80
Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val Ala
85 90 95
Ser Trp Val Gly Phe Leu His Ser Val Phe Gln Leu Ser Val Ile
100 105 110
Tyr Gly Leu Pro Phe Cys Asp Leu Asn Val Ile Asp His Phe Phe Cys
115 120 125
Asp Met His Pro Leu Leu Lys Leu Val Cys Thr Asp Thr His Val Ile
130 135 140
Gly Leu Leu Val Val Ala Asn Gly Gly Leu Gly Cys Thr Ile Val Phe
145 150 155 160
Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys Asn
165 170 175
Leu Ser Gln Lys Gly Arg Xaa Lys Ala Leu Ser Thr Cys Ser Ser His
180 185 190
Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Tyr Ala
195 200 205
Arg Pro Ala Arg Thr Phe Pro Ile Asp Lys Ser Val Ser Val Phe Tyr
210 215 220
Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
225 230 235 240
Ser Glu Met Thr Ser Ala Met Lys Lys Leu Trp Arg Arg Asp Phe Ile
245 250 255
Ser Ser Ser Thr Xaa Val
260

<210> 1940
<211> 309
<212> PRT
<213> Unknown (H38g858 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1940

```

Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1           5           10           15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Leu Thr
      20           25           30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
      35           40           45
Ala Ser Pro Ser Leu Gly Ser Ser Met Tyr Phe Phe Leu Ala Cys Leu
      50           55           60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
      65           70           75           80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
      85           90           95
Gly Gln Leu Phe Ile Asp His Leu Asp Gly Gly Ala Glu Val Val Leu
      100          105          110
Leu Val Val Lys Ala Cys Asp His His Val Asp Ile Trp Lys Pro Leu
      115          120          125
Arg Tyr Leu Thr Ile Met Asn Arg Gln Gly Xaa Met Arg Leu Leu Val
      130          135          140
Ala Val Val Thr Gly Gly Val Leu His Ser Leu Ser His Ile Val Ser
      145          150          155          160
Val Val Tyr Ser Leu Ala Tyr Cys Gly Pro Asn Val Ile Asp Tyr Phe
      165          170          175
Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr
      180          185          190
Phe Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val
      195          200          205
Val Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu
      210          215          220
Lys Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser
      225          230          235          240
Ser His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met
      245          250          255
Tyr Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val
      260          265          270
Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu
      275          280          285
Arg Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Lys
      290          295          300
Leu Thr Val Leu Glu
305

```

<210> 1941

<211> 305

<212> PRT

<213> Unknown (H38g859 protein)

<220>

<223> Synthetic construct

<400> 1941

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
      20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
      35           40           45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Val Gly Asn
      50           55           60

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Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
 65 70 75 80
 Leu Val Ile Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Cys
 100 105 110
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
 145 150 155 160
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
 180 185 190
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
 195 200 205
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
 210 215 220
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
 245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300
 Pro
 305

<210> 1942

<211> 316

<212> PRT

<213> Unknown (H38g860 protein)

<220>

<223> Synthetic construct

<400> 1942

Met Ile Cys Glu Asn His Thr Arg Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Thr Asn Asn Pro Glu Met Gln Val Ser Leu Phe Ile Phe Phe Leu
 20 25 30
 Ala Ile Tyr Thr Val Thr Leu Leu Gly Asn Phe Leu Ile Val Thr Val
 35 40 45
 Thr Ser Val Asp Leu Ala Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 Asn Leu Ser Leu Leu Glu Val Cys Phe Thr Leu Val Met Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Val Ser Pro Arg Lys Ile Ile Ser Phe Val Gly
 85 90 95
 Cys Gly Thr Gln Met Tyr Phe Phe Phe Phe Gly Ser Ser Glu Cys
 100 105 110
 Phe Leu Leu Ser Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met Asn Arg Ser Leu Cys Leu Trp Met
 130 135 140
 Ala Ile Gly Ser Trp Met Ser Gly Val Pro Val Ser Met Leu Gln Thr

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145          150          155          160
Ala Trp Met Met Ala Leu Pro Phe Cys Gly Pro Asn Ala Val Asp His
          165          170          175
Phe Phe Cys Asp Gly Pro Pro Val Leu Lys Leu Val Thr Val Asp Thr
          180          185          190
Thr Met Tyr Glu Met Gln Ala Leu Ala Ser Thr Leu Leu Phe Ile Met
          195          200          205
Phe Pro Phe Cys Leu Ile Leu Val Ser Tyr Thr Arg Ile Ile Ile Thr
          210          215          220
Ile Leu Arg Met Ser Ser Ala Thr Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ser
          245          250          255
Leu Thr Tyr Leu Arg Pro Lys Ser Asn Gln Ser Pro Glu Ser Lys Lys
          260          265          270
Leu Val Ser Leu Ser Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Gly Leu Arg Asn Asn Glu Val Lys Gly Ala Val Lys Arg Thr
          290          295          300
Ile Thr Gln Lys Val Leu Gln Lys Leu Asp Val Phe
305          310          315

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<210> 1943

<211> 309

<212> PRT

<213> Unknown (H38g861 protein)

<220>

<223> Synthetic construct

<400> 1943

```

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
1      5      10      15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Ser Val Ile
20     25     30
Tyr Ile Asn Ala Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr
35     40     45
Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Ala Tyr Leu
50     55     60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
65     70     75     80
Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Phe Asn Gly Cys Met
85     90     95
Thr Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu
100    105    110
Leu Thr Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Lys Pro Leu
115    120    125
His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
130    135    140
Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
145    150    155    160
Ile Cys Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
165    170    175
Cys Asp Leu Tyr Thr Leu Ile Asn Leu Ala Cys Thr Asn Thr His Thr
180    185    190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
195    200    205
Cys Leu Leu Leu Leu Val Ser Cys Val Val Ile Leu Tyr Ser Leu Lys
210    215    220
Thr His Ser Leu Glu Ala Arg His Glu Ala Leu Ser Thr Cys Val Ser
225    230    235    240

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His Ile Thr Val Val Ile Leu Ser Phe Ile Pro Cys Il Phe Val Tyr
 245 250 255
 Met Arg Pro Pro Ala Thr L u Pro Ile Asp Lys Ala Val Ala Val Phe
 260 265 270
 Tyr Thr Met Ile Thr Ser Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala
 290 295 300
 Ile Ser Ser Val Lys
 305

<210> 1944

<211> 164

<212> PRT

<213> Unknown (H38g862 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(164)

<223> Xaa = Any Amino Acid

<400> 1944

Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg
 1 5 10 15
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys
 20 25 30
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His
 35 40 45
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu
 50 55 60
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu
 65 70 75 80
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile
 85 90 95
 Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser
 100 105 110
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys
 115 120 125
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu
 130 135 140
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu
 145 150 155 160
 Leu Arg Thr His

<210> 1945

<211> 318

<212> PRT

<213> Unknown (H38g863 protein)

<220>

<223> Synthetic construct

<400> 1945

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala
 1 5 10 15
 Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val
 20 25 30
 Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn

```

      35      40      45
Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro
  50      55      60
Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr
  65      70      75      80
Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr
      85      90      95
Ile Ser Val Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu
      100      105      110
Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe
      115      120      125
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg
      130      135      140
Val Cys Leu Lys Leu Ala Ala Ala Ser Trp Phe Thr Gly Val Val Val
      145      150      155      160
Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr
      165      170      175
Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu
      180      185      190
Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser
      195      200      205
Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met
      210      215      220
His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His
      225      230      235      240
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe
      245      250      255
Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr
      260      265      270
Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro
      275      280      285
Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu
      290      295      300
Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr
      305      310      315

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<210> 1946
 <211> 291
 <212> PRT
 <213> Unknown (H38g864 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(291)
 <223> Xaa = Any Amino Acid

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<400> 1946
Ser Met Tyr Leu Val Thr Met Leu Arg Asn Leu Phe Ile Ile Leu Ala
  1      5      10      15
Gly Ser Ser Asp Pro His Phe His Thr Pro Met Tyr Phe Phe Leu Ser
      20      25      30
Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys
      35      40      45
Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
      50      55      60
Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp
      65      70      75      80
Met Leu Leu Thr Leu Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      85      90      95

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Ile Cys His Pro Leu His Tyr Arg Val Ile Met Asn Pro His Leu Cys
      100                      105                      110
Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      115                      120                      125
Leu His Ser Trp Ile Val Leu His Asn Ser Pro Phe Gln Glu Cys Gly
      130                      135                      140
Asn Leu Xaa Phe Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala
      145                      150                      155                      160
Cys Ser Asp Ser Ile Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro
      165                      170                      175
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys
      180                      185                      190
Ile Val Ser Ser Ile Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys
      195                      200                      205
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr
      210                      215                      220
Glu Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro
      225                      230                      235                      240
Arg Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Ile Pro Met
      245                      250                      255
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Ser Ala
      260                      265                      270
Leu Trp Arg Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His
      275                      280                      285
Pro Phe Ser
      290

```

<210> 1947

<211> 327

<212> PRT

<213> Unknown (H38g865 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1947

```

Met Asp Val Ser Ile Phe Leu Leu Leu Gly Thr Thr Glu Asp Pro Glu
  1          5          10          15
Arg Gln Pro Val Leu Thr Gly Leu Phe Leu Ser Met Cys Leu Val Thr
      20          25          30
Val Leu Gly Lys Leu Leu Ile Met Leu Ala Phe Ser Pro Asp Ser His
      35          40          45
Leu His Thr His Met Tyr Phe Phe Leu Ser Asn Leu Ser Leu Pro Asp
      50          55          60
Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Ala Asp Ile Gln
      65          70          75          80
Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser
      85          90          95
Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asp Met Leu Leu Ser Val
      100          105          110
Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser
      115          120          125
Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu Phe Phe
      130          135          140
Phe Phe Leu Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu
      145          150          155          160
Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Asp

```

Met 1	Gly	Asp	Lys	Gly 5	Thr	Gly	Asn	His	Ser 10	Asp	Val	Thr	Asp	Phe 15	Ile
Leu	Glu	Gly	Phe	Arg 20	Val	Arg	Pro	Glu 25	Phe	Tyr	Ile	Leu	Leu	Phe	Phe
Leu	Phe	Leu	Leu	Ile 35	Tyr	Ser	Met 40	Val	Leu	Leu	Gly	Asn 45	Ile	Ser	Val
Met 50	Thr	Ile	Ile	Val	Thr	Asp 55	Ser	Gln	Leu	Asn	Thr 60	Pro	Met	Tyr	Phe
Phe 65	Leu	Gly	Asn	Leu 70	Ser	Phe	Ile	Asp	Val	Ser 75	Tyr	Ser	Thr	Val	Ile 80
Ala	Pro	Lys	Ala	Met 85	Ala	His	Phe	Leu	Ser 90	Glu	Lys	Lys	Thr	Val	Ser
Phe	Ala	Gly	Cys	Val 100	Ala	Gln	Leu	Phe 105	Leu	Phe	Ala	Leu	Phe	Ile	Val
Thr	Glu	Gly	Phe	Val 115	Leu	Ala	Ala 120	Met	Ala	Tyr	Asp	Arg 125	Phe	Ser	Ala
Ile 130	Cys	Asn	Pro	Leu 135	Leu	His	Ser	Val	His	Met	Ser 140	Arg	Arg	Leu	Cys
Thr 145	Gln	Leu	Val	Ala 150	Gly	Ser	Tyr	Phe	Cys	Gly 155	Trp	Ala	Ser	Ser	Ile 160
Leu	Gln	Val	Ser	Val 165	Thr	Phe	Ser	Val	Ser 170	Phe	Cys	Ala	Ser	Arg	Val
Ile	Ala	His	Phe	Tyr 180	Cys	Asp	Ser	Tyr 185	Gln	Ile	Glu	Lys	Ile	Ser	Cys
Ser	Asn	Leu	Phe	Val 195	Asn	Lys	Met 200	Val	Ser	Leu	Ser 205	Leu	Ser	Val	Ile
Ile	Ile	Leu	Pro	Thr 210	Ile	Val	Val 215	Ile	Ile	Val	Ser 220	Tyr	Leu	Tyr	Ile
Val 225	Ser	Ser	Val	Leu 230	Lys	Ile	Pro	Ser	Ser 235	Glu	Arg	Lys	Lys	Asp	240

Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu
245 250

<210> 1949

<211> 335

<212> PRT

<213> Unknown (H38g367 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1949

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Ala Ser Lys Tyr Leu Leu Leu
1 5 10 15
Glu Leu Ser Glu Asp Pro Lys Leu Gln Leu Ala Leu Ser Gly Arg Glu
20 25 30
Pro Cys Thr Cys Thr Xaa Ser Leu Val Leu Glu Asn Leu Leu Ile Ile
35 40 45
Leu Ala Val Ser Ser Asp Phe His Leu His Thr Pro Met Tyr Phe Phe
50 55 60
Leu Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val
65 70 75 80
Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr
85 90 95
Ala Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met
100 105 110
Glu Glu Asn Met Leu Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala
115 120 125
Ile Cys His Pro Leu Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys
130 135 140
Gly Phe Leu Val Leu Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln
145 150 155 160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu
165 170 175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
180 185 190
Cys Asp Thr Phe Thr Asn Asn Ile Val Met Tyr Phe Leu Ala Ala Ile
195 200 205
Phe Gly Phe Leu Pro Ile Ser Arg Ile Ile Phe Ser Tyr Tyr Lys Ile
210 215 220
Val Ser Ser Met Leu Ser Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225 230 235 240
Phe Ser Thr Cys Gly Ser Pro Leu Ser Val Val Cys Leu Phe Tyr Gly
245 250 255
Lys Val Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
260 265 270
Lys Gly Ala Val Ala Ser Met Met Tyr Thr Val Ile Thr Pro Met Leu
275 280 285
Asn Pro Phe Ile Tyr Arg Leu Arg Asn Arg Asp Ile Lys Arg Val Leu
290 295 300
Trp Trp Leu His Gly Arg Thr Val Xaa Ser His Tyr Phe Ile Ile Cys
305 310 315 320
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
325 330 335

<210> 1950

<211> 317

<212> PRT

<213> Unknown (H38g868 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1950

```

Thr Gly Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
1      5      10      15
Leu Gln Pro Ala Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
20      25      30
Val Thr Val Leu Arg Asn Leu Phe Ser Ile Leu Ala Val Ser Ser Asp
35      40      45
Cys Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
50      55      60
Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp
65      70      75      80
Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
85      90      95
Met Ser Phe Leu Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
100     105     110
Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
115     120     125
Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
130     135     140
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
145     150     155     160
Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
165     170     175
Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
180     185     190
Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
195     200     205
Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
210     215     220
Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
225     230     235     240
Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu
245     250     255
Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
260     265     270
Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
275     280     285
Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Gly Ser Arg Ala
290     295     300
Phe Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
305     310     315

```

<210> 1951

<211> 313

<212> PRT

<213> Unknown (H38g869 protein)

<220>

<223> Synthetic construct

<400> 1951

```

Met Gly Asp Arg Gly Thr Ser Asn His Ser Glu Met Thr Asp Phe Ile
 1           5           10           15
Leu Ala Gly Phe Arg Val Arg Pro Glu Leu His Ile Leu Leu Phe Leu
          20           25           30
Leu Phe Leu Phe Val Tyr Ala Met Ile Leu Leu Gly Asn Val Gly Met
          35           40           45
Met Thr Ile Ile Met Thr Asp Pro Arg Leu Asn Thr Pro Met Tyr Phe
          50           55           60
Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Phe Tyr Ser Ser Val Ile
65           70           75           80
Glu Pro Lys Ala Met Ile Asn Phe Trp Ser Glu Asn Lys Ser Ile Ser
          85           90           95
Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Leu Ile Val
          100          105          110
Thr Glu Gly Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala
          115          120          125
Ile Cys Asn Pro Leu Leu Tyr Ser Val Gln Met Ser Thr Arg Leu Cys
          130          135          140
Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Cys Ile Ser Ser Val
145          150          155          160
Ile Gln Thr Ser Met Thr Phe Thr Leu Ser Phe Cys Ala Ser Arg Ala
          165          170          175
Val Asp His Phe Tyr Cys Asp Ser Arg Pro Leu Gln Arg Leu Ser Cys
          180          185          190
Ser Asp Leu Phe Ile His Arg Met Ile Ser Phe Ser Leu Ser Cys Ile
          195          200          205
Ile Ile Leu Pro Thr Ile Ile Val Ile Ile Val Ser Tyr Met Tyr Ile
          210          215          220
Val Ser Thr Val Leu Lys Ile His Ser Thr Glu Gly His Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Ser Ser His Leu Gly Val Val Ser Val Leu Tyr Gly
          245          250          255
Ala Val Phe Phe Met Tyr Leu Thr Pro Asp Arg Phe Pro Glu Leu Ser
          260          265          270
Lys Val Ala Ser Leu Cys Tyr Ser Leu Val Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Gln Glu Ala Leu Lys Lys
          290          295          300
Phe Leu Glu Lys Lys Asn Ile Ile Leu
305          310

```

<210> 1952

<211> 277

<212> PRT

<213> Unknown (H38g870 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(277)

<223> Xaa = Any Amino Acid

<400> 1952

```

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu
 1           5           10           15
Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa
          20           25           30
Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr
          35           40           45
Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser

```

```

      50              55              60
Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr
65              70              75              80
Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser
      85              90              95
Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met
      100              105              110
Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa
      115              120              125
Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln
      130              135              140
Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile
145              150              155              160
Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val
      165              170              175
Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe
      180              185              190
Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Phe His Xaa Pro Ser Gly
      195              200              205
Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly
      210              215              220
Leu Gly Thr Phe Met Tyr Leu Arg Ser Pro Glu Ala Met Gly Xaa Cys
225              230              235              240
Lys Phe Thr Val Ser Phe Thr Lys Met Gly Pro Val Met Asn Gly Leu
      245              250              255
Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro
      260              265              270
Leu Ser Phe Ser Ser
      275

```

<210> 1953

<211> 335

<212> PRT

<213> Unknown (H38g871 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1953

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Arg Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
      115      120      125
Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
130      135      140

```


Phe Leu Asp Leu Leu Ser Leu Phe Phe Phe Phe Phe Phe Phe Ser
 145 150 155 160
 Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
 165 170 175
 Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Cys
 180 185 190
 Cys Asp Thr Phe Thr Arg Asn Ile Asn Met Tyr Phe Pro Ala Ala Val
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Ile
 210 215 220
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Thr Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu
 290 295 300
 Arg Arg Pro His Ser Ser Ala Val Xaa Ser Gln Tyr Leu Leu Ile Cys
 305 310 315 320
 Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1954

<211> 342

<212> PRT

<213> Unknown (H38g872 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(342)

<223> Xaa = Any Amino Acid

<400> 1954

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ser Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Lys Arg His Ala Pro Glu Val Met Ala Tyr Asp Leu Phe Val Pro Ile
 115 120 125
 Cys His Leu Leu Tyr Arg Ser Thr Ile Leu Asn Pro Phe Val Arg Gly
 130 135 140
 Phe Leu Asn Leu Leu Ser Leu Phe Val Gly Phe Phe Phe Phe Ser Leu
 145 150 155 160
 Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr
 165 170 175
 Tyr Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln

```

      180      185      190
Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met
      195      200      205
Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu
      210      215      220
Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser
      225      230      235      240
Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
      245      250      255
Val Cys Xaa Phe Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp
      260      265      270
Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr
      275      280      285
Thr Val Val Thr Pro Met Leu Asn Ser Phe Ile Tyr Ser Leu Arg Asn
      290      295      300
Gly Asp Ile Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
      305      310      315      320
Ser Gln Tyr Val Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Asn
      325      330      335
Lys Asp Ser Lys Val Lys
      340

```

<210> 1955

<211> 348

<212> PRT

<213> Unknown (H38g873 protein)

<220>

<223> Synthetic construct

<400> 1955

```

Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val
  1          5          10          15
Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val
      20          25          30
Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile
      35          40          45
Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe
      50          55          60
Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr
      65          70          75          80
Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro
      85          90          95
Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe Phe His Leu Leu Ala Gly
      100          105          110
Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala
      115          120          125
Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln
      130          135          140
Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu
      145          150          155          160
Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val
      165          170          175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys
      180          185          190
Ala Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe
      195          200          205
Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val
      210          215          220
Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Lys Lys Lys Ala
      225          230          235          240

```

```
<210> 1956
<211> 230
<212> PRT
<213> Unknown (H38g874 protein)
```

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(230)
<223> Xaa = Any Amino Acid
```

<210> 1957
<211> 331

<212> PRT

<213> Unknown (H38g875 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1957

His	Thr	Glu	Pro	Arg	Asn	Leu	Thr	Ser	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Leu	Leu	Ala	Leu	Leu	Ser
			20					25					30		
Leu	Ser	Leu	Ser	Met	His	Leu	Val	Met	Val	Leu	Arg	Asn	Leu	Leu	Asn
		35					40					45			
Ile	Leu	Ala	Val	Ser	Ser	Asp	Ser	Pro	Leu	His	Thr	Pro	Thr	Tyr	Phe
	50					55					60				
Phe	Leu	Ser	Asn	Leu	Cys	Trp	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Ala	Thr
65					70					75					80
Val	Pro	Asn	Met	Ile	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Ser
				85					90					95	
His	Ala	Asp	Cys	Leu	Thr	Gln	Ile	Ser	Phe	Leu	Leu	Leu	Phe	Ala	Cys
			100					105						110	
Ile	Glu	Gly	Met	Leu	Leu	Thr	Val	Met	Thr	Tyr	Asp	Cys	Phe	Val	Ala
		115					120					125			
Ile	Cys	Cys	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His	Leu	Cys
	130					135					140				
Val	Phe	Phe	Val	Leu	Val	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln
145					150					155					160
Leu	His	Ser	Trp	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn	Val	Glu
				165					170					175	
Ile	Ser	Asn	Ser	Val	Cys	Asp	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys
			180					185						190	
Ser	Asp	Ser	Val	Ile	Asn	Ser	Ile	Phe	Met	His	Phe	His	Asn	Thr	Met
	195						200						205		
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Val	Ser	Tyr	Tyr	Lys	Ile
	210					215						220			
Val	Pro	Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala
225					230					235					240
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe	Tyr	Gly
				245					250					255	
Thr	Gly	Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Pro	Pro	Arg
			260					265					270		
Asn	Gly	Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu
	275						280					285			
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu
	290					295					300				
Trp	Arg	Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro
305					310					315					320
Phe	Ser	Cys	Val	Gly	Lys	Gly	Asn	His	Ile	Lys					
				325						330					

<210> 1958

<211> 322

<212> PRT

<213> Unknown (H38g876 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1958

```

His Arg Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Thr Pro Ile Tyr Phe
          50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65           70           75           80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Phe Ala Cys
          180          185          190
Ser Asp Ser Ile Ile Asn Ser Ile Phe Ile Tyr Phe His Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Ile Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
          260          265          270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Trp Gly Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
305          310          315          320
Phe Ser

```

<210> 1959

<211> 315

<212> PRT

<213> Unknown (H38g877 protein)

<220>

<223> Synthetic construct

<400> 1959

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val

```

<400> 1960															
Met	Thr	Asp	Tyr	Asn	Glu	Pro	Met	Glu	Pro	Met	Glu	Asp	Lys	Asn	Gln
1				5					10					15	
Thr	Val	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Thr	Asp	His	Pro	Tyr
			20					25					30		
Gln	Lys	Ile	Val	Leu	Phe	Phe	Met	Phe	Leu	Phe	Val	Tyr	Leu	Ile	Thr
		35					40					45			
Leu	Gly	Gly	Asn	Leu	Gly	Met	Ile	Thr	Leu	Ile	Trp	Ile	Asp	Pro	Arg
	50					55					60				
Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg	His	Leu	Ser	Phe	Val	Asp
65					70					75					80
Ile	Cys	Ser	Ser	Ser	Ser	Val	Val	Pro	Lys	Met	Leu	Cys	Asn	Ile	Phe
				85					90					95	
Ala	Glu	Lys	Lys	Asp	Ile	Thr	Phe	Leu	Gly	Cys	Ala	Ala	Gln	Met	Trp
			100					105					110		

Phe Phe Gly Leu Phe Glu Ala Ala Glu Cys Phe Leu Leu Ala Ala Met
 115 120 125
 Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pr Leu Leu Tyr Thr Leu
 130 135 140
 Ile Met Ser Gln Gln Val Cys Met Gln Leu Val Val Gly Pr Tyr Ala
 145 150 155 160
 Met Ala Leu Ile Ser Thr Met Thr His Thr Ile Phe Thr Phe Cys Leu
 165 170 175
 Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ile Phe
 180 185 190
 Pro Leu Leu Ser Leu Ala Cys Ala Asp Thr Trp Val Asn Lys Phe Val
 195 200 205
 Leu Phe Val Leu Ala Gly Ala Ile Gly Val Leu Ser Gly Leu Ile Ile
 210 215 220
 Met Val Ser Tyr Ile Cys Ile Leu Met Thr Ile Leu Lys Ile Gln Thr
 225 230 235 240
 Ala Asp Gly Lys Gln Lys Ala Phe Phe Thr Cys Phe Ser His Leu Ala
 245 250 255
 Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Leu Ile Tyr Val Arg Pro
 260 265 270
 Ser Ser Ser Ser Ser Leu Gly Ile Tyr Lys Val Ile Ser Leu Phe Tyr
 275 280 285
 Thr Val Val Ile Pro Met Val Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 290 295 300
 Lys Glu Val Lys Asp Ala Phe Arg Arg Lys Ile Glu Arg Lys Lys Phe
 305 310 315 320
 Ile Ile Gly

<210> 1961

<211> 229

<212> PRT

<213> Unknown (H38g879 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(229)

<223> Xaa = Any Amino Acid

<400> 1961

Phe Phe Ser Leu Asp Leu Ile Arg Ser Gln Ala Asn Thr Met Ser Lys
 1 5 10 15
 Lys His Trp Thr Ala Ile Ala Glu Phe Ile Pro Leu Gly Pro Thr Asp
 20 25 30
 Gln Ala Glu Leu Gln Leu Val Leu Phe Phe Phe Thr Phe Leu Val Ile
 35 40 45
 Tyr Leu Ile Met Val Met Gly Asn Leu Ser Met Ile Leu Ile Ile Arg
 50 55 60
 Ser Asp Xaa Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser His Leu
 65 70 75 80
 Ser Phe Ala Val Leu Cys Tyr Thr Leu Asn Val Thr Pro Gln Ile Leu
 85 90 95
 Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Phe Phe Ile Gly Cys Val
 100 105 110
 Ser Val Leu Xaa Phe Tyr Phe Phe Ile Val Leu Ile Ile Arg Asp Tyr
 115 120 125
 His Met Leu Thr Val Met Ala Asn Asp Cys Tyr Met Ala Ile Cys Lys
 130 135 140
 Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Phe Val Cys Leu Ser Leu

145 150 155 160
 Ala Ser Val Ser Xaa Ile Tyr Gly Phe Ala Asn Tyr Leu Ala Gln Thr
 165 170 175
 Ile Arg Met Leu Leu Ser Phe Xaa Gly Ser Asn Glu Ile Asn His
 180 185 190
 Phe Asp Cys Ala Asp Pro Pro Leu Leu Val Leu Pro Cys Ala Gly Thr
 195 200 205
 Cys Val Lys Xaa Ile Ile Met Leu Met Glu Pro His Cys Leu Leu Lys
 210 215 220
 Pro Gly Tyr Ile Leu
 225

<210> 1962

<211> 286

<212> PRT

<213> Unknown (H38g880 protein)

<220>

<223> Synthetic construct

<400> 1962

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
 1 5 10 15
 Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met
 35 40 45
 Ile Val Asp Met Gly Ser His Ser Arg Val Ile Ser Tyr Gly Gly Cys
 50 55 60
 Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met
 65 70 75 80
 Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
 85 90 95
 Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val
 100 105 110
 Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
 115 120 125
 Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
 130 135 140
 Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val
 145 150 155 160
 Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu
 165 170 175
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
 180 185 190
 Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys
 195 200 205
 Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 210 215 220
 Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
 225 230 235 240
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys
 260 265 270
 Asn Lys Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 275 280 285

<210> 1963

<211> 325

<212> PRT

<213> Unknown (H38g881 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1963

Met	Ala	Asn	Glu	Asn	Tyr	Thr	Lys	Val	Thr	Xaa	Phe	Ile	Phe	Thr	Gly
1				5					10					15	
Leu	Asn	Tyr	Asn	Pro	Gln	Leu	Arg	Val	Phe	Leu	Phe	Leu	Leu	Phe	Leu
			20					25					30		
Thr	Thr	Phe	Tyr	Val	Ile	Asn	Val	Thr	Gly	Asn	Leu	Gly	Met	Ile	Val
		35				40						45			
Leu	Ile	Arg	Ile	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	His	Leu	Ser	Phe	Val	Asp	Thr	Cys	Phe	Ser	Ser	Val	Val	Ser	Pro
65					70					75				80	
Lys	Met	Leu	Thr	Asp	Phe	Phe	Val	Lys	Arg	Lys	Ala	Ile	Ser	Phe	Leu
				85					90					95	
Gly	Cys	Ala	Leu	Gln	Gln	Trp	Phe	Phe	Gly	Phe	Phe	Val	Ala	Ala	Asp
			100					105					110		
Cys	Phe	Leu	Leu	Glu	Ser	Met	Ala	Tyr	Asp	Cys	Tyr	Val	Ala	Ile	Cys
		115					120					125			
Asn	Pro	Leu	Leu	Tyr	Ser	Val	Ala	Met	Ser	Gln	Arg	Leu	Cys	Ile	Gln
		130				135					140				
Leu	Val	Val	Gly	Pro	Tyr	Val	Ile	Gly	Leu	Met	Asn	Thr	Met	Thr	His
145					150					155					160
Thr	Thr	Asn	Ala	Phe	Cys	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asn
				165					170					175	
Pro	Phe	Phe	Cys	Asp	Met	Ser	Pro	Leu	Leu	Ser	Leu	Val	Cys	Ala	Asp
			180					185					190		
Thr	Arg	Leu	Asn	Lys	Leu	Ala	Val	Phe	Ile	Val	Ala	Gly	Ala	Val	Gly
		195				200						205			
Val	Phe	Ser	Gly	Leu	Thr	Ile	Leu	Ile	Ser	Tyr	Ile	Tyr	Ile	Leu	Met
		210				215					220				
Ala	Ile	Leu	Arg	Ile	Arg	Ser	Ala	Asp	Gly	Arg	Cys	Lys	Thr	Phe	Ser
225					230					235					240
Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Phe	Ile	Ser	Tyr	Gly	Thr	Leu
				245					250					255	
Phe	Phe	Ile	Tyr	Val	His	Pro	Ser	Ala	Thr	Phe	Ser	Leu	Asp	Leu	Asn
			260					265					270		
Lys	Val	Val	Ser	Val	Phe	Tyr	Thr	Ala	Val	Ile	Pro	Met	Leu	Asn	Pro
		275					280					285			
Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Asp	Ala	Ile	His	Arg
	290					295					300				
Thr	Val	Thr	Gln	Arg	Lys	Phe	Cys	Lys	Ala	Xaa	Ile	Leu	Ile	Gln	Lys
305					310					315					320
Glu	Leu	Gly	Arg	Lys											
				325											

<210> 1964

<211> 314

<212> PRT

<213> Unknown (H38g882 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1964

```

Met Glu Thr Glu Asn Asn Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1           5           10           15
Leu Thr Asp Asn Pro Met Leu Cys Ala Ile Phe Phe Val Phe Phe Leu
          20           25           30
Ala Val Tyr Ile Val Thr Ile Pro Gly Asn Ile Ser Ile Ile Leu Leu
          35           40           45
Ile Gln Ser Ser Pro Gln Leu His Thr Leu Met Tyr Leu Phe Leu Ser
          50           55           60
His Leu Ala Ser Val Asp Ile Gly Tyr Ser Ile Ser Val Thr Pro Ile
65           70           75           80
Ile Leu Ile Asn Phe Leu Arg Glu Lys Thr Thr Ile Pro Val Thr Gly
          85           90           95
Cys Ile Ala Gln Leu Gly Ser Asp Val Met Phe Gly Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Asp His Tyr Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser
          115          120          125
Ile Gln Met Pro Pro Val Val Cys Phe Leu Leu Leu Gly Ala Ser Tyr
          130          135          140
Leu Gly Gly Cys Leu Asn Ala Ser Ser Phe Thr Gly Cys Leu Met Asn
145          150          155          160
Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn His Phe Phe Cys Asp Leu
          165          170          175
Phe Pro Leu Leu Lys Leu Ser Cys Gly His Val Tyr Ile Ala Glu Ile
          180          185          190
Ser Pro Ala Ile Ser Ser Ala Ser Val Leu Ile Ser Thr Leu Phe Thr
          195          200          205
Ile Ile Val Ser Tyr Ile Tyr Ile Leu His Ser Ile Leu Lys Val Cys
          210          215          220
Ser Thr Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu
225          230          235          240
Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Leu Phe Val Tyr Val Met
          245          250          255
Pro Lys Ser Ser Tyr Ser Ala Asp Gln Val Lys Val Ala Phe Val Ile
          260          265          270
Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Glu Val Lys Glu Ala Met Arg Lys Leu Met Ala Arg Thr His
          290          295          300
Trp Phe Ser Xaa Ile Lys Ser Val Xaa Ser
305           310

```

<210> 1965

<211> 202

<212> PRT

<213> Unknown (H38g883 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1965

```

Ile Phe Ala Ile Leu Thr Thr Ile Asp Cys Cys Val Phe Val Trp Glu
 1           5           10           15

```

Phe Leu Glu Cys Thr Val Phe Val Asn Lys Arg Ala Cys Ala Gln Leu
 20 25 30
 Ala Cys Gly Ala Phe Cys Ile Gly Leu Ile Met Thr Val Val Xaa Ile
 35 40 45
 Thr Thr Val Ser Gln Arg Tyr Lys Arg Ser Thr Tyr Ala Ile Val Asp
 50 55 60
 Cys Phe Leu Phe Asp Thr Leu Leu Val Met Lys Leu Ser Cys Ile Asp
 65 70 75 80
 Asn Thr Ile Tyr Glu Ile Ile Gln Tyr Phe Ile His His Thr Cys Val
 85 90 95
 Gln Val Ser Met Gly Leu Val Cys Ile Ser Tyr Ile Asp Ile Pro Val
 100 105 110
 Thr Ser Ile Val Leu Arg Ile Ser Xaa Ser Glu Val Phe Ala Thr Cys
 115 120 125
 Val Pro Gln Pro Pro Pro His Gly His Cys Leu Tyr Val Cys Ala
 130 135 140
 Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly
 145 150 155 160
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile Ile His Ser Ala Ser Gly Pro
 165 170 175
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg
 180 185 190
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile
 195 200

<210> 1966

<211> 315

<212> PRT

<213> Unknown (H38g884 protein)

<220>

<223> Synthetic construct

<400> 1966

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1 5 10 15
 Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
 20 25 30
 Leu Leu Leu Phe Ala Tyr Leu Val Thr Thr Gly Gly Asn Leu Ser Ile
 35 40 45
 Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
 50 55 60
 Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
 65 70 75 80
 Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
 85 90 95
 Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
 100 105 110
 Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
 130 135 140
 Arg Met Leu Val Ala Ala Ser Leu Ala Cys Ala Phe Thr Asn Ala Leu
 145 150 155 160
 Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
 165 170 175
 Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
 180 185 190
 Ser Ser Thr Gln Leu Asn Glu Leu Leu Phe Ala Val Gly Phe Ile
 195 200 205
 Met Ala Gly Thr Pro Leu Val Leu Ile Ile Thr Ala Tyr Ser His Val

```

      210                215                220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
225                230                235                240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Ph Gly
      245                250                255
Arg Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Glu Glu Ala Ser Asp
      260                265                270
Lys Asp Lys Gly Val Gly Val Phe Asn Thr Val Ile Asn Pro Met Leu
      275                280                285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Pro Asp Val Gln Gly Ala Leu
      290                295                300
Trp Gln Ile Phe Leu Gly Arg Arg Ser Leu Thr
305                310                315

```

<210> 1967

<211> 309

<212> PRT

<213> Unknown (H38g885 protein)

<220>

<223> Synthetic construct

<400> 1967

```

Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
1      5      10      15
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
      20      25      30
Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
      35      40      45
Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
      65      70      75      80
Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly
      85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys
      100     105     110
Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
      115     120     125
Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu
      130     135     140
Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val
      145     150     155     160
Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe
      165     170     175
Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
      180     185     190
Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val
      195     200     205
Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile
      210     215     220
Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys
      225     230     235     240
Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile
      245     250     255
Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ile Glu Lys Asp Leu Val
      260     265     270
Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
      275     280     285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Val
      290     295     300

```

Gly Arg Asn Ile Ser
305

<210> 1968

<211> 320

<212> PRT

<213> Unknown (H38g886 protein)

<220>

<223> Synthetic construct

<400> 1968

Met	Leu	Gln	Arg	Val	Gly	Glu	Met	Asp	Gly	Gly	Asn	Gln	Ser	Glu	Gly	1	5	10	15
Ser	Glu	Phe	Leu	Leu	Gly	Ile	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Gln		20	25	30	
Met	Leu	Phe	Trp	Met	Phe	Leu	Val	Arg	Tyr	Leu	Val	Thr	Val	Leu	Gly	35	40	45	
Asn	Val	Leu	Ile	Ile	Leu	Ala	Ile	Ser	Ser	Asp	Ser	Arg	Leu	His	Thr	50	55	60	
Pro	Met	Tyr	Phe	Phe	Leu	Ala	Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	65	70	75	80
Val	Thr	Asn	Thr	Ile	Pro	Lys	Met	Leu	Val	Asn	Leu	Gln	Ser	Gln	Asn	85	90	95	
Lys	Ala	Ile	Ser	Tyr	Thr	Gly	Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	100	105	110	
Ser	Leu	Val	Ala	Leu	Asp	Asn	Leu	Asn	Leu	Ala	Val	Met	Ala	Tyr	Asp	115	120	125	
Arg	Tyr	Val	Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ile	130	135	140	
Pro	Gly	Leu	Cys	Ile	Leu	Leu	Leu	Ser	Leu	Cys	Trp	Val	Phe	Ser	Ala	145	150	155	160
Leu	Tyr	Gly	Leu	Ile	His	Ile	Leu	Leu	Met	Thr	Arg	Val	Thr	Phe	Cys	165	170	175	
Gly	Ser	Gln	Lys	Ile	His	Tyr	Leu	Phe	Cys	Glu	Met	Tyr	Phe	Leu	Leu	180	185	190	
Arg	Leu	Ala	Cys	Ser	Asn	Ile	His	Val	Asn	His	Thr	Val	Leu	Val	Ala	195	200	205	
Thr	Gly	Cys	Phe	Ile	Phe	Leu	Ile	Pro	Leu	Gly	Phe	Met	Ile	Thr	Ser	210	215	220	
Tyr	Ala	Arg	Ile	Val	Arg	Ala	Ile	Leu	Gln	Ile	Pro	Ser	Ala	Thr	Gly	225	230	235	240
Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Ala	Val	Val	Ser	245	250	255	
Leu	Phe	Tyr	Gly	Thr	Leu	Gly	Met	Val	Tyr	Leu	Gln	Pro	Leu	Gln	Thr	260	265	270	
Tyr	Ser	Met	Lys	Asp	Ser	Val	Ala	Thr	Val	Met	Tyr	Ala	Val	Val	Thr	275	280	285	
Pro	Met	Ile	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	His	290	295	300	
Gly	Ala	Leu	Gly	Arg	Leu	Arg	Gln	Gly	Lys	Ala	Phe	Gln	Lys	Leu	Thr	305	310	315	320

<210> 1969

<211> 276

<212> PRT

<213> Unknown (H38g887 protein)

<220>

<223> Synthetic construct

<400> 1969

```

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
 1           5           10           15
Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
 20           25           30
Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
 35           40           45
Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
 65           70           75           80
Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
 85           90           95
Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
100           105           110
Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
115           120           125
Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
130           135           140
Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
145           150           155           160
Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
165           170           175
Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
180           185           190
Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
195           200           205
Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
210           215           220
Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
225           230           235           240
Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
245           250           255
Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
260           265           270
Leu Ser Val Thr
275

```

<210> 1970

<211> 312

<212> PRT

<213> Unknown (H38g888 protein)

<220>

<223> Synthetic construct

<400> 1970

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
100           105           110

```

Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Il Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg Pro Lys
 305 310

<210> 1971

<211> 299

<212> PRT

<213> Unknown (H38g889 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400> 1971

Met Ala Asp Gly Asn Tyr Lys Arg Ile Thr Glu Phe Ile Phe Val Gly
 1 5 10 15
 Leu Arg Tyr His Leu Gln Leu Gln Val Phe Leu Phe Leu Pro Phe Leu
 20 25 30
 Pro Phe Tyr Leu Ile Thr Met Thr Glu Asn Leu Gly Met Met Val Arg
 35 40 45
 Ile Trp Leu Asp Ser Cys Phe His Thr Pro Met Tyr Phe Val Leu Ser
 50 55 60
 Tyr Leu Ser Phe Val Asp Ile Cys Phe Ser Ser Val Val Gly His Lys
 65 70 75 80
 Leu Leu Thr Asp Leu Phe Ala Val Arg Lys Ala Ile Ser Phe Leu Gly
 85 90 95
 Cys Pro Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Val Ile Glu Tyr
 100 105 110
 Leu Leu Leu Ala Ser Met Ala Tyr Asp Asn Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Val Ala Met Xaa Xaa Arg Leu Cys Ile Gln Leu
 130 135 140
 Val Val Val Arg Tyr Ala Ala Asp Phe Phe Asn Thr Ile Thr His Thr
 145 150 155 160
 Thr Ala Ala Phe His Phe Pro Phe Phe His Ser Asn Ile Ile Asn His

										165					170					175					
Phe	Phe	Cys	Asp	Met	Ser	Leu	Leu	Leu	Ser	Leu	Val	Cys	Ala	Asp	Ala										
				180					185					190											
Arg	Ile	Asn	Lys	Leu	Leu	Val	Phe	Ile	Val	Ala	Gly	Ala	Val	Leu	Val										
				195					200					205											
Val	Ser	Ser	Leu	Thr	Ile	Ile	Ile	Ser	Tyr	Phe	Tyr	Ile	Leu	Thr	Asp										
				210					215					220											
Ile	Leu	Arg	Ile	Cys	Ser	Ala	Asn	Gly	Lys	Asn	Lys	Thr	Phe	Ser	Thr										
				225					230					235											
Cys	Ser	Ser	His	Leu	Thr	Ala	Val	Ser	Ile	Phe	Tyr	Gly	Ser	Leu	Phe										
				245					250					255											
Phe	Ser	Tyr	Val	Arg	Pro	Gly	Ala	Thr	Phe	Tyr	Pro	Glu	Leu	Asn	Lys										
				260					265					270											
Ile	Val	Leu	Val	Phe	Cys	Ile	Ile	Pro	Met	Leu	Lys	Pro	Leu	Ile	Tyr										
				275					280					285											
Ser	Leu	Ile	Asn	Lys	Glu	Val	Ser	Xaa	Pro	Leu															
				290					295																

<210> 1972

<211> 311

<212> PRT

<213> Unknown (H38g890 protein)

<220>

<223> Synthetic construct

<400> 1972

Met 1	Glu	Lys	Ile	Asn 5	Asn	Val	Thr	Glu	Phe 10	Ile	Phe	Trp	Gly	Leu 15	Ser
Gln	Ser	Pro	Glu 20	Ile	Glu	Lys	Val	Cys 25	Phe	Val	Val	Phe	Ser 30	Phe	Phe
Tyr	Ile	Ile	Ile 35	Leu	Leu	Gly	Asn 40	Leu	Leu	Ile	Met	Leu 45	Thr	Val	Cys
Leu	Ser	Asn	Leu 50	Phe	Lys	Ser 55	Pro	Met	Tyr	Phe	Phe	Leu 60	Ser	Phe	Leu
Ser 65	Phe	Val	Asp 70	Ile	Cys	Tyr 75	Ser	Ser	Val	Thr	Ala	Pro	Lys	Met	Ile
Val	Asp	Leu	Leu 85	Ala	Lys	Asp 90	Lys	Thr	Ile	Ser	Tyr	Val	Gly 95	Cys	Met
Leu	Gln	Leu	Leu 100	Gly	Val	His 105	Phe	Phe	Gly	Cys	Thr	Glu	Ile 110	Phe	Ile
Leu	Thr	Val	Met 115	Ala	Tyr	Asp 120	Arg	Tyr	Val	Ala	Ile	Cys 125	Lys	Pro	Leu
His 130	Tyr	Met	Thr 135	Ile	Met	Asn 140	Arg	Glu	Thr	Cys	Asn	Lys	Met	Leu	Leu
Gly 145	Thr	Trp	Val 150	Gly	Gly	Phe 155	Leu	His	Ser	Ile	Ile	Gln	Val	Ala	Leu
Val	Val	Gln	Leu 165	Pro	Phe	Cys 170	Gly	Pro	Asn	Glu	Ile	Asp	His	Tyr 175	Phe
Cys	Asp	Val	His 180	Pro	Val	Leu 185	Lys	Leu	Ala	Cys	Thr	Glu	Thr 190	Tyr	Ile
Val	Gly	Val	Val 195	Val	Thr	Ala 200	Asn	Ser	Gly	Thr	Ile	Ala 205	Leu	Gly	Ser
Phe 210	Val	Ile	Leu 215	Leu	Ile	Ser 220	Tyr	Ser	Ile	Ile	Leu	Val	Ser	Leu	Arg
Lys 225	Gln	Ser	Ala 230	Glu	Gly	Arg 235	Arg	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser
His	Ile	Ala	Met 245	Val	Val	Ile 250	Phe	Phe	Gly	Pro	Cys	Thr	Phe	Met	Tyr
Met	Arg	Pro	Asp 260	Thr	Thr	Phe 265	Ser	Glu	Asp	Lys	Met	Val	Ala 270	Val	Phe

Tyr Thr Ile Ile Thr Pr Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Lys Lys Leu Trp Gly Arg Asn Val
 290 295 300
 Phe Leu Glu Ala Lys Gly Lys
 305 310

<210> 1973

<211> 318

<212> PRT

<213> Unknown (H38g891 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1973

Met Asp Tyr Arg Asn Gln Thr Leu Val Thr Glu Phe Phe Ser Val Gly
 1 5 10 15
 Leu Thr Asn Leu Phe Gln His Lys Ile Ala Leu Phe Leu Val Phe Leu
 20 25 30
 Phe Val Tyr Leu Val Thr Val Pro Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 Ile Trp Met Asp Ser Arg Leu Gln Thr Pro Lys Tyr Phe Ser Leu Cys
 50 55 60
 His Leu Ser Phe Val Asp Val Cys Ser Ser Ser Ala Ile Gly Pro Lys
 65 70 75 80
 Met Leu Thr Asp Ile Phe Val Glu Lys Lys Val Ile Ser Phe Gly Cys
 85 90 95
 Val Ala Gln Leu Trp Phe Phe Gly His Phe Val Val Thr Glu Cys Phe
 100 105 110
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Met Ala Ile Tyr Lys Pro
 115 120 125
 Leu Leu Tyr Thr Leu Ile Met Ser Gln Gln Val Cys Val Gln Leu Val
 130 135 140
 Val Gly Pro Tyr Ala Val Gly Leu Ile Ser Thr Met Thr His Met Thr
 145 150 155 160
 Phe Thr Phe Arg Leu Leu Tyr Cys Gly Pro Asn Ile Ile Asn His Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Val Leu Ser Leu Ala Tyr Ala Asp Thr His
 180 185 190
 Ile Asn Lys Cys Leu Leu Phe Ile Leu Val Gly Ala Leu Gly Val Leu
 195 200 205
 Ser Gly Val Ile Ile Leu Val Ser Tyr Ile Tyr Ile Val Ile Ala Ile
 210 215 220
 Leu Arg Ile Arg Ser Ala Asp Ala Arg Arg Lys Asp Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Met Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Phe
 245 250 255
 Ile Cys Val Cys Pro Ser Ser Ser Phe Ser Ile Asn Ile Asn Lys Val
 260 265 270
 Val Ser Leu Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ser Phe Ser Lys Lys Phe
 290 295 300
 Glu Arg Lys Lys Phe Leu Ile Gly Arg Xaa Thr Arg Ile Pro
 305 310 315

<210> 1974
 <211> 310
 <212> PRT
 <213> Unknown (H38g892 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(310)
 <223> Xaa = Any Amino Acid

<400> 1974

```

Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln
 1           5           10          15
Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu
      20           25          30
Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp
      35           40          45
Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu
      50           55          60
Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu
      65           70          75          80
Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala
      85           90          95
Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu
      100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu
      115          120          125
Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser
      130          135          140
Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met
      145          150          155          160
Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe
      165          170          175
Cys Asp Val Pro Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile
      180          185          190
Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr
      195          200          205
Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
      210          215          220
Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala
      225          230          235          240
Ser His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met
      245          250          255
Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val
      260          265          270
Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
      275          280          285
Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln
      290          295          300
Lys Leu Ser Leu Xaa Ser
305          310

```

<210> 1975
 <211> 309
 <212> PRT
 <213> Unknown (H38g893 protein)

<220>
 <223> Synthetic construct

<400> 1975

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
          20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
          35           40           45
Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
          65           70           75           80
Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
          85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
          100          105          110
Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
          130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
          145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
          165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
          180          185          190
His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
          195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
          210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
          225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
          245          250          255
Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
          260          265          270
Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn
          290          295          300
Lys Arg Ile Ser Ser
305

```

<210> 1976

<211> 309

<212> PRT

<213> Unknown (H38g894 protein)

<220>

<223> Synthetic construct

<400> 1976

```

Met Lys Lys Glu Asn Gln Ser Phe Asn Leu Asp Phe Ile Leu Leu Gly
 1           5           10           15
Val Thr Ser Gln Gln Glu Gln Asn Asn Val Phe Phe Val Ile Phe Leu
          20           25           30
Cys Ile Tyr Pro Ile Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala
          35           40           45
Ile Cys Ala Asp Ile Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Asn Leu Ser Leu Val Asp Ile Ile Phe Ser Ser Val Thr Ile Pro Lys

```

```

65          70          75          80
Val Leu Ala Asn His Leu Leu Gly Ser Lys Phe Ile Ser Phe Gly Gly
      85          90          95
Cys Leu Met Gln Met Tyr Phe Met Ile Ala Leu Ala Lys Ala Asp Ser
      100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Cys
      115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Leu Leu
      130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Thr Ser Ala Leu Pro His Thr
      145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
      165          170          175
Phe Tyr Cys Asp Ile Met Pro Leu Leu Lys Leu Ser Cys Ser Asp Val
      180          185          190
His Phe Asn Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Leu
      195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Val Gln Val Phe Ser Thr Val
      210          215          220
Phe Gln Val Pro Ser Thr Lys Ser Leu Phe Lys Ala Phe Cys Thr Cys
      225          230          235          240
Gly Ser His Leu Thr Val Val Phe Leu Tyr Tyr Gly Thr Thr Met Gly
      245          250          255
Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile
      260          265          270
Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr
      275          280          285
Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser
      290          295          300
Lys Arg Ile Ser Ser
305

```

<210> 1977

<211> 329

<212> PRT

<213> Unknown (H38g895 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1977

```

Ala Leu Leu Phe His Ser Tyr Lys His Pro Thr Gln Arg Arg Met Thr
1          5          10          15
Val Lys Ser His Ser Ile Val Thr Glu Phe Ser Leu Arg Gly Leu Thr
      20          25          30
Lys Gln Pro Asp Leu Gln Leu Phe His Phe Leu Ile Phe Leu Asp Ile
      35          40          45
His Met Val Thr Met Val Gly Asn Leu Gly Met Ile Thr Leu Ile Cys
      50          55          60
Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Phe Ser Asn Leu
      65          70          75          80
Ser Leu Leu Asp Leu Cys Tyr Ser Ser Ile Thr Asn Pro Lys Met Leu
      85          90          95
Val Asn Phe Val Leu Lys Lys Ser Ile Ile Ser Tyr Ala Gly Tyr Met
      100          105          110
Ser Xaa Phe Tyr Phe Phe Leu Val Phe Val Ile Ala Arg Cys Tyr Met
      115          120          125

```

```

Leu Met Val Lys Ala Cys Asp His Tyr Val Ala Ile Cys Cys Pro Leu
130                      135                      140
Leu Cys Asn Val Ile Met Ser His Val Thr Cys Ser Leu Met Val Ala
145                      150                      155                      160
Val Val Tyr Thr Met Gly Leu Val Val Ser Thr Ile Glu Thr Gly Leu
165                      170                      175
Ile Leu Lys Leu Pro Tyr Cys Glu Leu Leu Thr Ser Arg Cys Phe Cys
180                      185                      190
Asp Ile Leu Pro Leu Met Lys Leu Ser Xaa Ser Ser Ala Tyr Asp Val
195                      200                      205
Glu Met Ala Val Phe Phe Phe Ala Arg Phe Asn Leu Arg Ile Met Ile
210                      215                      220
Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Phe Ser Ile Leu His
225                      230                      235                      240
Ile Ser Thr Thr Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Ser Phe
245                      250                      255
His Leu Ala Ala Ile Gly Met Phe His Gly Xaa Thr Ala Phe Arg Tyr
260                      265                      270
Leu Lys Pro Ala Ile Thr Ser Ser Leu Ala Gln Glu Asn Val Ala Ser
275                      280                      285
Val Phe Tyr Thr Thr Val Ile Tyr Val Pro Asn Pro Leu Met Tyr Ser
290                      295                      300
Leu Lys Asn Lys Asp Val Lys Ala Ala Met Gln Lys Thr Leu Arg Ser
305                      310                      315                      320
Lys Phe Cys Cys Arg Cys Asn Tyr Leu
325

```

<210> 1978

<211> 316

<212> PRT

<213> Unknown (H38g896 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1978

```

Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu Leu Trp
1      5      10      15
Gly Leu Ser Asp Gln Pro Gln Gln His Ile Phe Phe Leu Leu Phe
20     25     30
Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile Val Leu
35     40     45
Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu
50     55     60
Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Ser Thr Thr Val Pro
65     70     75     80
Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser Tyr Ala
85     90     95
Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp
100    105    110
Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
115    120    125
His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys Ala Phe
130    135    140
Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Ala Met Thr Arg
145    150    155    160
Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu Pro Gly

```

				165				170					175				
Phe	Phe	Cys	Asp	Leu	Gly	Pr	Leu	Met	Lys	Val	Ser	Cys	Ser	Asp	Ala		
			180					185					190				
Gln	Val	Asn	Glu	Leu	Val	Leu	Leu	Phe	Leu	Gly	Gly	Ala	Val	Ile	Leu		
		195					200					205					
Ile	Pro	Phe	Met	Leu	Ile	Leu	Val	Ser	Tyr	Ile	Arg	Ile	Val	Ser	Ala		
	210					215					220						
Ile	Leu	Arg	Ala	Pro	Ser	Ala	Gln	Gly	Arg	Arg	Lys	Ala	Phe	Ser	Thr		
225					230					235					240		
Cys	Asp	Ser	His	Leu	Val	Val	Val	Ala	Leu	Phe	Phe	Gly	Thr	Val	Ile		
			245						250					255			
Arg	Ala	Tyr	Leu	Cys	Pro	Ser	Ser	Ser	Ser	Asn	Ser	Val	Lys	Glu			
		260						265					270				
Asp	Thr	Ala	Ala	Ala	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn		
	275						280					285					
Pro	Phe	Ile	Tyr	Ser	Met	Arg	Asn	Lys	Asp	Met	Lys	Ala	Ala	Val	Val		
	290					295					300						
Arg	Leu	Leu	Lys	Gly	Arg	Val	Ser	Phe	Ser	Gln	Gly						
305					310					315							

<210> 1979

<211> 336

<212> PRT

<213> Unknown (H38g897 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1979

Asp	Thr	Asp	Pro	Gln	Ser	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu		
1				5					10					15			
Lys	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Gln	Val	Val	Ala	Gly	Leu	Phe		
			20					25					30				
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu		
		35				40						45					
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu		
	50					55					60						
Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro		
65				70					75					80			
Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala		
			85					90					95				
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu		
		100						105				110					
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile		
	115					120					125						
Cys	His	Pro	Leu	Tyr	Cys	Ser	Ala	Ile	Phe	Asn	Pro	Cys	Phe	Cys	Gly		
	130					135					140						
Phe	Leu	Asp	Leu	Leu	Ser	Phe	Ile	Phe	Phe	Phe	Leu	Ser	Leu	Ser	Asp		
145				150					155						160		
Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp		
			165					170						175			
Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Ser	His	Leu		
		180					185					190					
Ala	Cys	Cys	Asp	Thr	Phe	Thr	Arg	Asn	Ile	Met	Tyr	Phe	Pro	Ala	Ala		
	195					200					205						
Ile	Phe	Gly	Phe	Leu	Pro	Ile	Leu	Gly	Thr	Leu	Phe	Ser	Tyr	Cys	Lys		
	210					215					220						

```

Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
225          230          235          240
Ala Phe Ser Thr Cys Gly Ser His L u Ser Val Val Cys Xaa Phe Tyr
          245          250          255
Gly Thr Gly Ile Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
260          265          270
Arg Lys Gly Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
275          280          285
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val
290          295          300
Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln His Leu Leu Ile
305          310          315          320
Cys Ser Ile Pro Phe Val Gly Trp Phe Lys Lys Gly Ala Lys Val Lys
          325          330          335

```

<210> 1980

<211> 309

<212> PRT

<213> Unknown (H38g898 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1980

```

Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
1          5          10          15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Leu Thr
          20          25          30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
          35          40          45
Thr Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
          50          55          60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
          65          70          75          80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
          85          90          95
Gly Gln Leu Phe Ile Tyr His Leu Phe Gly Gly Ser Glu Val Phe Leu
          100          105          110
Leu Val Val Met Ala Cys Asp His Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Leu Thr Ile Met Asn Arg Gln Val Xaa Ile Leu Leu Leu Val
          130          135          140
Val Val Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Val Val
          145          150          155          160
Val Tyr Ser Leu Ala Phe Cys Gly Pro Asn Val Ile Asp Tyr Phe Val
          165          170          175
Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe
          180          185          190
Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val Val
          195          200          205
Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys
          210          215          220
Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser Ser
          225          230          235          240
His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
          245          250          255
Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val Phe

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260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Ser Xaa
 290 295 300
 Leu Tyr Xaa Ser Lys
 305

<210> 1981

<211> 313

<212> PRT

<213> Unknown (H38g899 protein)

<220>

<223> Synthetic construct

<400> 1981

Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly
 1 5 10 15
 Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe
 20 25 30
 Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr
 35 40 45
 Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu
 50 55 60
 Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro
 65 70 75 80
 Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly
 85 90 95
 Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln
 100 105 110
 Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu
 130 135 140
 Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln
 145 150 155 160
 Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp
 165 170 175
 Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp
 180 185 190
 Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val
 195 200 205
 Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln
 210 215 220
 Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys
 245 250 255
 Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala
 260 265 270
 Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu
 290 295 300
 Arg Ser Pro Arg Thr Pro Ser Glu Val
 305 310

<210> 1982

<211> 318

<212> PRT

<213> Unknown (H38g900 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1982

```

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Thr Val Val Arg Asp Phe
 1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Ile Arg Ser Leu Leu Phe
      20           25           30
Leu Val Phe Phe Val Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
      35           40           45
Ile Leu Leu Thr Val Trp Ala Asp Pro Lys Leu Arg Ala Arg Pro Met
      50           55           60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
      65           70           75           80
Val Ile Val Pro Xaa Ile Ile Leu Asn Phe Thr Pro Ala Asn Lys Ala
      85           90           95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
      100          105          110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
      115          120          125
Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
      130          135          140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
      145          150          155          160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
      165          170          175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
      180          185          190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
      195          200          205
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
      210          215          220
Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
      225          230          235          240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
      245          250          255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
      260          265          270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
      275          280          285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
      290          295          300
Lys Arg Ile Thr Ala Gly Gln Gly Thr Glu Xaa Lys Xaa Val
      305          310          315

```

<210> 1983

<211> 310

<212> PRT

<213> Unknown (H38g901 protein)

<220>

<223> Synthetic construct

<400> 1983

```

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe

```

```

1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Ph
20           25           30
Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
35           40           45
Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
50           55           60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
65           70           75           80
Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
85           90           95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
100          105          110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
115          120          125
Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg
130          135          140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
145          150          155          160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
165          170          175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu
180          185          190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
195          200          205
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
210          215          220
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
225          230          235          240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
245          250          255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
260          265          270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
275          280          285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
290          295          300
Lys Arg Ile Thr Ala Gly
305          310

```

<210> 1984

<211> 300

<212> PRT

<213> Unknown (H38g902 protein)

<220>

<223> Synthetic construct

<400> 1984

```

Met Phe Ile Leu Thr Gly Phe Thr Asp Asp Phe Glu Leu Gln Val Phe
1           5           10           15
Leu Phe Leu Leu Phe Phe Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn
20           25           30
Leu Gly Leu Val Val Leu Val Ile Glu Asp Ser Trp Leu His Asn Pro
35           40           45
Met Tyr Tyr Phe Leu Ser Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser
50           55           60
Thr Val Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys
65           70           75           80
Ser Ile Ser Phe Ile Gly Cys Ala Thr Gln Met Leu Leu Phe Val Thr
85           90           95

```

```

Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp His
      100      105      110
Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro
      115      120      125
Arg Val Tyr Val Pro Leu Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu
      130      135      140
His Ala Thr Ile His Ile Val Ala Thr Phe Ser Leu Ser Phe Cys Gly
      145      150      155      160
Ser Asn Glu Ile Arg His Val Phe Cys Asp Met Pro Pro Leu Leu Ala
      165      170      175
Ile Ser Cys Ser Asp Thr His Thr Asn Gln Leu Leu Leu Phe Tyr Phe
      180      185      190
Val Gly Ser Ile Glu Ile Val Thr Ile Leu Ile Val Leu Ile Ser Cys
      195      200      205
Asp Phe Ile Leu Leu Ser Ile Leu Lys Met His Ser Ala Lys Gly Arg
      210      215      220
Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Gly Val Thr Ile
      225      230      235      240
Tyr His Gly Thr Ile Leu Val Ser Tyr Met Arg Pro Ser Ser Ser Tyr
      245      250      255
Ala Ser Asp His Asp Ile Ile Val Ser Ile Phe Tyr Thr Ile Val Ile
      260      265      270
Pro Lys Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      275      280      285
Lys Ala Val Lys Lys Met Leu Lys Leu Val Tyr Lys
      290      295      300

```

<210> 1985

<211> 324

<212> PRT

<213> Unknown (H38g903 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1985

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Leu Ala Val Arg Ser Glu Ser Pro Leu His Thr Thr Met Tyr Phe
      50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Lys Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Ph Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu

```

```

                165                170                175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                180                185                190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
                195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
                210                215                220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
                225                230                235                240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
                245                250                255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
                260                265                270
Asn Gly Val Val Val Ser Val Lys Xaa Ala Val Val Thr Pro Met Pro
                275                280                285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
                290                295                300
Arg Arg Leu Pro Asn Lys Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
                305                310                315                320
Phe Phe Trp Cys

```

<210> 1986
 <211> 335
 <212> PRT
 <213> Unknown (H38g904 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(335)
 <223> Xaa = Any Amino Acid

```

<400> 1986
Asp Thr Asp Pro Gln Ser Ile Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
                20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
                35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
                50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
                65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Lys Val Ile Tyr Ala Gly
                85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Lys
                100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Pro Ile Cys
                115          120          125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
                130          135          140
Leu Asn Leu Leu Ser Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln
                145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
                165          170          175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
                180          185          190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
                195          200          205

```

```

Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
 210                215                220
Val Ser S r Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
                245                250                255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
                260                265                270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
                275                280                285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
                290                295                300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
305                310                315                320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
                325                330                335

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<210> 1987

<211> 310

<212> PRT

<213> Unknown (H38g905 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1987

```

Met Glu Asn Arg Lys Asn Val Thr Xaa Phe Ile Leu Leu Gly Leu Thr
 1                5                10                15
Gln Asn Pro Glu Gly Gln Lys Val Leu Phe Val Thr Phe Leu Leu Ile
                20                25                30
Tyr Ile Val Thr Ile Met Gly Asn Leu Leu Ile Met Val Thr Ile Met
                35                40                45
Ala Ser Gln Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
                50                55                60
Ser Phe Ile His Thr Val Tyr Tyr Thr Ala Ile Ala Pro Lys Met Ile
                65                70                75                80
Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
                85                90                95
Ala Gln Leu Phe Met Asp His Leu Phe Ala Gly Ala Glu Val Ile Leu
                100                105                110
Leu Val Val Met Ala Tyr Asp Gln Tyr Val Ala Ile Cys Lys Pro Leu
                115                120                125
His Tyr Leu Ile Ile Met Asn Arg Arg Val Cys Val Leu Met Leu Leu
                130                135                140
Val Ala Trp Ile Gly Gly Phe Leu His Ser Leu Val Gln Phe Leu Phe
                145                150                155                160
Ile Tyr Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Asn Phe Leu
                165                170                175
Cys Asp Leu Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asn Thr Tyr Val
                180                185                190
Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Thr Val Thr
                195                200                205
Phe Phe Pro Leu Leu Leu Ser Tyr Gly Val Ile Leu Pro Ser Leu Lys
                210                215                220
Thr Gln Ser Leu Glu Gly Lys Cys Lys Ala Phe Tyr Thr Cys Ala Ser
                225                230                235                240
His Ile Thr Val Ile Thr Leu Phe Phe Val Pro Cys Ile Phe Leu Leu

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[illegible]

<210> 1988

<211> 308

<212> PRT

<213> Unknown (H38g906 protein)

<220>

<223> Synthetic construct

<400> 1988

[illegible]

<210> 1989

<211> 166
 <212> PRT
 <213> Unknown (H38g907 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(166)
 <223> Xaa = Any Amino Acid

<400> 1989
 Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn
 1 5 10 15
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala
 20 25 30
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly
 35 40 45
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg
 50 55 60
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys
 65 70 75 80
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 85 90 95
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr
 100 105 110
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 115 120 125
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala
 130 135 140
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa
 145 150 155 160
 Xaa His Leu Glu Leu Leu
 165

<210> 1990
 <211> 333
 <212> PRT
 <213> Unknown (H38g908 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(333)
 <223> Xaa = Any Amino Acid

<400> 1990
 Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His
 1 5 10 15
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa
 20 25 30
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa
 35 40 45
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser
 50 55 60
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val
 65 70 75 80
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys
 85 90 95
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Met

100	105	110
Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr		
115	120	125
Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Val		
130	135	140
Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr		
145	150	155
Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val		
165	170	175
Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser		
180	185	190
Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala		
195	200	205
Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile		
210	215	220
Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln		
225	230	235
Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr		
245	250	255
Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro		
260	265	270
Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met		
275	280	285
Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr		
290	295	300
Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr		
305	310	315
Pro Leu Trp Ser Val Arg Lys Asn Ser Lys Leu Lys		
325	330	

<210> 1991

<211> 308

<212> PRT

<213> Unknown (H38g909 protein)

<220>

<223> Synthetic construct

<400> 1991

Met Gly Thr Ser Asn Asn Glu Thr Glu Phe Ile Leu Leu Gly Ile Thr	
1 5 10 15	
Lys Asn Pro Glu Leu Arg Lys Ile Phe Ser Ala Leu Phe Leu Ala Met	
20 25 30	
Tyr Val Thr Thr Val Leu Gly Asn Leu Phe Ile Val Val Thr Leu Ala	
35 40 45	
Ala Ser Trp Ser Leu Arg Ser Pro Met Tyr Phe Ser Leu Thr Ser Leu	
50 55 60	
Ser Leu Met Gly Ala Thr Tyr Ser Ser Ile Thr Ala Pro Lys Met Thr	
65 70 75 80	
Val Asp Ser Leu Arg Ser Thr Thr Ile Ser Leu Glu Gly Cys Met Thr	
85 90 95	
Gln Leu Phe Ala Glu His Phe Ser Asp Gly Val Ala Ile Ile Leu Leu	
100 105 110	
Thr Val Met Val Cys Asp Cys Tyr Glu Ala Ile Ser Lys Pro Leu His	
115 120 125	
Asp Thr Thr Ile Met Ser Pro Arg Val Cys Cys Leu Leu Val Val Glu	
130 135 140	
Ala Trp Val Gly Gly Leu Thr His Ala Thr Ile Gln Leu Phe Ph Phe	
145 150 155 160	
Leu Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile	
165 170 175	

Cys Asp Leu Phe Pro Leu Leu Lys Leu Ala Tyr Met Asp Thr His Met
 180 185 190
 Leu Gly Leu Leu Val Ile Leu Asn Ser Gly Val Met Cys Met Ala Ile
 195 200 205
 Phe Leu Ile Leu Ile Ala Ser Tyr Ile Val Thr Leu Tyr Ser Leu Lys
 210 215 220
 Ser Cys Ser Ser Val Gly Arg Arg Asn Thr Leu Ser Thr Cys Gly Ser
 225 230 235 240
 His His Thr Val Val Ile Leu Phe Phe Val Glu Cys Ile Phe Leu Tyr
 245 250 255
 Ile Arg Pro Val Val Thr Tyr Pro Ile Asp Lys Asp Met Ala Ile Ser
 260 265 270
 Phe Thr Ile Val Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Gly Ile Lys Val Lys Asn Ala Ile Arg Lys Met Trp Met Lys Gln Gly
 290 295 300
 Thr Leu Gly Gly
 305

<210> 1992

<211> 318

<212> PRT

<213> Unknown (H38g910 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1992

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu
 20 25 30
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu
 35 40 45
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly
 50 55 60
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg
 65 70 75 80
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala
 85 90 95
 Cys Leu Ala Glu Met Tyr Phe Phe Val Thr Leu Gly Ile Thr Glu Ser
 100 105 110
 Tyr Leu Met Ala Ala Met Ser Xaa Arg Ala Arg Arg Arg Val Pro Ala
 115 120 125
 Pro Leu Tyr Gly Ala Leu Val Thr Pro Ser Ala Cys Ala Ser Leu Val
 130 135 140
 Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr Leu
 145 150 155 160
 Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro Phe
 165 170 175
 Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr Ser
 180 185 190
 Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu Ala
 195 200 205
 Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala Val
 210 215 220
 Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly Ala His

225 230 235 240
 Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser Val
 245 250 255
 Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu Ala
 260 265 270
 Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile Asn
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu Arg
 290 295 300
 Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala Asn Leu Ala
 305 310 315

<210> 1993

<211> 311

<212> PRT

<213> Unknown (H38g911 protein)

<220>

<223> Synthetic construct

<400> 1993

Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1 5 10 15
 Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
 20 25 30
 Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu
 35 40 45
 Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys
 50 55 60
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln
 65 70 75 80
 Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly
 85 90 95
 Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys
 100 105 110
 Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu
 130 135 140
 Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr
 145 150 155 160
 Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His
 165 170 175
 Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu
 195 200 205
 Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu
 245 250 255
 Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg
 260 265 270
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
 275 280 285
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Val
 290 295 300
 Trp Gly Arg Lys Thr Met Glu
 305 310

<210> 1994

<211> 316

<212> PRT

<213> Unknown (H38g912 protein)

<220>

<223> Synthetic construct

<400> 1994

```

Met Gln Asn Gln Ser Phe Val Thr Glu Phe Val Leu Leu Gly Leu Ser
 1           5           10           15
Gln Asn Pro Asn Val Gln Glu Ile Val Phe Val Val Phe Leu Phe Val
          20           25           30
Tyr Ile Ala Thr Val Gly Gly Asn Met Leu Ile Val Val Thr Ile Leu
          35           40           45
Ser Ser Pro Ala Leu Leu Val Ser Pro Met Tyr Phe Phe Leu Gly Phe
          50           55           60
Leu Ser Phe Leu Asp Ala Cys Phe Ser Ser Val Ile Thr Pro Lys Met
65           70           75           80
Ile Val Asp Ser Leu Tyr Val Thr Lys Thr Ile Ser Phe Glu Gly Cys
          85           90           95
Met Met Gln Leu Phe Ala Glu His Phe Phe Ala Gly Val Glu Val Ile
          100          105          110
Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
          115          120          125
Leu His Tyr Ser Ser Ile Met Asn Arg Arg Leu Cys Gly Ile Leu Met
          130          135          140
Gly Val Ala Trp Thr Gly Gly Leu Leu His Ser Met Ile Gln Ile Leu
145          150          155          160
Phe Thr Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe
          165          170          175
Met Cys Asp Leu Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr His
          180          185          190
Ile Phe Gly Leu Met Val Val Ile Asn Ser Gly Phe Ile Cys Ile Ile
          195          200          205
Asn Phe Ser Leu Leu Leu Val Ser Tyr Ala Val Ile Leu Leu Ser Leu
210          215          220
Arg Thr His Ser Ser Glu Gly Arg Trp Lys Ala Leu Ser Thr Cys Gly
225          230          235          240
Ser His Ile Ala Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val
          245          250          255
Tyr Thr Arg Pro Pro Ser Ala Phe Ser Leu Asp Lys Met Ala Ala Ile
          260          265          270
Phe Tyr Ile Ile Leu Asn Pro Leu Leu Asn Pro Leu Ile Tyr Thr Phe
          275          280          285
Arg Asn Lys Glu Val Lys Gln Ala Met Arg Arg Ile Trp Asn Arg Leu
          290          295          300
Met Val Val Ser Asp Glu Lys Glu Asn Ile Lys Leu
305          310          315

```

<210> 1995

<211> 310

<212> PRT

<213> Unknown (H38g913 protein)

<220>

<223> Synthetic construct

<400> 1995

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr

```

1           5           10           15
Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu
20           25           30
Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
35           40           45
Ala Ser Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
50           55           60
Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
65           70           75           80
Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
85           90           95
Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
100          105          110
Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
115          120          125
His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
130          135          140
Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
145          150          155          160
Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
165          170          175
Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
180          185          190
Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
195          200          205
Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
210          215          220
Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
225          230          235          240
His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
245          250          255
Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
260          265          270
Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
275          280          285
Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
290          295          300
Ile Thr Asp Asp Lys Arg
305          310

```

<210> 1996

<211> 321

<212> PRT

<213> Unknown (H38g914 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1996

```

Met Glu Thr Thr Asn His Ser Ala Val Thr Glu Phe Phe Leu Val Gly
1           5           10           15
Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu
20           25           30
Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Phe Leu Ile Ile Ile
35           40           45
Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Ph Leu Gly
50           55           60

```

```

Asn Leu S r Phe Leu Gly Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro
65          70          75          80
Met Leu Ile Ile Phe Val Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
85          90          95
Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Ile Glu Cys
100        105        110
Ile Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115        120        125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Val Leu Tyr Val Gln Met
130        135        140
Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Arg Thr
145        150        155        160
Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Ile Ile Asp His
165        170        175
Leu Thr Cys Glu Ile Leu Ala Leu Leu Lys Val Ile Cys Ser Asp Ile
180        185        190
Ser Ile Asn Val Phe Ile Met Thr Val Ser Ser Ile Val Leu Leu Val
195        200        205
Ile Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser Ile Leu
210        215        220
Arg Ile Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Phe Thr Cys Ser
225        230        235        240
Ala His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Val Leu Phe Met
245        250        255
His Met Lys Pro Lys Ser Lys Phe Thr Thr Ala Ser Asp Glu Ile Ile
260        265        270
Gly Leu Ser Tyr Glu Val Ile Thr Pro Met Asn Pro Ile Ile Tyr Ser
275        280        285
Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Lys Lys Ile Leu Ser Arg
290        295        300
His Val His Leu Trp Lys Ile Xaa Lys Ala Leu Arg His Val Thr Phe
305        310        315        320
Ser

```

<210> 1997

<211> 177

<212> PRT

<213> Unknown (H38g915 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 1997

```

Ala Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Phe Phe
1          5          10          15
Leu Lys Asn Leu Ser Val Leu Asp Leu Cys Tyr Ile Ser Val Thr Val
20        25        30
Pro Lys Ser Ile Arg Asn Ser Leu Thr Arg Arg Ser Ser Ile Ser Tyr
35        40        45
Leu Gly Cys Val Ala Gln Ala Tyr Phe Phe Ser Ala Phe Ala Ser Ala
50        55        60
Glu Leu Ala Phe Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile
65        70        75        80
Cys His Pro Leu Gln Tyr Arg Ala Val Met Thr Ser Gly Gly Cys Tyr
85        90        95
Gln Met Ala Val Thr Thr Trp Leu Ser Cys Phe Ser Tyr Ala Ala Val

```


Gln Ala Gln Ala Trp Pro Trp Val Pro Gly Ser Gly Gly Phe Val Ala
 20 25 30
 Ile Ala Val Pro Thr Ser Pro Ser Ser Ser Gly Leu Ser Phe Cys Gly
 35 40 45
 Pro Pro Val Ala Ile Asn His Phe Leu Ser Cys Asp Ile Ala Pr Leu
 50 55 60
 Ile Ala Leu Ala Cys Thr Gln His Thr Gly Ser Glu Ser Phe Val Ala
 65 70 75 80
 Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu
 85 90 95
 Val Ser His Met Cys Thr Ser Ser Ser Thr Ile Leu Arg Ile Pro Ser
 100 105 110
 Ala Ser Gly Arg Lys Gln Ser Leu Ser Pro Arg Ala Pro Arg His Leu
 115 120 125
 Thr Val Val Leu Ile Leu
 130

<210> 2000

<211> 196

<212> PRT

<213> Unknown (H38g924 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(196)

<223> Xaa = Any Amino Acid

<400> 2000

Thr Pro Pro Met Tyr Phe Leu Phe Leu Gly Glu Ala Glu Cys Phe Leu
 1 5 10 15
 Leu Ala Thr Met Glu Tyr Asp Arg Tyr Glu Asp Ile Cys Ser Pro Leu
 20 25 30
 Asn Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Gly
 35 40 45
 Asp Ser Trp Val Pro Ser Phe Pro Glu Ala Thr Glu Gln Ala Thr Met
 50 55 60
 Ala Leu Arg Phe Pro Phe Xaa Gly Thr Asn Lys Val Asn His Leu Phe
 65 70 75 80
 Leu Arg Gln Pro Ala Val Leu Lys Ala Gly Leu Met Gln Asp Thr Ala
 85 90 95
 Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Ala Met Asn
 100 105 110
 Pro Cys Leu Leu Ile Leu Ser Ser Tyr Thr Arg Ile Gly Ala Ala Ile
 115 120 125
 Pro Gln Glu Pro Ile Lys Leu Lys Gly Lys Gln Xaa Arg Pro Phe Ser
 130 135 140
 Thr Cys Ser Xaa His Leu Pro Trp Trp Pro Leu Phe Ser Asn Ile Ile
 145 150 155 160
 Ile Xaa Ala Ser Thr Tyr Phe Leu Gly Leu Lys Ser Asn Lys Phe Phe
 165 170 175
 Trp Arg Gly Lys Lys Val Val Phe Ile Tyr Thr Thr Leu Val Glu Thr
 180 185 190
 Pro Xaa Trp Asn
 195

<210> 2001

<211> 128

<212> PRT

<213> Unknown (H38g925 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(128)

<223> Xaa = Any Amino Acid

<400> 2001

```

His Cys Met Phe Leu Ala His Gly Ser Pro Leu Pro Pro Thr Gln Leu
 1           5           10          15
Pro Ile Xaa Phe Cys Asp Tyr Ile Ser His Arg Tyr Leu Thr Cys His
 20          25          30
Leu Ser Leu Pro Asn Ser Phe Ser Ser Phe Pro Tyr Gln Xaa Ile
 35          40          45
Leu Pro Leu Ser Leu Leu Ala Gln Ala Arg Asn Pro Gly Ile Ile Phe
 50          55          60
Phe Leu Pro Thr Phe Asn Ala Leu Xaa Ser Pro Val His Ser Thr Ser
 65          70          75          80
Xaa Arg Leu Ser Leu Ser Thr Tyr Tyr Tyr Ala Ser Gln Glu Thr Ile
 85          90          95
Ser Pro Arg Phe Asp Ser Thr Ala Val Ala Ser Tyr Leu Ile Phe Leu
100         105         110
His Leu Leu Trp Pro Ile Phe Asn Pro Phe Ile Tyr Cys Leu Arg Asn
115         120         125

```

<210> 2002

<211> 192

<212> PRT

<213> Unknown (H38g926 protein)

<220>

<223> Synthetic construct

<400> 2002

```

Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala Leu Leu Leu Thr Ser Met
 1           5           10          15
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Leu Ile
 20          25          30
Arg Met Arg Lys Arg Val Cys Ala Leu Met Ile Thr Gly Ser Trp Met
 35          40          45
Ile Gly Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala Leu Arg Ile
 50          55          60
Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Cys Asp Val Pro
 65          70          75          80
Ala Met Leu Thr Leu Ala Cys Thr Asp Thr Trp Val Tyr Glu Cys Thr
 85          90          95
Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile Cys Ile
100         105         110
Ala Cys Ser Tyr Gly Arg Ile Leu Leu Ala Val Tyr His Met His Ser
115         120         125
Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr His Leu Thr
130         135         140
Val Val Thr Phe Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro
145         150         155         160
Lys Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Phe
165         170         175
Phe Ile Ser Ser Phe Ser Ser Asn Pro Phe Met Tyr Thr Leu Arg Asn
180         185         190

```

<210> 2003

<211> 158
 <212> PRT
 <213> Unknown (H38g927 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(158)
 <223> Xaa = Any Amino Acid

<400> 2003
 Pro Met Tyr Phe Phe Leu Ser Met Leu Ser Ile Ser Glu Thr Cys Tyr
 1 5 10 15
 Met Val Ala Ile Thr Pro His Met Leu Ser Arg Leu Leu Asn Pro His
 20 25 30
 Xaa Leu Ile Val Met Gln Gly Cys Val Thr Gln Leu Phe Tyr Val Thr
 35 40 45
 Phe Gly Ile Asn Asn Cys Phe Leu Leu Ile Ala Met Gly Tyr Asp Cys
 50 55 60
 Tyr Val Val Phe Cys Asn Pro Leu Arg Tyr Ser Xaa Val Arg Gly Leu
 65 70 75 80
 Cys Val Xaa Leu Gly Ser Gly Ser Leu Arg Ile Gly Leu Gly Met Ala
 85 90 95
 Ile Val Gln Val Thr Ser Met Phe Gly Leu Pro Phe Cys Asp Asp Phe
 100 105 110
 Val Ile Ser His Phe Phe Cys Asp Val Arg Pro Leu Leu Lys Leu Ala
 115 120 125
 Cys Thr Asp Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val
 130 135 140
 Cys Val Leu Val Leu His Ile Ala Leu Ile Phe Ile Ser Tyr
 145 150 155

<210> 2004
 <211> 192
 <212> PRT
 <213> Unknown (H38g928 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(192)
 <223> Xaa = Any Amino Acid

<400> 2004
 Leu Leu Ala Thr Lys Ala Tyr Asp Xaa Tyr Val Pro Ile Arg His Pro
 1 5 10 15
 Phe Pro Tyr Pro Thr Arg Met Ser Pro Ala Met Cys Ala Ala Leu Val
 20 25 30
 Gly Met Ala Trp Leu Val Ser His Gly Asn Ser Leu Leu Tyr Ile Leu
 35 40 45
 Leu Met Ala Arg Leu Ser Phe Leu Cys Phe Pro Thr Lys Cys Thr His
 50 55 60
 Phe Phe Cys Asp Pro Pro Ser Leu Ser Xaa Arg Leu Ser Cys Ser Asp
 65 70 75 80
 Asn His Thr Ser Lys Leu Leu Ile Phe Thr Lys Gly Ala Ala Val Val
 85 90 95
 Val Thr Pro Leu Leu Leu Ile Leu Ala Ser Leu Trp Asp His Asn Lys
 100 105 110
 Leu Thr Val Leu Gln Leu Pro Ser Thr Ser Gly Arg Leu Arg Asp Leu

115	120	125
Xaa Pro Thr Cys Gly Ser His Leu Asp Val Val Ser Leu Phe Tyr Arg		
130	135	140
Thr Val Ile Ala Val Tyr Phe Gln Ala Thr Ser Ser Thr Arg Ala Glu		
145	150	155
Trp Asp Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu		
165	170	175
Asn Pro Ile Ile Tyr Ser Leu Thr Xaa Pro Arg Gly Arg Thr Leu Arg		
180	185	190

<210> 2005
 <211> 176
 <212> PRT
 <213> Unknown (H38g929 protein)

<220>
 <223> Synthetic construct

<400> 2005
Arg Val Pro Pro Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Val Phe
1 5 10 15
Asp Met Gly Phe Ser Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu
20 25 30
Met Gly Leu Gly Arg Leu Ile Ser Tyr Lys Asp Cys Val Cys Gln Leu
35 40 45
Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys Phe Leu Phe Thr Val
50 55 60
Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys Tyr Pro Leu Arg Tyr Thr
65 70 75 80
Val Ile Met Asn Pro Arg Ile Cys Val Ala Leu Ala Val Gly Thr Trp
85 90 95
Leu Leu Gly Cys Ile His Ser Ser Ile Leu Thr Ser Leu Thr Phe Thr
100 105 110
Leu Pro His Cys Gly Pro Asn Glu Val Asp His Phe Phe Cys Asp Ile
115 120 125
Pro Ala Leu Leu Pro Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg
130 135 140
Val Ser Phe Thr Asn Val Gly Leu Ile Ser Ala Gly Cys Phe Leu Leu
145 150 155 160
Asn Leu Leu Ser Tyr Thr Arg Ile Thr Asn Ile Tyr Leu Lys His Ser
165 170 175

<210> 2006
 <211> 44
 <212> PRT
 <213> Unknown (H38g930 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(44)
 <223> Xaa = Any Amino Acid

<400> 2006
Cys Ile Lys Leu Gly Thr Glu Leu Gly Ser Thr Ser Asn Gly Arg Gln
1 5 10 15
Cys Ala Gly Ile Arg Pro Ser Tyr Val Phe Thr Leu His Leu Xaa Ala
20 25 30
Asn Val Asn Pro Phe Ile Tyr Thr Leu Ser Asn Lys
35 40

<210> 2007
 <211> 187
 <212> PRT
 <213> Unknown (H38g931 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(187)
 <223> Xaa = Any Amino Acid

<400> 2007
 Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Leu Leu Leu
 1 5 10 15
 Ser Gln Leu Ser Leu Met Asp Leu Met Tyr Ile Ser Thr Thr Val Pro
 20 25 30
 Lys Met Ala Tyr Asn Phe Leu Ser Gly Gln Lys Gly Ile Ser Phe Leu
 35 40 45
 Gly Cys Gly Val Gln Ser Phe Phe Leu Thr Met Ala Cys Ser Glu
 50 55 60
 Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
 65 70 75 80
 His Ser Leu Tyr Tyr Pro Ile Arg Met Ser Lys Met Met Cys Val Lys
 85 90 95
 Met Ile Gly Gly Ser Trp Thr Leu Gly Ser Ile Asn Ser Leu Ala His
 100 105 110
 Thr Val Phe Ala Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asp
 115 120 125
 His Phe Phe Cys Asp Val Pro Ala Met Leu Leu Leu Ser Cys Thr Asp
 130 135 140
 Thr Trp Val Tyr Glu Tyr Met Val Leu Xaa Gly Gln Ser Leu Phe Leu
 145 150 155 160
 Leu Leu Pro Phe Ile Gly Ile Thr Ser Ser Glu Gly Arg Val Leu Ile
 165 170 175
 Ala Gly Tyr Ile Met His Ser Lys Glu Gly Arg
 180 185

<210> 2008
 <211> 62
 <212> PRT
 <213> Unknown (H38g934 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(62)
 <223> Xaa = Any Amino Acid

<400> 2008
 Gly Gly Asn Arg Lys Lys Arg Glu Lys Glu Gly Arg Lys Lys Arg Lys
 1 5 10 15
 Val Arg Lys Lys Thr Gly Xaa Gly Arg Xaa Glu Val Gly Leu Leu Lys
 20 25 30
 Gly Ser Asn Ile Val Met Tyr Met Ala Pro Lys Tyr Arg His Pro Glu
 35 40 45
 Glu Gln Gln Lys Val Leu Phe Leu Phe Tyr Ser Ser Phe Asn
 50 55 60

<210> 2009
 <211> 103
 <212> PRT
 <213> Homo sapien (1000494-1-1-323)

<400> 2009
 Pro Tyr Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Val Thr
 1 5 10 15
 Asp Thr Ser Cys Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val
 20 25 30
 Ile Ala Thr Pro Phe Val Cys Ile Leu Ala Pro Tyr Ala Arg Ile Leu
 35 40 45
 Val Ala Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe
 50 55 60
 Ser Ala Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr
 65 70 75 80
 Thr Ile Gly Val Tyr Leu Cys Arg Ser Ser Val Leu Thr Thr Ala Lys
 85 90 95
 Glu Lys Ala Ser Ala Val Met
 100

<210> 2010
 <211> 314
 <212> PRT
 <213> Homo sapien (1336040-1-1-945)

<400> 2010
 Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
 20 25 30
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
 35 40 45
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val
 65 70 75 80
 Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
 85 90 95
 Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
 100 105 110
 Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
 130 135 140
 Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val
 145 150 155 160
 His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
 165 170 175
 Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
 180 185 190
 Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
 195 200 205
 Glu Ile Ile Cys Phe Ile Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
 210 215 220
 Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
 245 250 255
 Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
 260 265 270

Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Il Pro Val Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
 290 295 300
 Lys Val Leu Arg Ser Lys Val Asp Ser Ser
 305 310

<210> 2011

<211> 317

<212> PRT

<213> Homo sapien (1336042-1-1-954)

<400> 2011

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
 20 25 30
 Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
 115 120 125
 Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
 195 200 205
 Thr Pro Leu Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
 245 250 255
 Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
 260 265 270
 Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
 290 295 300
 Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
 305 310 315

<210> 2012

<211> 318

<212> PRT

<213> Homo sapien (1369835-1-20155-22741)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2012

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
          20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
          35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
          50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
          85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
          100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
          115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
          130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
          145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
          165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
          180          185          190
Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
          195          200          205
Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
          210          215          220
Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
          225          230          235          240
Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu
          245          250          255
Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu Ser
          260          265          270
Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val Ser
          275          280          285
Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser Xaa
          290          295          300
Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro
          305          310          315

```

<210> 2013

<211> 319

<212> PRT

<213> Homo sapien (1857946-1-1-1049)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2013

```

Phe Ser Ser Val Asn Asn Ser Cys Pro Arg Asn Val Arg Pro Val Leu
 1          5          10          15
Ser Val Trp Ala Met Tyr Leu Val Met Ile Gly Ser Ile Val Met Thr
          20          25          30
Met Leu Gly Asn Met Ile Val Met Ile Ser Ile Ala His Phe Lys Gln

```

35	40	45
Leu His Ser Pro Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp		
50	55	60
Phe Leu Leu Ser Cys Val Val Met Pro Phe Ser Val Ile Thr Ser Ile		
65	70	75
Glu Ser Cys Trp Tyr Phe Gly Asp Leu Phe Cys Lys Val His Ser Cys		
85	90	95
Cys Asp Ile Ile Leu Cys Thr Thr Ser Ile Phe His Leu Cys Phe Ile		
100	105	110
Ser Val Asp Arg Tyr Asp Ala Val Xaa Asp Pro Leu Gln Tyr Val Thr		
115	120	125
Arg Ile Thr Ile Pro Val Ile Glu Leu Phe Leu Leu Ile Ser Trp Ser		
130	135	140
Ile Pro Ile Leu Phe Ala Phe Gly Leu Val Phe Ser Lys Leu Asn Ile		
145	150	155
Ile Gly Ala Glu Glu Phe Val Ala Ala Ile Asp Cys Thr Gly Leu Cys		
165	170	175
Val Leu Ile Phe Asn Lys Pro Gly Gly Val Leu Ala Ser Phe Ile Ala		
180	185	190
Phe Phe Leu Pro Gly Thr Thr Thr Val Gly Ile Tyr Ile His Ile Phe		
195	200	205
Thr Val Ala Arg Lys His Ala Met Gln Ile Gly Thr Gly Ser Arg Thr		
210	215	220
Lys Gln Ala Gly Ser Glu Ser Lys Lys Lys Trp His Pro Leu Lys Arg		
225	230	235
Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe Val		
245	250	255
Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe Ile		
260	265	270
Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu Gly		
275	280	285
Tyr Phe Asn Ser Ala Phe Asn Ser Ile Leu Tyr Gly Met Leu Tyr Pro		
290	295	300
Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe		
305	310	315

<210> 2014

<211> 134

<212> PRT

<213> Homo sapien (2358019-1-250070-250529)

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 2014

Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His	
1	5
Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe	
20	25
Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu	
35	40
Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly	
50	55
Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly	
65	70
Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe	
85	90
Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa	
100	105
	110

Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr
 115 120 125
 Phe Leu Arg Val Leu Ser
 130

<210> 2015
 <211> 127
 <212> PRT
 <213> Homo sapien (2447218-1-32642-33129)

<220>
 <221> VARIANT
 <222> (1)...(127)
 <223> Xaa = Any Amino Acid

<400> 2015
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser
 1 5 10 15
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu
 20 25 30
 Phe Gln Asn His Lys Leu Phe Leu Leu Phe Ala Gly Met Asn Val Phe
 35 40 45
 Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro
 50 55 60
 Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val
 65 70 75 80
 Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg
 85 90 95
 Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile
 100 105 110
 Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn
 115 120 125

<210> 2016
 <211> 216
 <212> PRT
 <213> Homo sapien (2921627-1-1-649)

<400> 2016
 Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met Leu Val
 1 5 10 15
 Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys Thr Ala
 20 25 30
 Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe Leu Leu
 35 40 45
 Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 50 55 60
 Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile Ala Gly
 65 70 75 80
 Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro Ile Thr
 85 90 95
 Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe Phe Cys
 100 105 110
 Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala Leu Tyr
 115 120 125
 Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile Pro Phe
 130 135 140
 Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val Gln Cys
 145 150 155 160
 Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser Ser
 165 170 175

His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr Thr Tyr
 180 185 190
 Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val Leu Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 2017

<211> 216

<212> PRT

<213> Homo sapien (2921629-1-1-649)

<400> 2017

Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val
 1 5 10 15
 Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys
 50 55 60
 Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu
 65 70 75 80
 Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
 115 120 125
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
 130 135 140
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
 145 150 155 160
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
 180 185 190
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Ile Val Thr Pro
 210 215

<210> 2018

<211> 212

<212> PRT

<213> Homo sapien (2921634-1-1-653)

<400> 2018

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly
 1 5 10 15
 Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe
 20 25 30
 Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala
 35 40 45
 Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr
 50 55 60
 Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys
 65 70 75 80
 Gly Phe Leu Asn Ala Pro Leu Arg Ile Val Asp Ile Phe Ser Leu Ser
 85 90 95
 Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro

```

      100      105      110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
      115      120      125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
      130      135      140
Thr Ser Tyr Leu Val Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
145      150      155      160
Gln Gly His Leu Lys Ala Trp Ser Thr Gly Ala Pro His Leu Ile Ala
      165      170      175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
      180      185      190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
      195      200      205
Val Phe Ile Ser
      210

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<210> 2019

<211> 215

<212> PRT

<213> Homo sapien (2921639-1-1-647)

<400> 2019

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Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1      5      10      15
Asn Ile Arg Thr Gln Ser Lys Val Val Thr Tyr Ala Gly Cys Ile Thr
      20      25      30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
      50      55      60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65      70      75      80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
      85      90      95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
      100      105      110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
      115      120      125
Asp Met Val Met Tyr Met Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
      130      135      140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
145      150      155      160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165      170      175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Gly Leu Gly Val Tyr
      180      185      190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
      195      200      205
Met Tyr Thr Val Val Thr Pro
      210      215

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<210> 2020

<211> 212

<212> PRT

<213> Homo sapien (2921641-1-1-636)

<220>

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 2020

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Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pr Lys Met Ile Val
 1          5          10          15
Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
          20          25          30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
          35          40          45
Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
          50          55          60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65          70          75          80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
          85          90          95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
          100          105          110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
          115          120          125
Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
          130          135          140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145          150          155          160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
          165          170          175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg
          180          185          190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
          195          200          205
Thr Ile Thr Pro
          210

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<210> 2021

<211> 216

<212> PRT

<213> Homo sapien (2921661-1-1-649)

<400> 2021

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Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala
 1          5          10          15
Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu
          20          25          30
Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu
          35          40          45
Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala
65          70          75          80
Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met
          85          90          95
Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys
          100          105          110
Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn
          115          120          125
Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val
          130          135          140
Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys
145          150          155          160
Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
          165          170          175
His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp
          180          185          190
Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser

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195 200 205
Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 2022
<211> 216
<212> PRT
<213> Homo sapien (2921667-1-1-649)

<400> 2022
Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
1 5 10 15
Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
20 25 30
Gln Leu Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu
35 40 45
Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr
50 55 60
Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
65 70 75 80
Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met
85 90 95
Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys
100 105 110
Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn
115 120 125
Glu Leu Leu Leu Phe Val Ala Ala Ala Phe Met Ala Val Ala Pro Leu
130 135 140
Val Phe Ile Ser Val Ser Tyr Ala His Val Val Ala Ala Val Pro Gln
145 150 155 160
Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175
His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr
180 185 190
Met Arg Leu Gly Ser Ala Glu Ser Ser Asp Lys Asp Lys Gly Val Gly
195 200 205
Val Phe Met Thr Val Ile Asn Pro
210 215

<210> 2023
<211> 215
<212> PRT
<213> Homo sapien (2921686-1-1-646)

<400> 2023
Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro Lys Met Ile Val
1 5 10 15
Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser Cys Leu Thr Gln
20 25 30
Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp Leu Leu Ile
35 40 45
Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Ser Pro His Tyr
50 55 60
Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe Val Leu Val Ser
65 70 75 80
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Thr Val Leu
85 90 95
Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys Asp
100 105 110
Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val Ile Asp Ser
115 120 125

Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe Leu Pro Ile Ser
 130 135 140
 Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser Ile Leu Arg Ile
 145 150 155 160
 Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr Cys Arg Ser His
 165 170 175
 Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr Leu
 180 185 190
 Thr Thr Ala Ala Gly Thr Thr Pro Arg Ser Gly Val Val Val Ser Val
 195 200 205
 Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2024

<211> 217

<212> PRT

<213> Homo sapien (2921715-1-1-652)

<400> 2024

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1 5 10 15
 Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
 20 25 30
 Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
 35 40 45
 Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
 50 55 60
 Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
 65 70 75 80
 Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
 85 90 95
 Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
 100 105 110
 Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
 115 120 125
 Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
 130 135 140
 Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
 145 150 155 160
 Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 165 170 175
 Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
 180 185 190
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
 195 200 205
 Ser Leu Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 2025

<211> 311

<212> PRT

<213> Homo sapien (3093312-1-33069-35776)

<400> 2025

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
 1 5 10 15
 Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
 20 25 30
 Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
 35 40 45
 Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe

50	55	60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser		
65	70	75
Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser		80
	85	90
Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr		95
	100	105
Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala		110
	115	120
Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys		125
	130	135
His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala		140
	145	150
Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln		155
	165	170
Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys		175
	180	185
Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile		190
	195	200
Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile		205
	210	215
Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val		220
	225	230
Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile		235
	245	250
Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp		255
	260	265
Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu		270
	275	280
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val		285
	290	295
Lys Arg Leu Met Gly Trp Glu		300
305	310	

<210> 2026

<211> 330

<212> PRT

<213> Homo sapien (3108020-1-23117-23433)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 2026

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly	
1	5
Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val	
	10
	15
	20
	25
Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile	
	30
	35
	40
	45
Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe	
	50
	55
	60
Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val	
	65
	70
	75
Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser	
	80
	85
	90
	95
Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu	
	100
	105
	110
Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile	
	115
	120
	125

Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly
 130 135 140
 Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu
 145 150 155 160
 His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile
 165 170 175
 Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser
 180 185 190
 Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu
 195 200 205
 Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val
 210 215 220
 Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr
 245 250 255
 Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser
 260 265 270
 Gly Ala Ile Ala Ser Val Arg Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys
 290 295 300
 Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Xaa Gly Leu
 305 310 315 320
 Lys Leu Tyr Pro Xaa Leu Gln Gly Ser Lys
 325 330

<210> 2027

<211> 319

<212> PRT

<213> Homo sapien (3108020-1-37593-38822)

<400> 2027

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ala Glu Asp Ser Asp Met Gln Leu Leu His Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr
 35 40 45
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly
 85 90 95
 Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn
 100 105 110
 Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
 145 150 155 160
 Leu Thr Ile Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His
 165 170 175
 Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Ile Asn Asn Ile Val Met Tyr Phe Val Thr Ile Val Leu Gly Val
 195 200 205
 Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser
 210 215 220

Val Leu Arg Val Ser Ala Arg Gly Gln His Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly
 245 250 255
 Val Tyr Leu Ser Ser Ala Val Thr Pro Ser Arg Thr Ser Leu Ala
 260 265 270
 Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu Leu
 290 295 300
 Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser
 305 310 315

<210> 2028

<211> 315

<212> PRT

<213> Homo sapien (3184261-1-5713-7336)

<400> 2028

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly
 1 5 10 15
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu
 20 25 30
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala
 35 40 45
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser
 100 105 110
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His
 115 120 125
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu
 130 135 140
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr
 145 150 155 160
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His
 165 170 175
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr
 180 185 190
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr
 195 200 205
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr
 210 215 220
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe
 245 250 255
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys
 260 265 270
 Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro
 305 310 315

<210> 2029

<211> 318

<212> PRT

<213> Homo sapien (3213020-1-101040-103030)

<400> 2029

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Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
1      5      10      15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
20      25      30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
35      40      45
Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
50      55      60
Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
65      70      75      80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
85      90      95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
100     105     110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
130     135     140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
145     150     155     160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
165     170     175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
180     185     190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu
195     200     205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
210     215     220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225     230     235     240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
245     250     255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
260     265     270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
275     280     285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
290     295     300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305     310     315

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<210> 2030

<211> 114

<212> PRT

<213> Homo sapien (32504-1-1-343)

<400> 2030

```

Val Cys His Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys
1      5      10      15
Gly Leu Leu Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu
20      25      30
Leu His Ile Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu
35      40      45
Ile Pro His Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys
50      55      60
Ser Asp Thr Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val

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65		70		75		80
Leu Gly Val Phe	Pro L u	Leu Gly Ile	Ile Phe Ser Tyr	Ser Arg Ile		
	85		90		95	
Ala Ser Ser Ile	Arg Lys Met Ser	Ser Ser Gly Gly Lys	Gln Lys Ala			
	100	105	110			
Leu Ser						

<210> 2031
 <211> 114
 <212> PRT
 <213> Homo sapien (32508-1-1-343)

<400> 2031

Ile Val Ser Pro	Leu Leu Tyr Thr	Val Ala Met Ser	Asp Arg Lys Cys
1	5	10	15
Val Glu Leu Val	Thr Gly Ser Trp	Ile Gly Gly Ile	Val Asn Thr Leu
	20	25	30
Ile His Thr Ile	Ser Leu Arg Arg	Leu Ser Phe Cys	Arg Leu Asn Ala
	35	40	45
Val Ser His Phe	Phe Cys Asp Ile	Pro Ser Leu Leu	Lys Leu Ser Cys
	50	55	60
Ser Asp Thr Ser	Met Asn Glu Leu	Leu Leu Thr Phe	Ser Gly Val
65	70	75	80
Ile Ala Met Ala	Thr Phe Leu Thr	Val Ile Ile Ser	Tyr Ile Phe Ile
	85	90	95
Ala Phe Ala Ser	Leu Arg Ile His	Ser Ala Ser Gly	Arg Gln Gln Ala
	100	105	110
Phe Ser			

<210> 2032
 <211> 112
 <212> PRT
 <213> Homo sapien (32509-1-1-338)

<400> 2032

Ile Cys His Pro	Leu Arg Tyr Thr	Thr Ile Met Lys	Glu Gly Leu Cys
1	5	10	15
Asn Leu Leu Val	Thr Val Ser Trp	Ile Leu Ser Cys	Thr Asn Ala Leu
	20	25	30
Ser His Thr Leu	Leu Leu Ala Gln	Leu Ser Phe Cys	Ala Asp Asn Thr
	35	40	45
Ile Pro His Phe	Phe Cys Asp Leu	Val Ala Leu Leu	Lys Leu Ser Cys
	50	55	60
Ser Asp Ile Ser	Leu Asn Glu Leu	Val Ile Phe Thr	Val Gly Gln Ala
65	70	75	80
Val Ile Thr Leu	Pro Leu Ile Cys	Ile Leu Ile Ser	Tyr Gly His Ile
	85	90	95
Gly Val Thr Ile	Leu Lys Ala Pro	Ser Thr Lys Gly	Ile Phe Lys Ala
	100	105	110

<210> 2033
 <211> 114
 <212> PRT
 <213> Homo sapien (32513-1-1-343)

<400> 2033

Ile Cys Tyr Pro	Leu Arg Tyr Thr	Ala Ile Met Asn	Pro Arg Ile Cys
1	5	10	15
Val Ala Leu Ala	Val Gly Thr Trp	Leu Leu Gly Cys	Ile His Ser Ser

```

      20      25      30
Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu
      35      40      45
Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys
      50      55      60
Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu
      65      70      75      80
Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile
      85      90      95
Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala
      100      105      110
Phe Ser

```

<210> 2034
 <211> 114
 <212> PRT
 <213> Homo sapien (32518-1-1-343)

```

<400> 2034
Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys
  1      5      10      15
Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu
      20      25      30
Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile
      35      40      45
Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys
      50      55      60
Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ser Gly Ser
      65      70      75      80
Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val
      85      90      95
Leu Phe Ala Ile Leu Lys Arg Lys Ser Asp Lys Gly Val Arg Lys Ala
      100      105      110
Phe Ser

```

<210> 2035
 <211> 148
 <212> PRT
 <213> Homo sapien (3289998-1-93404-94343)

```

<400> 2035
Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe
  1      5      10      15
Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe
      20      25      30
Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly Gly
      35      40      45
Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Ile Val Ser Ser Ile
      50      55      60
Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys
      65      70      75      80
Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu Gly
      85      90      95
Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala Thr
      100      105      110
Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe Ile
      115      120      125
Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser Phe
      130      135      140

```

Arg Gly Lys Gln
145

<210> 2036

<211> 312

<212> PRT

<213> Homo sapien (3402736-1-7079-10933)

<400> 2036

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
      20           25           30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
      35           40           45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Leu Arg Thr
      50           55           60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
      65           70           75           80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
      85           90           95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
      100          105          110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
      115          120          125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
      130          135          140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
      145          150          155          160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
      165          170          175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
      180          185          190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
      195          200          205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
      210          215          220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
      225          230          235          240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
      245          250          255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
      260          265          270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
      275          280          285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
      290          295          300
Gln Lys Thr Val Pro Met Glu Ile
      305          310

```

<210> 2037

<211> 305

<212> PRT

<213> Homo sapien (3522966-1-8581-12533)

<400> 2037

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
 1           5           10           15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20           25           30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu

```

35	40	45
His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu		
50	55	60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser		
65	70	75
Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu		
85	90	95
Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly		
100	105	110
Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile		
115	120	125
Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile		
130	135	140
Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro		
145	150	155
Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg		
165	170	175
Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val		
180	185	190
Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile		
195	200	205
Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp		
210	215	220
Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val		
225	230	235
Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro		
245	250	255
Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr		
260	265	270
Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys		
275	280	285
Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys		
290	295	300
Phe		
305		

<210> 2038
 <211> 142
 <212> PRT
 <213> Homo sapien (3738097-1-24383-25939)

<220>
 <221> VARIANT
 <222> (1)...(142)
 <223> Xaa = Any Amino Acid

<400> 2038
Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
1 5 10 15
Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys
20 25 30
Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
35 40 45
Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
50 55 60
Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
65 70 75 80
Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
85 90 95
Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
100 105 110

Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
 115 120 125
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
 130 135 140

<210> 2039
 <211> 297
 <212> PRT
 <213> Homo sapien (3738097-1-94180-96164)

<220>
 <221> VARIANT
 <222> (1)...(297)
 <223> Xaa = Any Amino Acid

<400> 2039
 Met Lys Xaa Met Ala Val Glu Asn Asn Ser Ser Val Thr Glu Phe Ile
 1 5 10 15
 Leu Val Arg Leu Thr Asn Ser Arg Cys Pro Ser Val Leu Phe Leu Met
 20 25 30
 Trp Ser Leu Trp Gly Glu Phe Glu His Asn Phe Met Ser Leu Asn Ser
 35 40 45
 His Leu His Thr Pro Thr His Phe Phe Leu Phe Thr Leu Ser Phe Ile
 50 55 60
 Asp Val Cys Tyr Ser Phe Val Cys Thr Thr Lys Ile Pro Met Gly Phe
 65 70 75 80
 Ile Ser Glu Arg Asn Ile Ile Ser Phe Val Gly Trp Pro Thr Xaa Leu
 85 90 95
 Tyr Phe Phe Cys Ile Phe Val Lys Glu Pro Lys Asn Gly Val Ile Val
 100 105 110
 Gly Ile Met Phe Ser Ala Lys Met Leu Val Cys Arg Glu Ile Met Asp
 115 120 125
 Xaa Ser Leu Met Xaa Asn Xaa Lys Met His Met Ala Leu Glu Arg Ser
 130 135 140
 Asp Phe Arg Met Gly Xaa Thr Gly Ser Ala Thr Lys Lys His Leu Ile
 145 150 155 160
 Ile Phe Leu Tyr Tyr Ser Asp Tyr Phe Gln Arg Xaa Xaa Gly Cys Arg
 165 170 175
 Ala Leu Gly Gln Gly Ser Leu Ala Lys Gln Asp Thr Xaa Leu Xaa Asn
 180 185 190
 Cys Thr Cys Thr Leu Lys Ser Leu Leu His Ile Ile Ile Cys Phe Tyr
 195 200 205
 Ile Trp Lys Gln Lys Lys Ile Ser Tyr Leu Tyr His Lys Ser Xaa Lys
 210 215 220
 Met Asp Leu Tyr Lys Ile Cys His Val Leu Trp Val Thr His Lys Lys
 225 230 235 240
 Asn Phe Leu Arg Pro Ser Ser Thr Ser Gln Met Val Gln Gly Lys Met
 245 250 255
 Leu Leu Lys Gly Tyr Ile Xaa Phe Trp Arg Met Ser Leu Pro Met Cys
 260 265 270
 Ala Ile Phe Ile Phe Val Arg Arg Tyr Tyr Tyr Leu Leu Lys Lys Leu
 275 280 285
 Lys Thr Leu Leu Tyr Lys Asn Ser Tyr
 290 295

<210> 2040
 <211> 325
 <212> PRT
 <213> Homo sapien (3746441-1-1-1386)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2040

```

Met Ala Asn Glu Asn Tyr Thr Lys Val Thr Xaa Phe Ile Phe Thr Gly
 1              5              10              15
Leu Asn Tyr Asn Pro Gln Leu Arg Val Phe Leu Phe Leu Leu Phe Leu
      20              25              30
Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
      35              40              45
Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50              55              60
Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
65              70              75              80
Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
      85              90              95
Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
      100              105              110
Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
      115              120              125
Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
      130              135              140
Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
145              150              155              160
Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
      165              170              175
Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
      180              185              190
Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
      195              200              205
Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
      210              215              220
Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
225              230              235              240
Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Leu Tyr Gly Thr Leu
      245              250              255
Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
      260              265              270
Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
      275              280              285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His Arg
      290              295              300
Thr Val Thr Gln Arg Lys Phe Cys Lys Ala Xaa Ile Leu Ile Gln Lys
305              310              315              320
Glu Leu Gly Arg Lys
      325

```

<210> 2041

<211> 328

<212> PRT

<213> Homo sapien (3766130-1-61888-64085)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2041

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
 1              5              10              15

```

Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
 20 25 30
 Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
 35 40 45
 Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
 50 55 60
 Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
 65 70 75 80
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
 85 90 95
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
 100 105 110
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
 130 135 140
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
 145 150 155 160
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
 165 170 175
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
 180 185 190
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
 195 200 205
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
 210 215 220
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
 245 250 255
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
 260 265 270
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
 290 295 300
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
 305 310 315 320
 Leu Ser Ser Lys Pro Lys Arg Arg
 325

<210> 2042

<211> 311

<212> PRT

<213> Homo sapien (3766130-1-85703-88675)

<400> 2042

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
 1 5 10 15
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
 20 25 30
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
 35 40 45
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
 65 70 75 80
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
 85 90 95
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
 100 105 110

Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
 130 135 140
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
 145 150 155 160
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
 180 185 190
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
 195 200 205
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
 210 215 220
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
 245 250 255
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile
 260 265 270
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr
 275 280 285
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr
 290 295 300
 Cys Gln Ala Ser Arg Ser Asp
 305 310

<210> 2043

<211> 216

<212> PRT

<213> Homo sapien (3831602-1-1-649)

<400> 2043

Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys Met Leu Ala
 1 5 10 15
 Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys Phe Leu
 20 25 30
 Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys Ile Leu Phe
 35 40 45
 Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu Leu
 50 55 60
 Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met Ala Ala Gly
 65 70 75 80
 Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr Ser His Val
 85 90 95
 Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His Phe Phe Cys
 100 105 110
 Asp Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr Ile Leu Lys
 115 120 125
 Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val Gly Thr Leu
 130 135 140
 Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser Ile Phe Ser
 145 150 155 160
 Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile Tyr Thr Tyr
 180 185 190
 Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys Val Ala Ser
 195 200 205
 Val Phe Tyr Thr Val Val Ile Pro
 210 215

<210> 2044
 <211> 217
 <212> PRT
 <213> Homo sapien (3831605-1-1-652)

<220>
 <221> VARIANT
 <222> (1)...(217)
 <223> Xaa = Any Amino Acid

<400> 2044
 Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Met Ile Glu
 1 5 10 15
 Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly Asp Cys Leu Thr
 20 25 30
 Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp Asp Met Ile Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu Asn
 50 55 60
 Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu Leu Val Leu Val
 65 70 75 80
 Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Val
 85 90 95
 Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys
 100 105 110
 Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp Ser Asp Ile Asn
 115 120 125
 Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly Phe Leu Arg Ile
 130 135 140
 Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe Pro Ile Leu Arg
 145 150 155 160
 Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser Thr Xaa Gly Ser
 165 170 175
 Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr
 180 185 190
 Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp Val Val Ala Ser
 195 200 205
 Val Met Tyr Ala Val Val Val Thr Pro
 210 215

<210> 2045
 <211> 214
 <212> PRT
 <213> Homo sapien (3831606-1-1-644)

<400> 2045
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu
 65 70 75 80
 Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
 100 105 110

Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 2046

<211> 278

<212> PRT

<213> Homo sapien (3831610-1-1-984)

<400> 2046

Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe
 1 5 10 15
 Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile
 20 25 30
 Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln
 35 40 45
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly
 50 55 60
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg
 65 70 75 80
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly
 85 90 95
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly
 100 105 110
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly
 115 120 125
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn
 130 135 140
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu
 145 150 155 160
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr
 165 170 175
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg
 180 185 190
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile
 195 200 205
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser
 210 215 220
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val
 225 230 235 240
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys
 245 250 255
 Arg Ala Leu Cys Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp
 260 265 270
 Pro Lys Lys Gly Ser Arg
 275

<210> 2047

<211> 227

<212> PRT

<213> Homo sapien (3831615-1-1-684)

<400> 2047

```

Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu
 1           5           10           15
Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala
 20           25           30
Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu
 35           40           45
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
 50           55           60
His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala
 65           70           75           80
Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp
 85           90           95
Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe
100           105           110
Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu
115           120           125
Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro
130           135           140
Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu
145           150           155           160
Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser
165           170           175
Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr
180           185           190
Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu
195           200           205
Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu
210           215           220
Leu Ser Trp
225

```

<210> 2048

<211> 217

<212> PRT

<213> Homo sapien (3831618-1-1-653)

<400> 2048

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
 1           5           10           15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
 20           25           30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
 35           40           45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 50           55           60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
 65           70           75           80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
 85           90           95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
100           105           110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
115           120           125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
130           135           140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
145           150           155           160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly

```

165 170 175
 Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr
 180 185 190
 Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val
 195 200 205
 Phe Tyr Ala Ile Val Thr Pro Met Leu
 210 215

<210> 2049

<211> 279

<212> PRT

<213> Homo sapien (3834584-1-78858-80128)

<400> 2049

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 1 5 10 15
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
 35 40 45
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
 50 55 60
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
 65 70 75 80
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu
 85 90 95
 His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr
 100 105 110
 Gly Ser Trp Val Val Ala Asn Ser Ala Leu Leu His Thr Leu Leu
 115 120 125
 Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe
 130 135 140
 Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu
 145 150 155 160
 Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
 165 170 175
 Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
 180 185 190
 Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
 195 200 205
 Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
 210 215 220
 Tyr Phe Arg Thr Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
 225 230 235 240
 Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
 245 250 255
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
 260 265 270
 Val Lys Phe Phe Ser Val Gln
 275

<210> 2050

<211> 310

<212> PRT

<213> Homo sapien (3924656-1-75882-77814)

<400> 2050

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu
 20 25 30

Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Il Met Val Thr
 35 40 45
 Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
 115 120 125
 Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu
 130 135 140
 Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Ile Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile
 195 200 205
 Ile Trp Phe Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr
 245 250 255
 Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser
 260 265 270
 Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys
 290 295 300
 Leu Val Ile Cys Arg Glu
 305 310

<210> 2051

<211> 123

<212> PRT

<213> Homo sapien (3962498-1-83664-84695)

<400> 2051

Met Ser Gly Ser Pro Thr Gln Leu Thr Ala Gly Pro Arg Thr Ala Ser
 1 5 10 15
 Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val Leu Ser Tyr Ile
 20 25 30
 Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala Ala Ser Arg Arg
 35 40 45
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Gly Met Val Leu Leu Phe
 50 55 60
 Tyr Gly Thr Gly Ser Ser Thr Tyr Met Arg Pro Thr Thr Arg Tyr Ser
 65 70 75 80
 Pro Leu Glu Gly Arg Leu Ala Ala Val Phe Tyr Ser Ile Leu Ile Pro
 85 90 95
 Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Met Lys Arg
 100 105 110
 Ala Leu Trp Lys Leu Tyr Leu Gln Val Pro Tyr
 115 120

<210> 2052

<211> 343

<212> PRT

<213> Homo sapien (3970959-1-83329-35626)

<220>

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 2052

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
          20           25           30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
          35           40           45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
          50           55           60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
          85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
          100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His
          115          120          125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
          130          135          140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
145          150          155          160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
          165          170          175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
          180          185          190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
          195          200          205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
          210          215          220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
225          230          235          240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
          245          250          255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
          260          265          270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
          290          295          300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
305          310          315          320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
          325          330          335
Tyr Leu Ser Tyr Thr His His
          340

```

<210> 2053

<211> 312

<212> PRT

<213> Homo sapien (3982606-1-1-939)

<400> 2053

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val L u Met Ser
 1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
 20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
 35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
 65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
 85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
 100     105     110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
 115     120     125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
 130     135     140
Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
 145     150     155     160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
 165     170     175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
 180     185     190
Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
 195     200     205
Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
 210     215     220
Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
 225     230     235     240
Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
 245     250     255
Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
 260     265     270
Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
 275     280     285
Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
 290     295     300
Leu Gly Lys Gly Arg Glu Val Gly
 305     310

```

<210> 2054

<211> 104

<212> PRT

<213> Homo sapien (3983513-1-17888-18909)

<220>

<221> VARIANT

<222> (1)...(104)

<223> Xaa = Any Amino Acid

<400> 2054

```

Val Pro Val Arg Cys Pro Gly Arg Val Arg Thr Leu Val Pro Glu Ile
 1      5      10      15
Ile Ser Val Asp Phe Pro Xaa Xaa Thr Leu Ile Xaa Gln Glu Val Tyr
 20      25      30
Gly Leu Leu Ser Thr Phe Pro Leu Phe Ala Gln Gly Val Cys Gly Pro
 35      40      45
Lys Ile Ile Ser Lys Ala Phe Cys Phe Ser Leu Leu Lys Gly Gly Cys
 50      55      60
Ser His Ser Leu Gln Leu Ala Lys Gly Gly Gly Val Leu Arg Lys Ala

```


65 70 75 80
 Gly Thr Leu Gly Met Leu Lys Val Ala Ser Val Cys Cys Ala Tyr His
 85 90 95
 Leu Leu Leu Val Leu Leu Ser Pro
 100

<210> 2055
 <211> 210
 <212> PRT
 <213> Homo sapien (4156137-1-118865-120877)

<220>
 <221> VARIANT
 <222> (1)...(210)
 <223> Xaa = Any Amino Acid

<400> 2055
 Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1 5 10 15
 Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
 20 25 30
 Leu Thr Phe Tyr Met Phe Thr Leu Gly Asn Ser Ala Ile Ile Leu
 35 40 45
 Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
 65 70 75 80
 Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
 85 90 95
 Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Thr Glu
 100 105 110
 Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
 115 120 125
 Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Tyr Leu His
 130 135 140
 Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
 145 150 155 160
 Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
 165 170 175
 Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
 180 185 190
 Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
 195 200 205
 Glu Leu
 210

<210> 2056
 <211> 310
 <212> PRT
 <213> Homo sapien (4156187-1-109107-111440)

<400> 2056
 Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35 40 45
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Ph Phe Leu Ser His
 50 55 60
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met

65		70		75		80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg						
	85		90		95	
Met Met Gln Thr Phe Leu Ph Ser Thr Phe Ala Val Thr Glu Cys Leu						
	100		105		110	
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro						
	115		120		125	
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala						
	130		135		140	
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val						
	145		150		155	
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe						
	165		170		175	
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His						
	180		185		190	
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly						
	195		200		205	
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile						
	210		215		220	
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Cys Thr Cys						
	225		230		235	
Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr Gly Thr Ala Ile Ile						
	245		250		255	
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr						
	260		265		270	
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile						
	275		280		285	
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu						
	290		295		300	
Gly Val Glu Arg Ala Leu						
305		310				

<210> 2057

<211> 127

<212> PRT

<213> Homo sapien (4156187-1-27673-28734)

<220>

<221> VARIANT

<222> (1)...(127)

<223> Xaa = Any Amino Acid

<400> 2057

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe													
1		5		10		15							
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg													
	20		25		30								
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr													
	35		40		45								
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe													
	50		55		60								
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val													
	65		70		75								
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Tyr Phe Val													
	85		90		95								
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu													
	100		105		110								
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile													
	115		120		125								

<210> 2058

<211> 312
 <212> PRT
 <213> Homo sapien (4156187-1-8673-10070)

<220>
 <221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 2058

```

Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
          20           25           30
Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
          35           40           45
Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
          50           55           60
Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
          65           70           75           80
Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
          85           90           95
Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
          100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
          115          120          125
Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
          130          135          140
Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
          145          150          155          160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
          165          170          175
Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
          180          185          190
Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
          195          200          205
Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
          210          215          220
Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys
          225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val
          245          250          255
Val Tyr Leu Val Pro Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile
          260          265          270
Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu
          290          295          300
Gln Lys Lys Arg Thr Met Xaa Met
          305          310

```

<210> 2059
 <211> 315
 <212> PRT
 <213> Homo sapien (4160227-1-768-2100)

<220>
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 2059

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Ph Ile Leu Leu Gly
 1          5          10          15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
          20          25          30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
          35          40          45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
          50          55          60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
65          70          75          80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
          85          90          95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
          100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
          165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
          180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
          195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
          245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
          260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp
305          310          315

```

<210> 2060

<211> 311

<212> PRT

<213> Homo sapien (4190944-1-137143-138613)

<400> 2060

```

Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1          5          10          15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
          20          25          30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
          35          40          45
Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
65          70          75          80
Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
          85          90          95
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp

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```

      100      105      110
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
      115      120      125
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
      130      135      140
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
145      150      155      160
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
      165      170      175
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
225      230      235      240
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Gln Asp Arg Ile Tyr Arg
305      310

```

<210> 2061

<211> 145

<212> PRT

<213> Homo sapien (4190944-1-141327-142434)

<220>

<221> VARIANT

<222> (1)...(145)

<223> Xaa = Any Amino Acid

<400> 2061

```

Met Thr Thr Pro Phe Asn Ser Ser Leu Ile Met Phe Ser Leu Leu Asp
1      5      10      15
Ser Ser Met Pro Glu Ile Leu Cys Pro Leu Pro Tyr Phe Phe Leu Gly
      20      25      30
Ser His Ala Thr His Ser Ser Xaa Leu Ser Ser Leu Thr Leu Ile Asn
      35      40      45
Arg Xaa Asn Met Phe Ser Glu Leu Asn Ser Pro Tyr Phe Ser Ile Glu
      50      55      60
Leu Asn Leu Lys Tyr Leu Tyr Ile Cys Asn Lys Leu Thr Leu Glu Lys
65      70      75      80
Pro Asn Thr Phe Phe Xaa Thr Phe Cys Val Leu Ser Thr Asn Glu Arg
      85      90      95
Pro Met Val Leu Phe Leu Tyr Cys Ile Gln Pro Ala Phe Trp Ile Pro
      100      105      110
Ile Trp Xaa Asn Lys Glu Leu Ala Arg Arg Phe Leu Val Tyr Ser Gln
      115      120      125
Gly Leu Cys Ser Ser Ile Xaa Asp Asn Val Thr Arg Cys Pro Glu Ala
      130      135      140
Cys
145

```

<210> 2062

<211> 318

<212> PRT

<213> Homo sapien (4190944-1-15386-17112)

<400> 2062

```

Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1          5          10          15
Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
          20          25          30
Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
          35          40          45
Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
          50          55          60
Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
          65          70          75          80
Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
          85          90          95
Ala Arg Cys Leu Ala Gln Phe Phe Phe Tyr Ala Phe Gly Val Thr
          100          105          110
Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
          130          135          140
Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
          145          150          155          160
Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
          165          170          175
Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
          180          185          190
Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
          195          200          205
Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
          210          215          220
Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
          225          230          235          240
Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
          245          250          255
Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
          260          265          270
Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
          275          280          285
Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
          290          295          300
Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
          305          310          315

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<210> 2063

<211> 317

<212> PRT

<213> Homo sapien (4190944-1-176262-177597)

<400> 2063

```

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
 1          5          10          15
Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
          20          25          30
Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
          35          40          45
Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
          50          55          60
Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala

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65          70          75          80
Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
      85          90          95
Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
      100          105          110
Asp Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      115          120          125
Ala Ile Arg Asn Pro Leu Leu Tyr Thr Thr Ala Met Ser Gln Arg Leu
      130          135          140
Cys Leu Ala Leu Leu Gly Ala Ser Gly Leu Gly Gly Ala Val Ser Ala
145          150          155          160
Phe Val His Thr Thr Leu Thr Phe Arg Leu Ser Phe Cys Arg Ser Arg
      165          170          175
Lys Ile Asn Ser Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Ile Ser
      180          185          190
Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly
      195          200          205
Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe
      210          215          220
Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg
225          230          235          240
Ala Ala Ser Thr Gly Gly Ser His Leu Thr Ala Val Ala Met Met Tyr
      245          250          255
Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu
      260          265          270
Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser
      275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
      290          295          300
Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln
305          310          315

```

<210> 2064

<211> 314

<212> PRT

<213> Homo sapien (4190944-1-2029-4183)

<400> 2064

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
1          5          10          15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
      20          25          30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
      35          40          45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
      50          55          60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
      85          90          95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
      100          105          110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
      115          120          125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
      130          135          140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
145          150          155          160
Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
      165          170          175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr

```

180 185 190
 Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser
 195 200 205
 Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg
 260 265 270
 Ile Ile Thr Val Val Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met Lys Trp
 290 295 300
 Met Ser Arg Met Gln Thr Phe Phe Phe Arg
 305 310

<210> 2065

<211> 216

<212> PRT

<213> Homo sapien (438406-1-1-648)

<400> 2065

Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
 1 5 10 15
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
 20 25 30
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Gly Ile Cys Gln Ala Leu Thr
 50 55 60
 Tyr Arg Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
 65 70 75 80
 Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Gly Met
 85 90 95
 Ser Thr Leu Asn Phe Cys Gly Pro Asn Val Ile Asn His Phe Tyr Cys
 100 105 110
 Asp Leu Pro Gln Leu Phe Lys Leu Ser Cys Ser Ser Thr Gln Leu Asn
 115 120 125
 Glu Leu Leu Phe Ala Val Gly Phe Ile Met Ala Gly Thr Pro Met
 130 135 140
 Ala Leu Ile Val Ile Ser Tyr Ile His Val Ala Ala Val Leu Arg
 145 150 155 160
 Ile Arg Ser Val Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Ala Ile Phe Tyr Gly Ser Gly Ile Phe Asn Tyr
 180 185 190
 Met Arg Leu Gly Ser Thr Lys Leu Ser Asp Lys Asp Lys Ala Val Gly
 195 200 205
 Ile Phe Asn Thr Val Ile Asn Pro
 210 215

<210> 2066

<211> 318

<212> PRT

<213> Homo sapien (4581418-1-11548-14170)

<400> 2066

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
 1 5 10 15

Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
 20 25 30
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
 35 40 45
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met
 130 135 140
 Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
 145 150 155 160
 Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His
 165 170 175
 Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr
 180 185 190
 Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu
 195 200 205
 Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
 210 215 220
 Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
 245 250 255
 Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
 260 265 270
 Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
 290 295 300
 Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys
 305 310 315

<210> 2067

<211> 257

<212> PRT

<213> Homo sapien (4581418-1-39007-42459)

<220>

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2067

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu
 1 5 10 15
 Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His
 20 25 30
 Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys
 35 40 45
 Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys
 50 55 60
 His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu
 65 70 75 80
 Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser

```
<210> 2068
<211> 309
<212> PRT
<213> Homo sapien (5081803-1-1-930)
```

Met	Lys	Lys	Glu	Asn	Gln	Ser	Phe	Asn	Leu	Asp	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Val	Thr	Ser	Gln	Gln	Glu	Gln	Asn	Asn	Val	Phe	Phe	Val	Ile	Phe	Leu
			20					25					30		
Cys	Ile	Tyr	Pro	Ile	Thr	Leu	Thr	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala
		35					40					45			
Ile	Cys	Ala	Asp	Ile	Arg	Leu	His	Asn	Pro	Met	Tyr	Phe	Leu	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Ile	Ile	Phe	Ser	Ser	Val	Thr	Ile	Pro	Lys
65					70						75				80
Val	Leu	Ala	Asn	His	Leu	Leu	Gly	Ser	Lys	Phe	Ile	Ser	Phe	Gly	Gly
				85					90					95	
Cys	Leu	Met	Gln	Met	Tyr	Phe	Met	Ile	Ala	Leu	Ala	Lys	Ala	Asp	Ser
			100					105					110		
Tyr	Thr	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Ala	Val	Ala	Ile	Ser	Cys
		115					120					125			
Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg	Ser	Cys	Ile	Leu	Leu
	130					135					140				
Ile	Ala	Gly	Ser	Trp	Val	Ile	Gly	Asn	Thr	Ser	Ala	Leu	Pro	His	Thr
145					150					155					160
Leu	Leu	Thr	Ala	Ser	Leu	Ser	Phe	Cys	Gly	Asn	Gln	Glu	Val	Ala	Asn
				165					170					175	
Phe	Tyr	Cys	Asp	Ile	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Val
			180					185					190		
His	Phe	Asn	Val	Lys	Met	Met	Tyr	Leu	Gly	Val	Gly	Val	Phe	Ser	Leu
		195					200					205			
Pro	Leu	Leu	Cys	Ile	Ile	Val	Ser	Tyr	Val	Gln	Val	Phe	Ser	Thr	Val
	210					215					220				
Phe	Gln	Val	Pro	Ser	Thr	Lys	Ser	Leu	Phe	Lys	Ala	Phe	Cys	Thr	Cys
225					230					235					240
Gly	Ser	His	Leu	Thr	Val	Val	Phe	Leu	Tyr	Tyr	Gly	Thr	Thr	Met	Gly

245 250 255
 Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser
 290 295 300
 Lys Arg Ile Ser Ser
 305

<210> 2069

<211> 272

<212> PRT

<213> Homo sapien (5262456-1-1-1993)

<400> 2069

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
 20 25 30
 Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35 40 45
 His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
 65 70 75 80
 Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
 85 90 95
 Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
 100 105 110
 Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
 130 135 140
 Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
 145 150 155 160
 Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
 165 170 175
 Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
 180 185 190
 Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
 195 200 205
 Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
 210 215 220
 Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
 225 230 235 240
 Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
 245 250 255
 Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
 260 265 270

<210> 2070

<211> 356

<212> PRT

<213> Homo sapien (5262456-1-22068-24947)

<220>

<221> VARIANT

<222> (1)... (356)

<223> Xaa = Any Amino Acid

<400> 2070

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
          65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
          130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
          145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
          210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
          225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
          290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
          305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
          340          345          350
Arg Xaa Tyr Pro
          355

```

<210> 2071

<211> 338

<212> PRT

<213> Homo sapien (5679453-1-2929-5456)

<220>

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 2071

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
 1           5           10           15

```

Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Ph Ser Asp Arg Pro
 20 25 30
 Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val
 35 40 45
 Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
 50 55 60
 Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
 65 70 75 80
 Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
 85 90 95
 Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
 100 105 110
 Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130 135 140
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
 145 150 155 160
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
 165 170 175
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
 180 185 190
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
 195 200 205
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
 210 215 220
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
 225 230 235 240
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
 245 250 255
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
 260 265 270
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
 275 280 285
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
 290 295 300
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
 305 310 315 320
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
 325 330 335
 Phe Ile

<210> 2072

<211> 308

<212> PRT

<213> Homo sapien (5791525-1-119325-122054)

<400> 2072

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1 5 10 15
 Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
 20 25 30
 Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
 35 40 45
 Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
 65 70 75 80
 Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
 85 90 95

Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
 100 105 110
 Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
 130 135 140
 Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
 145 150 155 160
 Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
 165 170 175
 Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
 180 185 190
 Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
 195 200 205
 Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
 210 215 220
 Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
 245 250 255
 Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
 260 265 270
 Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
 290 295 300
 Leu Lys Arg Thr
 305

<210> 2073

<211> 314

<212> PRT

<213> Homo sapien (5791525-1-456-2065)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2073

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1 5 10 15
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
 20 25 30
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
 100 105 110
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Val Leu Ser Pro Lys Asn Cys Ala Leu
 130 135 140
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His
 145 150 155 160
 Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Ph Tyr

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      165      170      175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
      180      185      190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Ph
      195      200      205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
      210      215      220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
      225      230      235      240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
      245      250      255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
      260      265      270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
      275      280      285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
      290      295      300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
      305      310

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<210> 2074
 <211> 138
 <212> PRT
 <213> Homo sapien (5823349-1-32238-32756)

<220>
 <221> VARIANT
 <222> (1)...(138)
 <223> Xaa = Any Amino Acid

```

<400> 2074
Leu Met Leu Leu Asp Leu Leu Ser Asp Ala Glu Val His Ala Val Ser
  1           5           10           15
Ser Ser His Cys Ser Leu His Leu Thr Lys Glu Ile Phe Ser Ile Val
      20           25           30
Ser Asn Gln Ala Leu Ser Pro Glu Ser Thr Leu Gly Leu His Met His
      35           40           45
Leu Cys Ala Phe Leu Thr Leu Phe Pro Leu Pro Arg Thr Pro Leu Pro
      50           55           60
Ser Phe Leu Ile His Arg Asn Leu Ile His Leu Ser Ser His Ala Gln
      65           70           75           80
Gln Leu Ser Phe Pro Xaa Leu Leu Xaa Lys Tyr Ser Leu Phe Asn Leu
      85           90           95
Tyr Val Ile Leu Ser Arg Ile Leu Phe Pro Leu His Pro Leu Val Tyr
      100          105          110
Glu Gln Phe Lys Ser Gly Cys Tyr Gly Xaa Phe Ile Ile Lys Ile Leu
      115          120          125
Asn Phe Cys Leu Leu Xaa Val Met Asn Leu
      130          135

```

<210> 2075
 <211> 162
 <212> PRT
 <213> Homo sapien (5931513-1-1-2929)

```

<400> 2075
Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
  1           5           10           15
Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
      20           25           30
Ser Leu Phe Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala

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      35      40      45
Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr
  50      55      60
Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser
65      70      75      80
Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile
      85      90      95
Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
      100      105      110
Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu
      115      120      125
Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu
      130      135      140
Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe
145      150      155      160
Leu Ile

```

<210> 2076

<211> 318

<212> PRT

<213> Homo sapien (6087993-15-1-2211)

<400> 2076

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
  1      5      10      15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
      20      25      30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
      35      40      45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
      50      55      60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu
65      70      75      80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
      85      90      95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
      100      105      110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
      115      120      125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
      130      135      140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145      150      155      160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
      165      170      175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
      180      185      190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val
      195      200      205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
      210      215      220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
225      230      235      240
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
      245      250      255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg
      260      265      270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
      275      280      285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys

```


290 295 300
 Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
 305 310 315

<210> 2077

<211> 314

<212> PRT

<213> Homo sapien (6087993-21-1-3660)

<400> 2077

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu
 1 5 10 15
 Leu Val Gly Ile Pro Gly Leu Glu Ser Gln His Trp Ile Ala Leu
 20 25 30
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35 40 45
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50 55 60
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr
 65 70 75 80
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly
 85 90 95
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser
 100 105 110
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130 135 140
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile
 145 150 155 160
 Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
 165 170 175
 Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
 180 185 190
 Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
 195 200 205
 Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
 210 215 220
 Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
 245 250 255
 Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
 260 265 270
 His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
 275 280 285
 Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
 290 295 300
 Arg Val Leu Arg Val Phe Thr Gln Lys Asp
 305 310

<210> 2078

<211> 327

<212> PRT

<213> Homo sapien (6087993-34-2575-6318)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2078

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
 1 5 10 15
 Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe
 20 25 30
 Cys Phe Met Phe Phe Leu Ser Leu Thr Gly Asn Gly Val Leu Leu Phe
 35 40 45
 Leu Ile Arg Thr Glu Cys Ser Leu Arg Gln Pro Met Phe Leu Phe Leu
 50 55 60
 Ala Met Leu Ser Phe Val Asp Leu Val Leu Ser Leu Ser Thr Leu Pro
 65 70 75 80
 Lys Met Leu Ala Ile Phe Trp Phe Gly Ala Thr Ala Ile Ser Ser His
 85 90 95
 Ser Cys Leu Ser Gln Met Phe Phe Ile His Ala Phe Ser Ala Met Glu
 100 105 110
 Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Ser Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Ala Thr Ile Leu Pro Pro Val Val Ala Lys
 130 135 140
 Ile Gly Gly Leu Val Val Leu Xaa Gly Val Gly Leu Thr Ile Ser Phe
 145 150 155 160
 Pro Ser Leu Ala His Arg Leu His Tyr His Gly Ser His Met Ile Ala
 165 170 175
 Tyr Thr Phe Cys Glu His Met Ala Val Val Lys Leu Ala Cys Glu Ala
 180 185 190
 Thr Thr Val Asp Asn Leu Tyr Ala Phe Val Val Ala Ile Phe Leu Gly
 195 200 205
 Gly Gly Asp Val Val Cys Ile Ala Tyr Ser Tyr Gly Leu Ile Val Arg
 210 215 220
 Thr Val Met His Phe Pro Ser Pro Glu Glu Arg Ala Lys Ala Gly Ser
 225 230 235 240
 Thr Cys Thr Ala His Val Cys Val Ile Leu Phe Phe Tyr Gly Leu Gly
 245 250 255
 Phe Leu Ser Val Val Met Gln Arg Phe Gly Ala Pro Thr Ala Ser Thr
 260 265 270
 Ala Lys Val Ile Leu Ala Asn Leu Tyr Leu Leu Phe Pro Pro Ala Leu
 275 280 285
 Asp Pro Ile Val Tyr Gly Met Glu Thr Lys Gln Ile Xaa Glu Arg Leu
 290 295 300
 Leu Met Ile Leu Ser Pro Lys Gln Ile Glu Leu Thr Xaa Val Xaa Leu
 305 310 315 320
 Ser Pro Ala Gly Leu Gln Gly
 325

<210> 2079

<211> 135

<212> PRT

<213> Homo sapien (6087993-36-10518-12399)

<220>

<221> VARIANT

<222> (1)...(135)

<223> Xaa = Any Amino Acid

<400> 2079

Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1 5 10 15
 Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
 20 25 30
 Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
 35 40 45

Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
 50 55 60
 His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
 65 70 75 80
 Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
 85 90 95
 Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
 100 105 110
 Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
 115 120 125
 Arg Arg Leu Xaa Lys Ile Lys
 130 135

<210> 2080

<211> 141

<212> PRT

<213> Homo sapien (6094601-37-1-3120)

<220>

<221> VARIANT

<222> (1)...(141)

<223> Xaa = Any Amino Acid

<400> 2080

Met Leu Thr Cys Phe Trp Lys His Leu Xaa Tyr Leu Pro Leu Xaa Phe
 1 5 10 15
 Val Asp Phe Val Leu Ser Lys Lys Lys Pro Ser Asn Xaa Ser Val Ser
 20 25 30
 Ile Asn Val Phe Leu Leu Leu Thr Tyr Xaa Xaa Ser Phe Ala Leu Val
 35 40 45
 Tyr Leu Cys Phe Asp Lys Leu Phe Trp Ile Cys Asn Pro Leu Ser Gly
 50 55 60
 Leu Met Thr Leu Arg Arg Thr Arg Cys Ala Gly Ile Leu Gly Ala Cys
 65 70 75 80
 Trp Thr Tyr Ala Phe Thr Ser Thr Ile Arg Xaa Val Phe Phe Phe Phe
 85 90 95
 Asn Leu Lys Asp Lys Leu Phe Phe Gln Met Ser Asn Phe Leu Ser Leu
 100 105 110
 Xaa Glu Leu Met Xaa Gly Pro Phe Phe Leu Glu Asn Ser His Met Tyr
 115 120 125
 Ser Tyr Thr His Lys Leu Cys Leu Leu Phe Xaa Gly Val
 130 135 140

<210> 2081

<211> 315

<212> PRT

<213> Homo sapien (6249440-1-23422-29767)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 2081

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1 5 10 15
 Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
 20 25 30
 Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35 40 45
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

50		55		60
Phe Phe Leu Ser Thr	Leu Ser Ser Leu Glu Met Cys Tyr Ser Il Ser			
65	70	75	80	
Trp Glu Leu Xaa Val	Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile			
	85	90	95	
Ser Tyr Asn Ser Cys Ser Val Gln Met	Ile Thr His Leu Phe Leu Gly			
	100	105	110	
Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val				
	115	120	125	
Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val				
	130	135	140	
Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala				
145	150	155	160	
Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val				
	165	170	175	
Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys				
	180	185	190	
Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe				
	195	200	205	
Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile				
	210	215	220	
Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly				
225	230	235	240	
Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met				
	245	250	255	
Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val				
	260	265	270	
Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr				
	275	280	285	
Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys				
	290	295	300	
Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn				
305	310	315		

<210> 2082

<211> 295

<212> PRT

<213> Homo sapien (6739493-1-1-1041)

<400> 2082

Met Tyr Ser Phe Met Ala Gly Ser Ile Phe Ile Thr Ile Phe Gly Asn	
1	5
Leu Ala Met Ile Ile Ser Ile Ser Tyr Phe Lys Gln Leu His Thr Pro	
	20
Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp Phe Leu Leu Gly	
	35
Phe Thr Ile Met Pro Tyr Ser Met Ile Arg Ser Val Glu Asn Cys Trp	
	50
Tyr Phe Gly Leu Thr Phe Cys Lys Ile Tyr Tyr Ser Phe Asp Leu Met	
65	70
Leu Ser Ile Thr Ser Ile Phe His Leu Cys Ser Val Ala Ile Asp Arg	
	85
Phe Tyr Ala Ile Cys Tyr Pro Leu Leu Tyr Ser Thr Lys Ile Thr Ile	
	100
Pro Val Ile Lys Arg Leu Leu Leu Cys Trp Ser Val Pro Gly Ala	
	115
Phe Ala Phe Gly Ala Val Phe Ser Glu Ala Tyr Ala Asp Gly Ile Glu	
	130
Gly Tyr Asp Ile Leu Val Ala Cys Ser Ser Ser Cys Pro Val Met Phe	
145	150
Asn Lys Leu Trp Gly Thr Thr Leu Phe Met Ala Gly Ph Phe Thr Pro	
	155
	160

Leu 1	Ser	Ser	Met	Cys 5	Leu	Thr	Ile	Val	Met 10	His	Cys	Glu	Phe	Phe 15	Leu
Met	Asp	Leu	Thr 20	Asp	Asp	Pro	Gln	Leu 25	His	Pro	Thr	Phe	Ser 30	Ala	Leu
Phe	Leu	Pro 35	Ile	Tyr	Val	Val	Met 40	Val	Met	Ala	Asn	Leu 45	Gly	Leu	Leu
Ala	Phe 50	Ile	Val	Val	Ser	Pro 55	Gln	Phe	Leu	Thr	Pro 60	Met	Tyr	Phe	Phe
Leu 65	Ser	Asn	Trp	Ser	Ser 70	Val	Asp	Phe	Cys	Tyr 75	Ser	Ser	Val	Thr	Val
Pro	Lys	Ile	Ser	Met 85	Gly	Phe	Phe	Ser	Asp 90	Cys	Gln	Val	Phe 95	Ser	Phe
Ser	Gly	Cys	Met 100	Ala	Gln	Leu	Ser	Cys 105	Phe	Xaa	Ile	Phe	Ala 110	Asp	Thr
Glu	Phe 115	Phe	Leu	Leu	Ala	Ser	Met 120	Val	Tyr	Tyr	Arg	Xaa 125	Glu	Ala	Val
Cys	Asn 130	Pro	Leu	Leu	Tyr	His 135	Ile	Thr	Met	Ser	Pro 140	Lys	Leu	Cys	Leu
Gln 145	Leu	Val	Ala	Thr 150	Ser	Met	Asn	Met	Val	Leu 155	Pro	Ser	Ser	Thr	Ile 160
Phe	His	Leu	Ile 165	Phe	Cys	Lys	Ser	Arg	Ala 170	Ile	Ile	His	Xaa 175	Phe	Cys
Tyr	Phe	Ser	Pro 180	Pro	Pro	Arg	Leu	Xaa 185	Lys	Leu	Ser	Cys	Ser 190	Asp	Met
Gln	Gly 195	Leu	Gln	Leu	Leu	Thr	Phe 200	Ala	Ser	Ser	Ser	Phe 205	Asn	Val	Ser
Val	Ser 210	Arg	Thr	Ile	Phe 215	Leu	Val	Ser	Tyr	Leu 220	Ile	Met	Arg	Met	Pro
Ser 225	Val	Xaa	Gly	Lys 230	His	Cys	Ala	Ser	His 235	Leu	Thr	Ala	Val	Ser	Leu
Cys	Tyr	Gly	Thr 245	Thr	Val	Phe	Leu	His 250	Leu	His	Leu	Ser	Leu 255	Lys	Cys

Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
 260 265 270
 Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys
 275 280 285
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu
 290 295 300

<210> 2084

<211> 274

<212> PRT

<213> Homo sapien (6911343-1-22015-25112)

<220>

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 2084

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1 5 10 15
 Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
 20 25 30
 Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
 35 40 45
 Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
 50 55 60
 Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
 65 70 75 80
 Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
 85 90 95
 Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
 100 105 110
 Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
 115 120 125
 Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
 130 135 140
 Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
 145 150 155 160
 Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
 165 170 175
 Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
 180 185 190
 Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
 195 200 205
 Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
 210 215 220
 Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
 225 230 235 240
 Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
 245 250 255
 Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
 260 265 270
 Ile Leu

<210> 2085

<211> 323

<212> PRT

<213> Homo sapien (6911343-1-65670-69060)

<220>

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 2085

```

Val Glu Asn Ser Pro Met Val Thr Asp Phe Ile Phe Leu Gly Met Thr
1      5      10      15
Asp Asn Ser Gln Leu Glu Val Leu Leu Phe Gly Val Phe Leu Ile Ala
20      25      30
Tyr Ile Ile Thr Val Leu Glu Asn Leu Gly Leu Val Val Leu Ile Arg
35      40      45
Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Gln
50      55      60
Ser Phe Leu Asp Val Cys Phe Ser Ser Ile Thr Ile Pro Gln Asn Leu
65      70      75      80
Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr
85      90      95
Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe
100     105     110
Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu
115     120     125
Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala
130     135     140
Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser
145     150     155     160
Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe
165     170     175
Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile
180     185     190
Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr
195     200     205
Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile
210     215     220
Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys
225     230     235     240
Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr
245     250     255
Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile
260     265     270
Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile
275     280     285
Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu
290     295     300
Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile
305     310     315     320
Leu Xaa Arg

```

<210> 2086

<211> 318

<212> PRT

<213> Homo sapien (7024122-10-14004-16338)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2086

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
1      5      10      15

```

```

Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe
      20      25      30
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met
      35      40      45
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe
      50      55      60
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile
      65      70      75      80
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr
      85      90      95
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr
      100      105      110
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile
      115      120      125
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val
      130      135      140
Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile
      145      150      155      160
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu
      165      170      175
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile
      180      185      190
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile
      195      200      205
Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser
      210      215      220
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser
      225      230      235      240
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val
      245      250      255
Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile
      260      265      270
Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys
      290      295      300
Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile
      305      310      315

```

<210> 2087

<211> 318

<212> PRT

<213> Homo sapien (7024122-5-2648-5354)

<400> 2087

```

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala
  1      5      10      15
Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val
      20      25      30
Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn
      35      40      45
Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro
      50      55      60
Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr
      65      70      75      80
Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr
      85      90      95
Ile Ser Val Gly Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu
      100      105      110
Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe
      115      120      125

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```

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg
 130                135                140
Val Cys Leu Lys Leu Ala Ala Ala Ser Trp Phe Thr Gly Val Val Val
145                150                155                160
Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr
                165                170                175
Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu
                180                185                190
Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser
                195                200                205
Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met
                210                215                220
His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His
225                230                235                240
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe
                245                250                255
Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr
                260                265                270
Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro
                275                280                285
Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu
290                295                300
Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr
305                310                315

```

<210> 2088

<211> 317

<212> PRT

<213> Homo sapien (7024122-6-11866-14009)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2088

```

Met Gly Asp Lys Gly Thr Gly Asn His Ser Asp Val Thr Asp Phe Ile
 1                5                10                15
Leu Glu Gly Phe Arg Val Arg Pro Glu Phe Tyr Ile Leu Leu Phe Phe
                20                25                30
Leu Phe Leu Leu Ile Tyr Ser Met Val Leu Leu Gly Asn Ile Ser Val
                35                40                45
Met Thr Ile Ile Val Thr Asp Ser Gln Leu Asn Thr Pro Met Tyr Phe
50                55                60
Phe Leu Gly Asn Leu Ser Phe Ile Asp Val Ser Tyr Ser Thr Val Ile
65                70                75                80
Ala Pro Lys Ala Met Ala His Phe Leu Ser Glu Lys Lys Thr Val Ser
                85                90                95
Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Phe Ile Val
100                105                110
Thr Glu Gly Phe Val Leu Ala Ala Met Ala Tyr Asp Arg Phe Ser Ala
115                120                125
Ile Cys Asn Pro Leu Leu His Ser Val His Met Ser Arg Arg Leu Cys
130                135                140
Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Trp Ala Ser Ser Ile
145                150                155                160
Leu Gln Val Ser Val Thr Phe Ser Val Ser Phe Cys Ala Ser Arg Val
                165                170                175
Ile Ala His Phe Tyr Cys Asp Ser Tyr Gln Ile Glu Lys Ile Ser Cys
180                185                190
Ser Asn Leu Phe Val Asn Lys Met Val Ser Leu Ser Leu Ser Val Ile

```

195	200	205
Ile Ile Leu Pro Thr Ile Val Val Ile Ile Val Ser Tyr Leu Tyr Ile		
210	215	220
Val Ser Ser Val Leu Lys Ile Pro Ser Ser Glu Gly Arg Lys Lys Asp		
225	230	235
Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu Xaa Gly		
245	250	255
Thr Val Ser Phe Val Tyr Leu Thr Pro Pro Ser Asn Pro Glu Leu Arg		
260	265	270
Lys Val Ala Ser Val Phe Tyr Ile Cys Val Thr Pro Met Leu Asn Pro		
275	280	285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys		
290	295	300
Ile Leu Cys Asn Lys Lys Ala Leu Ser Xaa Phe Tyr Phe		
305	310	315

<210> 2089

<211> 315

<212> PRT

<213> Homo sapien (7107785-12-32121-33524)

<400> 2089

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu		
1	5	10
Ala Gly Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val		
20	25	30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val		
35	40	45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe		
50	55	60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile		
65	70	75
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe		
85	90	95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser		
100	105	110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile		
115	120	125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe		
130	135	140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly		
145	150	155
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val		
165	170	175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys		
180	185	190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu		
195	200	205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile		
210	215	220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala		
225	230	235
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly		
245	250	255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp		
260	265	270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu		
275	280	285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu		
290	295	300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val		

305

310

315

<210> 2090

<211> 141

<212> PRT

<213> Homo sapien (7107785-6-1204-2472)

<220>

<221> VARIANT

<222> (1)...(141)

<223> Xaa = Any Amino Acid

<400> 2090

Arg	Asn	Ile	Arg	Ile	Ser	Leu	Pro	Ile	Tyr	Phe	Leu	Ser	Val	Xaa	Glu
1				5					10					15	
Glu	Arg	Phe	Gly	Arg	Glu	Glu	Phe	Leu	Arg	Val	Trp	Thr	Tyr	Xaa	Leu
			20					25					30		
Ile	Ser	Met	Arg	Asn	Cys	Phe	Leu	Arg	Gly	Cys	Leu	Met	Tyr	Xaa	Met
		35					40					45			
Ile	Phe	Ser	Trp	Ser	Cys	Thr	Glu	Tyr	Val	Val	His	Met	Phe	Phe	Ser
	50					55					60				
Leu	Leu	Asn	Ser	Gly	Ile	Ser	Thr	Glu	Cys	Gln	Ile	Ser	Tyr	Gln	Gln
65				70					75					80	
Asn	Lys	Asp	Ile	Ala	Ile	Phe	Phe	Leu	His	Asn	Leu	Xaa	Xaa	Lys	Glu
			85					90						95	
Asn	Phe	Glu	Ile	Phe	Leu	Tyr	Glu	Asp	Tyr	Cys	Ser	His	Ile	Arg	Asp
		100					105						110		
Leu	Thr	Lys	Ile	Ser	Leu	Gly	Glu	Ala	Gly	Xaa	Asn	Tyr	Xaa	Gly	Lys
		115					120					125			
Ser	Thr	Thr	Ile	Glu	Phe	Leu	Phe	Leu	Ala	Leu	Leu	Phe			
	130					135					140				

<210> 2091

<211> 202

<212> PRT

<213> Homo sapien (7134787-10-3417-6169)

<220>

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 2091

Ile	Phe	Ala	Ile	Leu	Thr	Thr	Ile	Asp	Cys	Cys	Val	Phe	Val	Trp	Glu
1				5					10					15	
Phe	Leu	Glu	Cys	Thr	Val	Phe	Val	Asn	Lys	Arg	Ala	Cys	Ala	Gln	Leu
			20					25					30		
Ala	Cys	Gly	Ala	Phe	Cys	Ile	Gly	Leu	Ile	Met	Thr	Val	Val	Xaa	Ile
		35					40					45			
Thr	Thr	Val	Ser	Gln	Arg	Tyr	Lys	Arg	Ser	Thr	Tyr	Ala	Ile	Val	Asp
	50					55					60				
Cys	Phe	Leu	Phe	Asp	Thr	Leu	Leu	Val	Met	Lys	Leu	Ser	Cys	Ile	Asp
65				70					75					80	
Asn	Thr	Ile	Tyr	Glu	Ile	Ile	Gln	Tyr	Phe	Ile	His	His	Thr	Cys	Val
			85				90						95		
Gln	Val	Ser	Met	Gly	Leu	Val	Cys	Ile	Ser	Tyr	Ile	Asp	Ile	Pro	Val
		100					105					110			
Thr	Ser	Ile	Val	Leu	Arg	Ile	Ser	Xaa	Ser	Glu	Val	Phe	Ala	Thr	Cys
		115					120					125			
Val	Pro	Gln	Pro	Pro	Pro	His	His	Gly	His	Cys	Leu	Tyr	Val	Cys	Ala
	130					135					140				

Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly
 145 150 155 160
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile Ile His Ser Ala Ser Gly Pro
 165 170 175
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg
 180 185 190
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile
 195 200

<210> 2092

<211> 276

<212> PRT

<213> Homo sapien (7134787-7-358-5219)

<400> 2092

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
 20 25 30
 Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
 35 40 45
 Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
 65 70 75 80
 Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
 85 90 95
 Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
 130 135 140
 Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
 145 150 155 160
 Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
 165 170 175
 Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
 180 185 190
 Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
 195 200 205
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
 210 215 220
 Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
 225 230 235 240
 Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
 260 265 270
 Leu Ser Val Thr
 275

<210> 2093

<211> 310

<212> PRT

<213> Homo sapien (7139676-7-1545-4565)

<400> 2093

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu

20 25 30
 Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
 35 40 45
 Ala S r Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
 50 55 60
 Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
 65 70 75 80
 Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
 85 90 95
 Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
 100 105 110
 Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
 130 135 140
 Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
 145 150 155 160
 Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
 165 170 175
 Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
 180 185 190
 Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
 195 200 205
 Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
 210 215 220
 Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
 225 230 235 240
 His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
 245 250 255
 Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
 260 265 270
 Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
 275 280 285
 Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
 290 295 300
 Ile Thr Asp Asp Lys Arg
 305 310

<210> 2094

<211> 311

<212> PRT

<213> Homo sapien (7139676-9-1-2285)

<400> 2094

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
 20 25 30
 Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
 35 40 45
 Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50 55 60
 Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
 65 70 75 80
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
 85 90 95
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
 100 105 110
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile

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      130              135              140
Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu
145              150              155              160
Thr Ile Phe Val Pro Phe Cys Gly Pr Asn Glu Ile Asp His Tyr Phe
      165              170              175
Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met
      180              185              190
Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr
      195              200              205
Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg
      210              215              220
Ala Tyr Ser Ala Glu Arg Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser
      225              230              235              240
His Val Ile Val Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr
      245              250              255
Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe
      260              265              270
Tyr Thr Ile Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg
      275              280              285
Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile
      290              295              300
Leu Leu Lys Arg Asn Gln Leu
305              310

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<210> 2095

<211> 319

<212> PRT

<213> Homo sapien (7144617-1-1-995)

<400> 2095

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Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
1      5      10      15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20      25      30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35      40      45
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
      50      55      60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
      65      70      75      80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
      85      90      95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
      100      105      110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
      115      120      125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
      130      135      140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
      145      150      155      160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
      165      170      175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
      180      185      190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
      195      200      205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
      210      215      220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
      225      230      235      240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser

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1231

<210> 2097
 <211> 247
 <212> PRT
 <213> Homo sapien (7144976-1-1-1194)

<220>
 <221> VARIANT
 <222> (1)...(247)
 <223> Xaa = Any Amino Acid

<400> 2097
 Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
 20 25 30
 Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
 35 40 45
 Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
 50 55 60
 Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
 65 70 75 80
 Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
 85 90 95
 Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
 100 105 110
 Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
 115 120 125
 Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
 130 135 140
 Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
 145 150 155 160
 Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
 165 170 175
 Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
 180 185 190
 Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
 195 200 205
 Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
 210 215 220
 Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
 225 230 235 240
 Arg Pro Ile Leu Gly Asn Ser
 245

<210> 2098
 <211> 329
 <212> PRT
 <213> Homo sapien (7145001-12-25597-26388)

<220>
 <221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 2098
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu
 20 25 30
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile

35	40	45
Ile Phe Ile Ser Pro Ala Leu Gly Ser Pro Met Tyr Ser Phe Pro Ser		
50	55	60
Tyr Leu Phe Ile Ile Asp Ile Phe Cys Ser Ser Ile Ala Pro Lys		
65	70	75
Met Asn Phe Asp Leu Ile Ser Glu Lys Asn Thr Ile Ser Phe Asn Gly		
	85	90
Cys Met Thr Gln Leu Phe Thr Glu His Phe Phe Thr Glu His Phe Phe		
	100	105
Glu Ala Ala Glu Ile Ile Leu Leu Ser Val Met Ala Tyr Asp His Tyr		
	115	120
Val Ala Ile Arg Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro		
	130	135
Met Cys Gly Phe Leu Met Val Val Ala Gly Ile Leu Gly Phe Val His		
145	150	155
Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro		
	165	170
Asn Val Ile Asn His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu		
	180	185
Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser		
	195	200
Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val		
	210	215
Ile Ile Leu Cys Phe Leu Arg Thr His Ser Ser Glu Gly Arg Arg Lys		
225	230	235
Ala Leu Ser Ser Cys Ala Ser His Ile Phe Ile Val Ile Leu Phe Phe		
	245	250
Val Pro Phe Ser Tyr Leu Tyr Leu Arg Pro Ile His Ser Phe Pro Thr		
	260	265
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu Asn		
	275	280
Pro Leu Ile Tyr Thr Leu Lys Asn Lys Glu Val Lys Asn Val Ile Lys		
	290	295
Lys Leu Trp Lys Gln Ile Met Thr Thr Asp Asp Lys Xaa Val Leu Xaa		
305	310	315
His Lys His Leu Gly Lys Asn Ile Trp		
	325	

<210> 2099

<211> 264

<212> PRT

<213> Homo sapien (7145001-12-45102-50811)

<400> 2099

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala	
1	5
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp	
	20
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu	
	35
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe	
	50
Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met	
65	70
Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile	
	85
Thr Met Asn Arg Gln Val Cys Gly Leu Val Ala Met Ala Trp Val	
	100
Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu	
	115
Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe	
	120
	125

130 135 140
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe
 145 150 155 160
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu
 165 170 175
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser
 180 185 190
 Thr Cys Ala Phe His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys
 195 200 205
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala
 210 215 220
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile
 225 230 235 240
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp
 245 250 255
 Ser Gln Ile Ile Trp Gly Asn Asn
 260

<210> 2100

<211> 309

<212> PRT

<213> Homo sapien (7145001-8-11112-14684)

<400> 2100

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1 5 10 15
 Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
 20 25 30
 His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
 35 40 45
 Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
 50 55 60
 Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
 65 70 75 80
 Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
 100 105 110
 Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
 115 120 125
 His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
 130 135 140
 Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
 145 150 155 160
 Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
 165 170 175
 Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
 180 185 190
 Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
 195 200 205
 Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
 210 215 220
 Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
 225 230 235 240
 His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
 245 250 255
 Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
 260 265 270
 Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg

290
Ser Leu Gly Glu Lys
305

295

300

<210> 2101
<211> 296
<212> PRT
<213> Homo sapien (7145013-16-7265-9434)

<400> 2101
Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met
1 5 10 15
Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His
20 25 30
Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu
35 40 45
Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg
50 55 60
Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr
65 70 75 80
Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Thr Val Met Ser Tyr
85 90 95
Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met
100 105 110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
115 120 125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
130 135 140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
145 150 155 160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
165 170 175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
180 185 190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
195 200 205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
210 215 220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
225 230 235 240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
245 250 255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
260 265 270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
275 280 285
Glu Lys Arg Met Arg Ala Val Leu
290 295

<210> 2102
<211> 162
<212> PRT
<213> Homo sapien (7211526-1-1-487)

<400> 2102
Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30
Pro Leu Val His Val Ser Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45

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Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50                      55                      60
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Phe Ile Phe Gly
65                      70                      75                      80
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
                        85                      90                      95
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
          100                      105                      110
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
          115                      120                      125
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
          130                      135                      140
Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145                      150                      155                      160
Leu Leu

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<210> 2103
<211> 162
<212> PRT
<213> Homo sapien. (7211533-1-1-487)

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<220>
<221> VARIANT
<222> (1)...(162)
<223> Xaa = Any Amino Acid

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<400> 2103
Met Ala Ile Val Asn Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile
 1                      5                      10                      15
Val Cys Ile Val Leu Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Ser
          20                      25                      30
Ser Leu Thr His Thr Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro
          35                      40                      45
Asn Val Ile Ser His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu
          50                      55                      60
Ser Cys Ser Glu Thr Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser
65                      70                      75                      80
Gly Ile Ile Ala Thr Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile
          85                      90                      95
Phe Ile Val Ala Ala Ile Leu Arg Ile Arg Xaa Glu Ala Gly Arg Arg
          100                      105                      110
Lys Ala Phe Ser Thr Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe
          115                      120                      125
Tyr Gly Ser Ile Ser Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser
          130                      135                      140
Leu Glu Gln Glu Lys Val Val Ser Val Phe Tyr Thr Leu Val Val Pro
145                      150                      155                      160
Met Leu

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<210> 2104
<211> 162
<212> PRT
<213> Homo sapien (7211534-1-1-485)

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<400> 2104
Val Gly Ile Cys Asn Pro Leu Leu Tyr Thr Val Thr Met Ser Pro Gln
 1                      5                      10                      15
Lys Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ile Phe Gly
          20                      25                      30

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Ser Phe Cys Gly Asp
 35 40 45
 Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
 50 55 60
 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Val Phe Ile Ile Val
 65 70 75 80
 Thr Val Gly Ile Gly Val Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly
 85 90 95
 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
 115 120 125
 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
 130 135 140
 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro
 145 150 155 160
 Met Phe

<210> 2105

<211> 162

<212> PRT

<213> Homo sapien (7211536-1-1-487)

<400> 2105

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
 1 5 10 15
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
 20 25 30
 Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
 35 40 45
 Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
 65 70 75 80
 Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
 85 90 95
 Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
 115 120 125
 Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 130 135 140
 Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
 145 150 155 160
 Leu Leu

<210> 2106

<211> 162

<212> PRT

<213> Homo sapien (7211538-1-1-487)

<400> 2106

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15
 Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
 20 25 30
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45
 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

```

      50      55      60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65      70      75      80
Val Val Val Ile Thr Leu Pr  Phe Met Cys Il  Leu Val Ser Tyr Gly
      85      90      95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100      105      110
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115      120      125
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130      135      140
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145      150      155      160
Met Leu

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<210> 2107

<211> 159

<212> PRT

<213> Homo sapien (7211540-1-1-478)

<400> 2107

```

Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln
1      5      10      15
Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His
      20      25      30
Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
      35      40      45
Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu
      50      55      60
Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser
65      70      75      80
Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala
      85      90      95
Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys
      100      105      110
Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe
      115      120      125
Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
      130      135      140
Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu
145      150      155

```

<210> 2108

<211> 162

<212> PRT

<213> Homo sapien (7211541-1-1-488)

<400> 2108

```

Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys
1      5      10      15
Val Cys Leu Cys Leu Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn
      20      25      30
Gly Leu Ser Gln Thr Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro
      35      40      45
Asn Asp Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu
      50      55      60
Ala Cys Ser Asp Thr Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala
65      70      75      80
Gly Ser Asn Leu Ile Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr
      85      90      95

```

Phe Ile Phe Thr Ala Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg
 100 105 110
 Lys Ala Phe Ser Thr Cys Gly Ser His Val Thr Ala Val Thr Val Phe
 115 120 125
 Tyr Gly Thr Leu Phe Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser
 130 135 140
 Ile Gln Gln Gly Lys Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro
 145 150 155 160
 Met Leu

<210> 2109
 <211> 162
 <212> PRT
 <213> Homo sapien (7211542-1-1-487)

<400> 2109
 Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
 1 5 10 15
 Leu Cys Thr Leu Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr
 20 25 30
 Ile Phe Pro Pro Leu Met Leu Leu Gln Leu Asp Tyr Cys Ala Ser
 35 40 45
 Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60
 Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
 65 70 75 80
 Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
 85 90 95
 Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
 115 120 125
 Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
 130 135 140
 Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
 145 150 155 160
 Met Leu

<210> 2110
 <211> 243
 <212> PRT
 <213> Homo sapien (7230851-8-1-2360)

<220>
 <221> VARIANT
 <222> (1)...(243)
 <223> Xaa = Any Amino Acid

<400> 2110
 Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser
 1 5 10 15
 Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser
 20 25 30
 Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 35 40 45
 Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys
 50 55 60
 Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met
 65 70 75 80

```

Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
      85      90      95
Gly Ser Pro Ile Pr  Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
      100      105      110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Leu Val Leu
      115      120      125
Ile His Pro Ile Xaa Ile Xaa Arg Cys Lys Leu Ile Ile Leu Leu Tyr
      130      135      140
Glu Pro Phe Lys Ile Ile Glu Asp Ser Tyr Val Leu Phe Leu Ile Ile
      145      150      155      160
Thr Ile Leu Ser Ser His Xaa Leu Ile His Asn Cys Xaa Xaa Val Met
      165      170      175
Asp Phe Leu Leu Lys Gln Pro Leu Phe Tyr His Leu Met Leu Leu Val
      180      185      190
Met Gln Gln Leu Thr Leu Asn Ala Leu Phe Ile Phe Xaa Thr Xaa Xaa
      195      200      205
Leu Leu Leu Thr Ser Leu Xaa Asp Leu Lys Ile Ser Leu Cys Thr Val
      210      215      220
Val Ser Gln Xaa Ile Thr Thr Ile Ile Leu Lys Asn Lys Ile Lys Val
      225      230      235      240
Val Ser Met

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<210> 2111

<211> 313

<212> PRT

<213> Homo sapien (7239533-11-790-4930)

<220>

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 2111

```

Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser
  1      5      10      15
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn
      20      25      30
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys
      35      40      45
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn
      50      55      60
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val
      65      70      75      80
Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe
      85      90      95
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His
      100      105      110
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg
      115      120      125
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Leu Gly Leu Ile
      130      135      140
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly
      145      150      155      160
Ser Asn Lys Ile Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys
      165      170      175
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn
      180      185      190
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr
      195      200      205
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys

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210	215	220
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe		
225	230	235
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu		240
	245	250
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn		255
	260	265
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg		270
	275	280
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys		285
	290	295
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr		300
305	310	

<210> 2112

<211> 311

<212> PRT

<213> Homo sapien (7239533-19-11510-15318)

<400> 2112

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly		
1	5	10
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu		15
	20	25
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu		30
	35	40
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser		45
	50	55
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys		60
65	70	75
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly		80
	85	90
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val		95
	100	105
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn		110
	115	120
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu		125
	130	135
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu		140
145	150	155
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His		160
	165	170
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile		175
	180	185
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser		190
	195	200
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr		205
	210	215
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr		220
225	230	235
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu		240
	245	250
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys		255
	260	265
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val		270
	275	280
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val		285
	290	295
Met Gly Ser Lys Ile His Ser		300
305	310	

<210> 2113
 <211> 287
 <212> PRT
 <213> Homo sapien (7239533-20-19626-20657)

<220>
 <221> VARIANT
 <222> (1)...(287)
 <223> Xaa = Any Amino Acid

<400> 2113

Tyr	Ile	Leu	Leu	Asp	Ile	Tyr	Ile	Cys	Leu	Asn	Asn	Thr	His	Val	Xaa
1				5					10					15	
Leu	Cys	Val	Glu	Ser	Gln	Arg	Gln	Phe	Lys	Ile	Ser	Phe	Tyr	Phe	Ser
		20						25					30		
Phe	Phe	Leu	Leu	Ala	Ile	Thr	Xaa	Phe	Xaa	Xaa	Xaa	Ile	Leu	Ile	Ile
		35					40					45			
Met	Lys	Thr	Xaa	Gln	Tyr	Phe	Leu	Lys	His	Lys	His	Leu	Lys	Lys	Lys
	50				55						60				
Phe	Ser	Xaa	Cys	Leu	Val	Tyr	Ile	Leu	Thr	Tyr	Ile	Leu	Ser	Leu	Xaa
65				70					75					80	
Ser	Lys	Phe	Phe	Ala	Leu	Cys	Xaa	Ile	Phe	Ala	Asp	Lys	Ala	Phe	Gln
				85					90					95	
Glu	Gln	Val	Ser	Gly	Asn	Xaa	Xaa	Ser	Arg	Ser	Xaa	Glu	Ser	Pro	Val
		100						105					110		
His	Tyr	Thr	Leu	Thr	Met	Ser	Gln	Lys	Phe	Cys	Ser	Ile	His	Pro	Ala
	115						120					125			
Gly	Cys	Tyr	Asp	Gln	Gly	Ile	Xaa	Ser	Ile	Pro	Gly	His	Ser	Phe	Ser
	130					135					140				
His	Cys	Ile	Ala	Tyr	Cys	Gly	His	Asn	Val	Val	Asn	Ile	Phe	Xaa	Asn
145				150					155					160	
Lys	Tyr	Ser	Val	Ala	Ile	Ser	Asp	Ser	Cys	Ser	Ser	Ser	Trp	Ile	Ala
			165						170					175	
Asp	Phe	Cys	Leu	Phe	Val	Cys	Phe	Ala	Leu	Val	Asn	Phe	Asp	Xaa	Leu
			180					185					190		
Arg	Asn	Leu	Arg	Val	Leu	Leu	Leu	Ser	Phe	His	Phe	Gln	Leu	Val	Xaa
	195							200					205		
Lys	Ala	Leu	Ser	Ala	Ser	Ala	His	Gln	Pro	Ser	Pro	Pro	Ile	Ser	His
	210					215					220				
Ile	Ser	Thr	Ile	Phe	Leu	Thr	Leu	Val	Pro	Asn	Ser	Lys	Asn	Ser	Gln
225				230					235					240	
Ala	Ile	Val	Lys	Ala	His	Ser	Val	Cys	Tyr	Ala	Met	Leu	Ile	Pro	Met
			245						250					255	
Leu	Asn	Ser	Gln	Thr	Cys	Ser	Met	Arg	Tyr	Lys	Asn	Val	Asn	Glu	Ser
		260						265					270		
Leu	Gln	Lys	Leu	Met	Asp	Phe	Lys	Ile	Phe	Xaa	His	Xaa	Lys	Gln	
	275						280					285			

<210> 2114
 <211> 256
 <212> PRT
 <213> Homo sapien (7239533-8-1261-3491)

<400> 2114

Met	Tyr	Phe	Phe	Leu	Ser	His	Leu	Ser	Phe	Leu	Asp	Thr	Cys	Tyr	Ser
1				5					10					15	
Asn	Val	Phe	Thr	Pro	Lys	Leu	Leu	Glu	Ile	Leu	Val	Val	Glu	Asp	Arg
		20						25					30		
Thr	Ile	Ser	Phe	Lys	Gly	Cys	Met	Val	Gln	Phe	Phe	Phe	Gly	Cys	Ala
		35					40					45			
Phe	Val	Ile	Thr	Glu	Met	Phe	Met	Leu	Ala	Val	Met	Ala	Tyr	Asp	Leu

50	55	60
Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro		
65	70	75
Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly L u		80
	85	90
Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly		95
	100	105
Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser		110
	115	120
Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile		125
	130	135
Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr		140
145	150	155
Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro		160
	165	170
Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile		175
	180	185
Phe His Gly Val Ile Leu Leu Leu Tyr Cys Val Pro Asn Ser Lys Ser		190
	195	200
Ser Trp Leu Leu Val Lys Val Ala Thr Val Leu Phe Thr Val Ile Ile		205
	210	215
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys		220
225	230	235
Gly Thr Val Arg Lys Leu Ile Asn Ser Gln Ser Pro Phe His Ser Lys		240
	245	250
		255

<210> 2115

<211> 314

<212> PRT

<213> Homo sapien (7239533-9-1-1650)

<400> 2115

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu		
1	5	10
Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val		15
	20	25
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile		30
	35	40
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe		45
	50	55
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr		60
65	70	75
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr		80
	85	90
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr		95
	100	105
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile		110
	115	120
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala		125
	130	135
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val		140
145	150	155
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile		160
	165	170
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser		175
	180	185
Asp Ile Leu Ile Pro His Leu Leu Phe Ser Phe Ala Thr Phe Asn		190
	195	200
Glu Met Cys Thr Leu Leu Ile Leu Thr Ser Tyr Val Phe Ile Phe		205
210	215	220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe		

225 230 235 240
 Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
 260 265 270
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
 275 280 285
 Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
 290 295 300
 Lys Leu Ile His Thr Gln Val Pro Phe His
 305 310

<210> 2116

<211> 308

<212> PRT

<213> Homo sapien (7239554-20-1-1871)

<400> 2116

Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe
 1 5 10 15
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe
 20 25 30
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile
 35 40 45
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn
 50 55 60
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala
 65 70 75 80
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys
 85 90 95
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu
 100 105 110
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala
 130 135 140
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly
 145 150 155 160
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe
 165 170 175
 Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val
 195 200 205
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile
 210 215 220
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr
 245 250 255
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu
 260 265 270
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe
 290 295 300
 Pro Phe Phe Arg
 305

<210> 2117

<211> 157

<212> PRT
 <213> Homo sapien (7239554-9-1-1342)

<220>
 <221> VARIANT
 <222> (1)...(157)
 <223> Xaa = Any Amino Acid

<400> 2117
 Met Gly Glu Ala Arg Asn Arg Thr Val Val Gln Glu Phe Ile Leu Glu
 1 5 10 15
 Gly Phe Pro Ala Val Gln His Leu Gly Asn Val Leu Phe Leu Val His
 20 25 30
 Leu Leu Ala Tyr Leu Ala Ser Ile Met Ala Asn Met Leu Ile Ile Thr
 35 40 45
 Ile Thr Trp Ala Asp His His Leu Gln Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Ser Phe Ser Phe Cys Glu Cys Cys Phe Ile Thr Thr Val Ile Pro
 65 70 75 80
 Lys Leu Leu Val Ile Leu Leu Ser Gly Arg Ala Lys Ile Pro Leu Ser
 85 90 95
 Thr Thr Leu Ser His Ala Val Pro Phe Ser Phe Leu Tyr Ser Trp Val
 100 105 110
 Asn Ser Phe Ser Ser Leu Asn Gly Cys Asp Val Pro Leu Asp Xaa Tyr
 115 120 125
 Leu Ala Ile Cys Lys Pro Leu His Tyr Ser Thr Ile Met Ser Leu Arg
 130 135 140
 Thr Ser Phe His Lys Val Thr Ala Trp Leu Cys Pro Gly
 145 150 155

<210> 2118
 <211> 129
 <212> PRT
 <213> Homo sapien (7239558-10-440-1325)

<400> 2118
 Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1 5 10 15
 Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
 20 25 30
 Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
 35 40 45
 Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
 65 70 75 80
 Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro

<210> 2119
 <211> 313
 <212> PRT
 <213> Homo sapien (7248974-19-1-3170)

<220>

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 2119

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1          5          10          15
Pro Gly Ser Gln Glu Val Arg Arg Ile Leu Phe Val Asn Phe Phe Phe
          20          25          30
Leu Tyr Ala Val Thr Val Met Gly Asn Thr Val Ile Ile Val Thr Val
          35          40          45
Cys Val Asp Lys His Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
          50          55          60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Ala Pro Phe Met
65          70          75          80
Leu Trp Gly Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
          85          90          95
Cys Ala Ala Gln Leu Leu Tyr Leu Ser Leu Gly Thr Ser Glu Leu Ala
          100          105          110
Leu Met Gly Val Met Ala Val Asp His Tyr Val Ala Val Cys Asn Pro
          115          120          125
Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Cys Val Trp Met Val
          130          135          140
Ile Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val Tyr
          145          150          155          160
Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Asn Val Leu Asp His Phe
          165          170          175
Tyr Cys Asp Xaa Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr Leu
          180          185          190
Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile Gly
          195          200          205
Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr Ile
          210          215          220
Leu Lys Ile Pro Leu Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr Cys
          225          230          235          240
Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Ser Ser Cys Leu Phe
          245          250          255
Leu Tyr Thr Lys Pro Lys Gln Thr Gln Ala Ala Lys Tyr Asn Arg Ile
          260          265          270
Ala Ser Leu Leu Val Leu Val Val Thr Pro Phe Leu Asn Pro Phe Ile
          275          280          285
Phe Thr Leu Arg Asn Asp Lys Phe Ile Gln Ala Phe Gly Asp Gly Met
          290          295          300
Lys His Cys Tyr Gln Leu Leu Arg Ile
          305          310

```

<210> 2120

<211> 138

<212> PRT

<213> Homo sapien (7248974-26-1-596)

<220>

<221> VARIANT

<222> (1)...(138)

<223> Xaa = Any Amino Acid

<400> 2120

```

Leu Leu Ser Leu Trp Ile Phe Thr Leu Phe Cys Tyr Tyr Val Xaa Tyr
 1          5          10          15
Cys Asp Glu Lys Pro Leu Phe Val Tyr Thr Leu Ile Pro Lys Cys Val
          20          25          30

```

Ser Asp Ile Xaa Gly Met Asn Phe Tyr Lys Cys Asn Cys Trp Val Met
 35 40 45
 Gly Met Ser Asn Phe Asn Ser Phe Tyr Gln Val Phe Ile Glu His Arg
 50 55 60
 Val Phe Ile Val Xaa Pro Ala Val Gly Gly Cys Phe Phe Ile Val Ser
 65 70 75 80
 Asn Ile Val Cys Xaa Xaa Thr Leu Gly Lys Lys Leu Asn Ile Phe Ile
 85 90 95
 Lys Ser Asn Ser His Leu Thr Thr Ile Ser Ile Tyr Gln Arg Gly Gly
 100 105 110
 Met Val Thr Trp Ile Gly His Ser Asn Ser Ser Ser Tyr Gln Xaa Thr
 115 120 125
 Xaa Asp Tyr Ser Leu Leu Tyr Xaa Leu Ile
 130 135

<210> 2121
 <211> 161
 <212> PRT
 <213> Homo sapien (7248974-31-3444-4455)

<220>
 <221> VARIANT
 <222> (1)...(161)
 <223> Xaa = Any Amino Acid

<400> 2121
 Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser
 20 25 30
 Ile Val Ile Arg Asn Tyr Val Ile Ile Val Cys Val Glu Lys Cys
 35 40 45
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu
 50 55 60
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr
 65 70 75 80
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu
 85 90 95
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val
 100 105 110
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn
 115 120 125
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu
 130 135 140
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu
 145 150 155 160
 Pro

<210> 2122
 <211> 169
 <212> PRT
 <213> Homo sapien (7249005-11-1-1318)

<220>
 <221> VARIANT
 <222> (1)...(169)
 <223> Xaa = Any Amino Acid

<400> 2122
 Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe

```

1           5           10           15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
                20                25                30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
        35                40                45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
        50                55                60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
65                70                75                80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
                85                90                95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
        100                105                110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
        115                120                125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
        130                135                140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
145                150                155                160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
                165

```

<210> 2123

<211> 110

<212> PRT

<213> Homo sapien (7249007-9-15200-16107)

<220>

<221> VARIANT

<222> (1)...(110)

<223> Xaa = Any Amino Acid

<400> 2123

```

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
1           5           10           15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
        20                25                30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
        35                40                45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
        50                55                60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65                70                75                80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
        85                90                95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
        100                105                110

```

<210> 2124

<211> 241

<212> PRT

<213> Homo sapien (7249007-9-22951-24848)

<220>

<221> VARIANT

<222> (1)...(241)

<223> Xaa = Any Amino Acid

<400> 2124

```

Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
1           5           10           15

```



```

Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
      20                25                30
Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
      35                40                45
Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
      50                55                60
Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
      65                70                75                80
His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
      85                90                95
Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
      100               105               110
Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
      115               120               125
Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
      130               135               140
Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
      145               150               155               160
His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
      165               170               175
Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
      180               185               190
Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
      195               200               205
Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
      210               215               220
Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
      225               230               235               240
Pro

```

<210> 2125

<211> 318

<212> PRT

<213> Homo sapien (7249162-23-8972-11111)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2125

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
  1                5                10                15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
      20                25                30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
      35                40                45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
      50                55                60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
      65                70                75                80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
      85                90                95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
      100               105               110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
      115               120               125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
      130               135               140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro

```

145					150					155				160
Asp	Val	Phe	Leu	Val	Lys	Arg	Leu	Pro	Phe	Cys	His	Ser	Asn	Leu
				165					170					175
Pro	His	Thr	Tyr	Cys	Glu	His	Met	Ala	Val	Ala	Lys	Phe	Ala	Cys
			180					185					190	
Asp	Ile	His	Val	Asn	Val	Trp	Tyr	Gly	Leu	Ser	Val	Leu	Leu	Tyr
		195					200					205		
Val	Val	Leu	Asp	Ala	Leu	Leu	Ile	Leu	Val	Ser	Xaa	Ser	Phe	Ile
		210				215					220			
Tyr	Thr	Gly	Phe	His	Leu	Pro	Ser	Pro	Gly	Ala	Arg	Gln	Lys	Ala
225					230					235				240
Gly	Thr	Cys	Gly	Ser	Pro	Leu	Arg	Val	Ile	Ser	Met	Phe	Tyr	Leu
				245					250					255
Gly	Ile	Phe	Thr	Ile	Ile	Thr	Gln	Arg	Phe	Gly	His	His	Val	Pro
			260					265					270	
His	Thr	His	Ile	Leu	Leu	Gly	Asn	Val	Trp	Val	Leu	Ala	Pro	Pro
		275					280					285		Met
Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Ile	Asn	Thr	Arg	Gln	Ile	Gln	Glu
	290					295					300			Cys
Val	Leu	Ser	Leu	Leu	Ser	Ser	Gln	Arg	Lys	Xaa	Cys	Xaa	Ile	
305					310					315				

<210> 2126

<211> 322

<212> PRT

<213> Homo sapien (7249220-22-20773-24242)

<220>

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 2126

Met	Ser	Val	Val	Glu	Ala	Asn	Asn	Ile	Ser	Gly	Pro	Val	Ser	Glu	Phe
1				5					10					15	
Ile	Leu	Leu	Gly	Phe	Pro	Cys	Arg	Cys	Arg	Glu	Thr	Lys	Ile	Leu	Leu
			20					25					30		
Phe	Val	Val	Phe	Ser	Leu	Ile	Tyr	Leu	Leu	Thr	Leu	Met	Gly	Asn	Thr
		35				40						45			
Ser	Ile	Ile	Cys	Ala	Val	Trp	Ser	Ser	Gln	Lys	Leu	His	Thr	Pro	Met
	50					55					60				
Tyr	Ile	Leu	Leu	Ala	Asn	Phe	Ser	Phe	Leu	Glu	Ile	Cys	Cys	Ile	Ser
65				70					75					80	
Ser	Asp	Val	Pro	Asn	Met	Leu	Ala	Asn	Leu	Ile	Ser	His	Ile	Lys	Ser
				85				90						95	
Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Leu	Gln	Phe	Phe	Tyr	Phe	Ser	Met	Cys
		100						105					110		
Ala	Ala	Glu	Gly	Tyr	Phe	Leu	Ser	Val	Met	Ser	Phe	Asp	Arg	Phe	Leu
		115					120					125			
Thr	Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Thr	Val	Met	Thr	His	His	Leu
	130					135					140				
Cys	Val	Xaa	Leu	Val	Ala	Phe	Cys	Arg	Ala	Gly	Gly	Phe	Leu	Ser	Ile
145				150					155					160	
Leu	Met	Pro	Ala	Val	Leu	Met	Ser	Arg	Val	Pro	Phe	Cys	Gly	Pro	Asn
				165					170					175	
Ile	Thr	Asp	His	Phe	Phe	Cys	Asn	Leu	Gly	Pro	Leu	Leu	Ala	Leu	Ser
		180						185					190		
Cys	Ala	Pro	Val	Pro	Lys	Thr	Thr	Leu	Thr	Cys	Ala	Thr	Val	Ser	Ser
		195					200					205			
Leu	Ile	Ile	Phe	Ile	Thr	Phe	Leu	Tyr	Ile	Leu	Gly	Ser	His	Ile	Leu
	210					215					220				

Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr
 245 250 255
 Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pr
 260 265 270
 Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr A'a Thr Pro Phe
 275 280 285
 Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala
 290 295 300
 Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Ser Trp Asn Thr
 305 310 315 320
 Leu Lys

<210> 2127

<211> 311

<212> PRT

<213> Homo sapien (7249282-10-14985-16332)

<400> 2127

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1 5 10 15
 Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
 20 25 30
 Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
 35 40 45
 Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
 85 90 95
 Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
 100 105 110
 Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
 115 120 125
 Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
 130 135 140
 Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
 145 150 155 160
 Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
 165 170 175
 Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
 180 185 190
 Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
 195 200 205
 Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
 210 215 220
 Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
 245 250 255
 Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
 260 265 270
 Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
 290 295 300
 Gln Arg Arg Gln Asp Ser Arg
 305 310

<210> 2128
 <211> 306
 <212> PRT
 <213> Homo sapien (7249282-10-21300-24853)

<220>
 <221> VARIANT
 <222> (1)...(306)
 <223> Xaa = Any Amino Acid

<400> 2128

Thr	Ala	Gly	Ser	Asn	Phe	Thr	Glu	Val	Thr	Val	Phe	Ile	Leu	Ser	Gly
1				5					10					15	
Tyr	Ala	Asn	His	Pro	Glu	Leu	Gln	Val	Ser	Phe	Phe	Leu	Met	Phe	Leu
			20				25						30		
Phe	Ile	Tyr	Leu	Phe	Thr	Ile	Leu	Gly	Asn	Leu	Gly	Leu	Ile	Met	Leu
		35				40						45			
Ile	Arg	Met	Asp	Ser	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50				55						60				
Asn	Leu	Ala	Phe	Ile	Asp	Ile	Phe	Tyr	Ser	Ser	Ser	Val	Thr	Pro	Lys
65				70					75					80	
Thr	Leu	Ala	Asn	Phe	Gln	Ser	Asn	Gln	Arg	Ser	Ile	Ser	Phe	Val	Gly
			85					90						95	
Cys	Phe	Val	Gln	Met	Tyr	Phe	Ser	Val	Gly	Leu	Val	Cys	Thr	Glu	Cys
			100				105						110		
Phe	Leu	Leu	Gly	Ser	Met	Ala	Tyr	Asp	Cys	Tyr	Val	Ala	Ile	Trp	Asn
		115				120						125			
Pro	Tyr	Ser	Val	Val	Ile	Ser	Xaa	Lys	Ala	Cys	Asn	Trp	Leu	Gly	Val
	130				135						140				
Met	Ser	Tyr	Thr	Ile	Gly	Phe	Thr	Asn	Ser	Leu	Val	Ser	Val	Trp	Val
145				150					155					160	
Ile	Ser	Gly	Leu	Phe	Cys	Asp	Ser	Ser	Ile	Asn	Phe	Phe	Phe	Cys	Asp
			165					170						175	
Thr	Thr	Ala	Leu	Leu	Ala	Leu	Ser	Cys	Val	Asp	Ala	Phe	Ser	Thr	Glu
			180				185						190		
Met	Val	Ser	Phe	Ala	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Gly	Ser	Ile	Leu
		195				200						205			
Ile	Ile	Thr	Val	Thr	Tyr	Ile	Ala	Ile	Thr	Ser	Ala	Ile	Leu	Lys	Asn
	210				215						220				
Gln	Trp	Ala	Ala	Gly	Trp	Gln	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Phe	His
225				230					235					240	
Leu	Met	Ala	Leu	Thr	Ile	Phe	Tyr	Gly	Ser	Leu	Ile	Phe	Thr	Tyr	Leu
			245					250						255	
Gln	Leu	Asp	Lys	Thr	Ser	Ser	Leu	Ile	His	Ala	Gln	Leu	Ala	Phe	Val
		260					265						270		
Phe	Tyr	Met	Thr	Val	Ile	Pro	Met	Leu	Asn	Pro	Leu	Ile	Xaa	Ser	Leu
		275				280						285			
Arg	Asn	Lys	Asp	Val	Lys	Asn	Ala	Leu	Leu	Arg	Val	Ile	His	Arg	Lys
	290				295						300				
Leu	Phe														
305															

<210> 2129
 <211> 327
 <212> PRT
 <213> Homo sapien (7249282-10-488-2060)

<220>
 <221> VARIANT
 <222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2129

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
 1 5 10 15
 Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
 20 25 30
 Leu Ala Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
 35 40 45
 Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
 50 55 60
 Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
 85 90 95
 Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
 115 120 125
 Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
 130 135 140
 Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
 145 150 155 160
 Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
 165 170 175
 His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
 180 185 190
 Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
 195 200 205
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
 210 215 220
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
 260 265 270
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
 290 295 300
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
 305 310 315 320
 Val Lys Leu Gln Ile Ile Leu
 325

<210> 2130

<211> 319

<212> PRT

<213> Homo sapien (7249282-11-14537-16718)

<400> 2130

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr
 1 5 10 15
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro
 20 25 30
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn
 35 40 45
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser

65		70		75		80
Thr Val Ile Ala	Pro Lys Met Leu Val	Asn Phe Ile Val	His Lys Asn			
	85	90	95			
Thr Ile Ser Tyr	Asn Trp Tyr Ala Thr	Gln Leu Ala Phe Phe	Glu Ile			
	100	105	110			
Phe Ile Ile Ser	Glu Leu Phe Ile Leu	Ser Ala Met Ala Tyr	Asp Arg			
	115	120	125			
Tyr Val Ala Ile	Cys Lys Pro Leu Leu	Tyr Val Ile Ile	Met Ala Glu			
	130	135	140			
Lys Val Leu Trp	Val Leu Val Ile Val	Pro Tyr Leu Tyr	Ser Thr Phe			
	145	150	155			160
Val Ser Leu Phe	Leu Thr Ile Lys Leu	Phe Lys Leu Ser	Phe Cys Gly			
	165	170	175			
Ser Asn Ile Ile	Ser Tyr Phe Tyr Cys	Asp Cys Ile Pro	Leu Met Ser			
	180	185	190			
Ile Leu Cys Ser	Asp Thr Asn Glu Leu	Glu Leu Ile Ile	Leu Ile Phe			
	195	200	205			
Ser Gly Cys Asn	Leu Leu Phe Ser Leu	Ser Ile Val Leu	Ile Ser Tyr			
	210	215	220			
Met Phe Ile Leu	Val Ala Ile Leu Arg	Met Asn Ser Arg	Lys Gly Arg			
	225	230	235			240
Tyr Lys Ala Phe	Ser Thr Cys Ser Ser	His Leu Thr Val	Val Ile Met			
	245	250	255			
Phe Tyr Gly Thr	Leu Leu Phe Ile Tyr	Leu Gln Pro Lys	Ser Ser His			
	260	265	270			
Thr Leu Ala Ile	Asp Lys Met Ala Ser	Val Phe Tyr Thr	Leu Leu Ile			
	275	280	285			
Pro Met Leu Asn	Pro Leu Ile Tyr Ser	Leu Arg Asn Lys	Glu Val Lys			
	290	295	300			
Asp Ala Leu Lys	Arg Thr Leu Thr Asn	Arg Phe Lys Ile	Pro Ile			
	305	310	315			

<210> 2131

<211> 317

<212> PRT

<213> Homo sapien (7249282-11-25530-27263)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2131

Met Gly Gln Lys	Asn Leu Thr Val Leu	Thr Glu Leu Ile Leu	Met Glu
1	5	10	15
Ile Thr Arg Arg	Leu Glu Leu Gln Leu	Ser Leu Phe Trp Val	Phe Leu
	20	25	30
Ile Ile Cys Thr	Phe Thr Val Val Ser	Lys Glu Cys Ile Ile	Ile Leu
	35	40	45
Asn Asn Val Asp	Leu Gly Leu Gln Thr	Phe Val Tyr Phe	Leu Ile Arg
	50	55	60
Tyr Leu Asn Phe	Ile Asn Leu Gly Asn	Ser Met Val Ile Tyr	Pro Lys
	65	70	75
Ile Leu Val Asn	Phe Val Val Ala Gln	Asn Ala Ile Pro	Cys Tyr Ala
	85	90	95
Cys Thr Met Gln	Met Ala Phe Phe Ile	Met Phe Ile Ile	Cys Glu Leu
	100	105	110
Phe Val Ser Ser	Ala Met Ala Tyr Asp	His Tyr Val Asp	Ile His Ser
	115	120	125
Leu Leu Pro Xaa	Asn Val Met Ser Gln	Glu Leu Cys His	Val Leu Val
	130	135	140

Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
 145 150 155 160
 Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
 165 170 175
 Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
 180 185 190
 Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
 195 200 205
 Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
 210 215 220
 Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
 225 230 235 240
 Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
 245 250 255
 Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
 260 265 270
 Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
 275 280 285
 Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
 290 295 300
 Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
 305 310 315

<210> 2132

<211> 318

<212> PRT

<213> Homo sapien (7249282-5-5312-7865)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2132

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr
 1 5 10 15
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro
 20 25 30
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn
 35 40 45
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser
 65 70 75 80
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys
 85 90 95
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val
 100 105 110
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Ser Pro
 130 135 140
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile
 145 150 155 160
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala
 180 185 190
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe
 195 200 205
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr

210	215	220
Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg		
225	230	235
Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val		240
	245	250
Phe Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His		255
	260	265
Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile		270
	275	280
Pro Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asn Val Lys		285
	290	295
Asp Ala Leu Lys Arg Phe Leu Asp Asn Pro Cys Arg Ser Leu		300
305	310	315

<210> 2133

<211> 279

<212> PRT

<213> Homo sapien (7264174-61-26274-29247)

<220>

<221> VARIANT

<222> (1)...(279)

<223> Xaa = Any Amino Acid

<400> 2133

Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu	
1 5 10 15	
Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys	
20 25 30	
Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser	
35 40 45	
Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met	
50 55 60	
Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu	
65 70 75 80	
Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp	
85 90 95	
Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile	
100 105 110	
Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe	
115 120 125	
Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val	
130 135 140	
Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala	
145 150 155 160	
His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa	
165 170 175	
Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys	
180 185 190	
Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu	
195 200 205	
Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu	
210 215 220	
Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr	
225 230 235 240	
Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe	
245 250 255	
Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu	
260 265 270	
Ser Ile Ile Leu Thr Leu Val	
275	

<210> 2134
 <211> 314
 <212> PRT
 <213> Homo sapien (7283250-10-5473-8590)

<400> 2134

```

Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly
 1              5              10              15
Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr
      20              25              30
Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu
      35              40              45
Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser
      50              55              60
Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys
65              70              75              80
Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu
      85              90              95
Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe
      100             105             110
Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser
      115             120             125
Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu
      130             135             140
Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr
145             150             155             160
Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His
      165             170             175
Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile
      180             185             190
Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu
      195             200             205
Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr
      210             215             220
Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr
225             230             235             240
Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile
      245             250             255
Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys
      260             265             270
Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe
      275             280             285
Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala
      290             295             300
Val Gly Arg Arg Thr Glu Leu Ala Gln Arg
305             310

```

<210> 2135
 <211> 309
 <212> PRT
 <213> Homo sapien (7283250-11-11521-16137)

<400> 2135

```

Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser
 1              5              10              15
Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile
      20              25              30
Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr
      35              40              45
Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

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<210> 2136
<211> 313
<212> PRT
<213> Homo sapien (7283250-5-1-3004)
```

<400> 2136																
Met	Glu	Lys	Arg	Asn	Leu	Thr	Val	Val	Arg	Glu	Phe	Val	Leu	Leu	Gly	
1				5					10					15		
Leu	Pro	Ser	Ser	Ala	Glu	Gln	Gln	His	Leu	Leu	Ser	Val	Leu	Phe	Leu	
			20					25					30			
Cys	Met	Tyr	Leu	Ala	Thr	Thr	Leu	Gly	Asn	Met	Leu	Ile	Ile	Ala	Thr	
		35					40					45				
Ile	Gly	Phe	Asp	Ser	His	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ala	Phe	Val	Asp	Ile	Cys	Phe	Thr	Ser	Thr	Thr	Val	Pro	Gln	
65					70					75					80	
Met	Val	Val	Asn	Ile	Leu	Thr	Gly	Thr	Lys	Thr	Ile	Ser	Phe	Ala	Gly	
			85						90					95		
Cys	Leu	Thr	Gln	Leu	Phe	Phe	Phe	Val	Ser	Phe	Val	Asn	Met	Asp	Ser	
			100					105					110			
Leu	Leu	Leu	Cys	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	His	Tyr	Thr	Ala	Arg	Met	Asn	Leu	Cys	Leu	Cys	Val	Gln	Leu	
	130					135						140				
Val	Ala	Gly	Leu	Trp	Leu	Val	Thr	Tyr	Leu	His	Ala	Leu	Leu	His	Thr	
145					150					155					160	
Val	Leu	Ile	Ala	Gln	Leu	Ser	Phe	Cys	Ala	Ser	Asn	Ile	Ile	His	His	

```

      165      170      175
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Val
      180      185      190
Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Gly Leu Leu Ala Leu
      195      200      205
Thr Pro Leu Val Cys Ile Leu Val Ser Tyr Gly Leu Ile Phe Ser Thr
      210      215      220
Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala Val Ser Thr
      225      230      235      240
Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly Thr Ala Ile
      245      250      255
Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu Ser Asp Thr
      260      265      270
Leu Ser Thr Ile Met Tyr Ser Met Val Ala Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Arg Gly Leu Gln Lys Met
      290      295      300
Leu Leu Lys Cys Thr Val Phe Gln Gln
      305      310

```

<210> 2137

<211> 310

<212> PRT

<213> Homo sapien (7283250-6-1-1725)

<220>

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 2137

```

Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln
  1           5           10           15
Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu
      20           25           30
Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp
      35           40           45
Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu
      50           55           60
Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu
      65           70           75           80
Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala
      85           90           95
Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu
      100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu
      115          120          125
Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser
      130          135          140
Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met
      145          150          155          160
Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe
      165          170          175
Cys Asp Val Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile
      180          185          190
Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr
      195          200          205
Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
      210          215          220
Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala
      225          230          235          240

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Ser His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met
 245 250 255
 Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val
 260 265 270
 Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln
 290 295 300
 Lys Leu Ser Leu Xaa Ser
 305 310

<210> 2138

<211> 320

<212> PRT

<213> Homo sapien (7321521-20-4435-9278)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2138

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe
 1 5 10 15
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln
 20 25 30
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met
 35 40 45
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His
 50 55 60
 Thr Pro Met Tyr Thr Leu Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp
 65 70 75 80
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys
 85 90 95
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu
 100 105 110
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln
 130 135 140
 Val Cys Thr Gly Leu Ile Phe Ala Trp Ser Cys Val Phe Val Ile
 145 150 155 160
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro
 165 170 175
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu
 180 185 190
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe
 195 200 205
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr
 210 215 220
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys
 225 230 235 240
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu
 245 250 255
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His
 260 265 270
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr
 275 280 285
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys
 290 295 300
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile

305

310

315

320

<210> 2139

<211> 331

<212> PRT

<213> Homo sapien (7321521-21-4479-8486)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 2139

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
      20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Lys
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
      115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
      210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
      245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
      260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
      290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Ile Lys Ile Asp Cys
305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
      325          330

```

<210> 2140

<211> 313

<212> PRT

<213> Homo sapien (7321521-22-8611-12801)

<400> 2140

```

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Ph Val Leu Thr Gly
1      5      10      15
Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Ph Val Ile Phe Leu
20      25      30
Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
35      40      45
Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
50      55      60
Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
65      70      75      80
Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
85      90      95
Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
100      105      110
Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
115      120      125
Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
130      135      140
Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
145      150      155      160
Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
165      170      175
Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
180      185      190
Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
195      200      205
Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
210      215      220
Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
225      230      235      240
Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
245      250      255
Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
260      265      270
Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
275      280      285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
290      295      300
Thr Lys Tyr Ile Leu Cys Lys Glu Lys
305      310

```

<210> 2141

<211> 134

<212> PRT

<213> Homo sapien (7321637-16-2663-3767)

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 2141

```

His Met Val Asp Ile Leu Asn Arg Gln Thr Leu Leu Tyr Leu Val Leu
1      5      10      15
Gly Leu Trp Leu Glu His Val Leu Pro Ser Ser Phe Gly Thr Val Met
20      25      30
Val Pro Leu Cys Gly Pro Arg Met Thr Ala Arg Leu Leu Phe Leu Pro
35      40      45
Val Pro Leu Ser Ala Glu Asn Glu Leu Arg Arg Ala Leu Leu Ser Thr
50      55      60

```

Glu Ala His Thr Ile Ser Leu Val Gly Gln Arg Leu Ala Ile Pro Cys
 65 70 75 80
 Asn Asn Ile Ser Xaa Phe Ile Tyr Leu Ile Lys Asn Arg Asn Leu Gly
 85 90 95
 Gln Gln Pro Ala Tyr Ser Thr Cys Trp Asp His Xaa Leu Leu Val Ser
 100 105 110
 Leu Phe Tyr Phe Lys Thr Phe His Ile Xaa Thr His Gly Ser Thr Ser
 115 120 125
 Phe Thr Phe Ile Lys Leu
 130

<210> 2142

<211> 315

<212> PRT

<213> Homo sapien (7327747-39-1-1406)

<400> 2142

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
 20 25 30
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
 145 150 155 160
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
 165 170 175
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly
 210 215 220
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
 260 265 270
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
 290 295 300
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 2143

<211> 308

<212> PRT

<213> Homo sapien (7328761-32-2018-4643)

<220>

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 2143

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
 1           5           10           15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
          20           25           30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
 35           40           45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
 50           55           60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
 65           70           75           80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
          85           90           95
Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
          100          105          110
Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
          115          120          125
Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
          130          135          140
Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
          145          150          155          160
Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
          165          170          175
Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
          180          185          190
Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
          195          200          205
Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
          210          215          220
Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
          225          230          235          240
Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
          245          250          255
Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
          260          265          270
Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
          275          280          285
Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
          290          295          300
Trp Lys Asp Ser
305

```

<210> 2144

<211> 101

<212> PRT

<213> Homo sapien (7341899-1-693-1026)

<220>

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 2144

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val

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1           5           10           15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
20           25           30
Ile Ile Ser Tyr Asn Tyr Phe Ile Il Ile Cys His Pr Leu Xaa Tyr
35           40           45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
50           55           60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
65           70           75           80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
85           90           95
Cys Cys Leu Ala Glu
100

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<210> 2145

<211> 326

<212> PRT

<213> Homo sapien (7341899-24-747-1936)

<400> 2145

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Met Glu Arg Ala Asn Asp Ser Thr Phe Ser Gly Phe Ile Leu Leu Gly
1           5           10           15
Phe Ser Asn Arg Pro Gln Leu Glu Thr Ala Leu Phe Val Val Ile Leu
20           25           30
Ile Ile Tyr Phe Leu Ser Phe Leu Gly Asn Gly Thr Ile Ile Leu Leu
35           40           45
Ser Ile Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Phe Met Asp Leu Cys Leu Thr Thr Cys Thr Val Pro Gln
65           70           75           80
Thr Leu Val Asn Phe Lys Gly Lys Asp Lys Thr Ile Thr Tyr Gly Gly
85           90           95
Cys Val Thr Gln Leu Phe Ile Ala Leu Gly Leu Gly Gly Ser Glu Cys
100           105           110
Val Leu Leu Ser Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg
115           120           125
Ser Leu His Tyr Met Val Ser Met His Pro Gln Leu Cys Leu Gln Leu
130           135           140
Val Val Thr Thr Trp Leu Thr Gly Phe Gly Asn Ser Val Ile Gln Thr
145           150           155           160
Ala Leu Thr Met Thr Leu Pro Leu Cys Asp Lys Asn Gln Val Asp His
165           170           175
Phe Phe Cys Glu Val Pro Val Met Leu Lys Leu Ser Cys Thr Asn Thr
180           185           190
Ser Ile Asn Glu Ala Glu Ile Phe Ala Val Ser Val Phe Phe Leu Val
195           200           205
Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly His Ile Thr His Ala
210           215           220
Val Leu Lys Ile Lys Ser Ala Gln Gly Arg Gln Lys Ala Phe Gly Thr
225           230           235           240
Cys Gly Ser His Leu Leu Val Val Ile Ile Phe Phe Gly Thr Leu Ile
245           250           255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Tyr Ser Gln Asp Val Asn Lys
260           265           270
Ser Ile Ala Leu Phe Tyr Thr Leu Val Thr Pro Leu Leu Asn Pro Leu
275           280           285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Thr Lys Lys Thr
290           295           300
Ser Gly Glu Asp Il Ala Cys Met Arg Lys Leu Thr Gln Gly Leu Gln
305           310           315           320
Phe Gln Thr Phe Val His

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325

<210> 2146
 <211> 155
 <212> PRT
 <213> Homo sapien (7341899-6-1-567)

<220>
 <221> VARIANT
 <222> (1)...(155)
 <223> Xaa = Any Amino Acid

<400> 2146
 Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His Val Leu Leu Ala
 1 5 10 15
 Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu Glu Met Ser Val
 20 25 30
 Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu Ile Ser Asn Phe
 35 40 45
 Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met Asn Thr Ser Asn
 50 55 60
 Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His His His Arg
 65 70 75 80
 Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile Ile Val Xaa Met
 85 90 95
 Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln Glu Arg Phe Phe
 100 105 110
 Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys Leu Leu Val Tyr
 115 120 125
 Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg Arg Ile Leu Arg
 130 135 140
 Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn
 145 150 155

<210> 2147
 <211> 318
 <212> PRT
 <213> Homo sapien (7341900-14-7037-9080)

<220>
 <221> VARIANT
 <222> (1)...(318)
 <223> Xaa = Any Amino Acid

<400> 2147
 Met Ala Glu Ser Gly Thr Thr Val Thr Glu Phe Phe Leu Arg Gly Phe
 1 5 10 15
 Arg Leu Lys Ala Glu Leu Gln Ile Gly Leu Phe Phe Val Phe Leu Val
 20 25 30
 Ile Phe Leu Ile Thr Met Gly Gly Asn Leu Gly Met Ile Val Leu Met
 35 40 45
 Leu Ile Gln Thr Asp Pro Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser His Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Ile Gly Pro
 65 70 75 80
 Gln Leu Leu Glu Thr Leu Ala Thr Asp Lys Met Ile Ile Thr Tyr Glu
 85 90 95
 Arg Cys Ala Ser Gln Phe Phe Phe Phe Thr Leu Cys Ala Ser Ile Glu
 100 105 110
 Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
 115 120 125

Asn Pro Leu Leu Tyr Ala Ile Val Met Thr Pro Lys Thr Arg Leu Ala
 130 135 140
 Leu Leu Ala Gly Ala Tyr Ser Gly Ala Ile Val Asn Ser Val Ile Cys
 145 150 155 160
 Thr Gly Cys Thr Phe Ser Ile Ser Phe Ser Lys Ser Asn His Val Asp
 165 170 175
 Phe Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Glu
 180 185 190
 Thr Arg Pro Arg Glu Trp Val Ile Tyr Leu Ser Ala Phe Leu Val Ile
 195 200 205
 Thr Thr Ser Ile Ser Val Ile Leu Thr Ser Tyr Leu Phe Ile Ile Gln
 210 215 220
 Ser Val Leu Lys Ile Arg Thr Ala Gly Gly Arg Ala Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Met Thr Ala Leu Thr Leu Phe Phe Gly Thr Leu
 245 250 255
 Ile Phe Ile Tyr Leu Lys Gly Asn Met Gly Glu Ser Leu Glu Glu Asp
 260 265 270
 Lys Ile Val Ser Ile Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Met Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys
 290 295 300
 Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu
 305 310 315

<210> 2148

<211> 317

<212> PRT

<213> Homo sapien (7341900-15-17952-19084)

<400> 2148

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1 5 10 15
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
 20 25 30
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
 35 40 45
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
 50 55 60
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
 100 105 110
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
 130 135 140
 Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
 145 150 155 160
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
 165 170 175
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
 195 200 205
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
 210 215 220
 Il Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
 225 230 235 240

Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile
 260 265 270
 Asn Phe Asn Lys Val Val S r Val Phe Tyr Ser Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
 290 295 300
 Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln
 305 310 315

<210> 2149

<211> 314

<212> PRT

<213> Homo sapien (7341900-16-17098-20843)

<400> 2149

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1 5 10 15
 Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
 35 40 45
 Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
 65 70 75 80
 Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
 85 90 95
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
 130 135 140
 Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
 145 150 155 160
 Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
 165 170 175
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
 195 200 205
 Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
 210 215 220
 Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
 245 250 255
 Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
 290 295 300
 Ala Arg Arg Leu Gln Val Ser Leu Ser Met
 305 310

<210> 2150

<211> 311

<212> PRT

<213> Homo sapien (7341900-6-1691-2778)

<220>

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 2150

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Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1           5           10           15
Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
      20           25           30
Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
      35           40           45
Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
      50           55           60
Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
65           70           75           80
Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
      85           90           95
Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
      100          105          110
Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
      115          120          125
Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
      130          135          140
Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
145          150          155          160
Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
      165          170          175
Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
      180          185          190
Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met
      195          200          205
Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
      210          215          220
Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
225          230          235          240
Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
      245          250          255
Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
      260          265          270
Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
      275          280          285
Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
      290          295          300
Ile Gly Asn Phe Trp Val Phe
305          310

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<210> 2151

<211> 306

<212> PRT

<213> Homo sapien (7406632-1-90980-93013)

<400> 2151

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Met Glu Gly Lys Asn Gln Thr Asn Ile Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Phe Ser Ser Trp Gln Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu
      20           25           30
Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
      35           40           45

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Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Ph Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Gln Thr Gln Thr Ile Ser Tyr Pro Gly
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
 100 105 110
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
 130 135 140
 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
 145 150 155 160
 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
 180 185 190
 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
 195 200 205
 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
 210 215 220
 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr
 245 250 255
 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
 260 265 270
 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 290 295 300
 Leu Ser
 305

<210> 2152

<211> 314

<212> PRT

<213> Homo sapien (7407927-19-1-4216)

<400> 2152

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
 65 70 75 80
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
 85 90 95
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160

Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
 195 200 205
 Ile Ser Phe Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
 210 215 220
 Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
 290 295 300
 Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
 305 310

<210> 2153

<211> 117

<212> PRT

<213> Homo sapien (7407927-23-3086-3824)

<220>

<221> VARIANT

<222> (1)...(117)

<223> Xaa = Any Amino Acid

<400> 2153

Ser Ile Thr Glu Ala Leu Cys Leu Lys Tyr Val His Leu Asn Asn Lys
 1 5 10 15
 Glu Met Tyr Phe Met Tyr Leu Gly Lys Asn Arg Ser Arg Ile Ile Asn
 20 25 30
 Val Cys Ser Leu Val Leu Gln Ile Ile Thr Thr Ile Ile Leu Ile Leu
 35 40 45
 Pro Ser Pro Trp Leu Ser Leu Ile Ile Ser Gly Thr Phe Trp Ile Ile
 50 55 60
 Xaa Pro Leu His Ser Phe Pro His Gln Ile Ile Xaa Asn Ile Asn Thr
 65 70 75 80
 Ala Thr Glu Cys Thr Ile Ser Lys Leu Leu Tyr His Leu Gly Ser
 85 90 95
 Lys Leu Phe Asn Val Lys Ala Gln Phe Ser Thr Xaa Leu Leu Pro Asn
 100 105 110
 Glu Leu Tyr Val Leu
 115

<210> 2154

<211> 338

<212> PRT

<213> Homo sapien (7407958-12-642-1844)

<220>

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 2154

Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg

1	5	10	15
Gly Val Val His Phe His Ph His Phe Phe Ser Thr Asp Leu Val Val			
20	25	30	
Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val			
35	40	45	
Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His			
50	55	60	
Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu			
65	70	75	80
Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu			
85	90	95	
Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met			
100	105	110	
Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val			
115	120	125	
Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn			
130	135	140	
Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu			
145	150	155	160
Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His			
165	170	175	
Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met			
180	185	190	
Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser			
195	200	205	
Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser			
210	215	220	
Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met			
225	230	235	240
His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His			
245	250	255	
Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu			
260	265	270	
Cys Pro Ser Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu			
275	280	285	
Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val			
290	295	300	
Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met			
305	310	315	320
Ser Leu Xaa Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro			
325	330	335	
Xaa Leu			

<210> 2155

<211> 314

<212> PRT

<213> Homo sapien (7467565-10-15924-18962)

<400> 2155

Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu			
1	5	10	15
Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu			
20	25	30	
Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu			
35	40	45	
Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met			
50	55	60	
Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser			
65	70	75	80
Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met			

				85					90					95		
Ile	Ser	Leu	Ser	Glu	Cys	Met	Ile	Gln	Phe	Phe	S	r	Phe	Ala	Phe	Gly
			100					105						110		
Gly	Thr	Thr	Glu	Cys	Phe	Leu	Leu	Ala	Thr	Met	Ala	Tyr	Asp	Arg	Tyr	
		115						120					125			
Val	Ala	Ile	Cys	Lys	Pro	Leu	Leu	Tyr	Pro	Val	Ile	Met	Asn	Asn	Ser	
	130					135					140					
Leu	Cys	Ile	Arg	Leu	Leu	Ala	Phe	Ser	Phe	Leu	Gly	Gly	Phe	Leu	His	
145					150					155					160	
Ala	Leu	Ile	His	Glu	Val	Leu	Ile	Phe	Arg	Leu	Thr	Phe	Cys	Asn	Ser	
			165						170					175		
Asn	Ile	Ile	His	His	Phe	Tyr	Cys	Asp	Ile	Ile	Pro	Leu	Phe	Met	Ile	
		180						185					190			
Ser	Cys	Thr	Asp	Pro	Ser	Ile	Asn	Phe	Leu	Met	Val	Phe	Ile	Leu	Ser	
	195						200					205				
Gly	Ser	Ile	Gln	Val	Phe	Thr	Ile	Val	Thr	Val	Leu	Asn	Ser	Tyr	Thr	
	210					215					220					
Phe	Ala	Leu	Phe	Thr	Ile	Leu	Lys	Lys	Lys	Ser	Val	Arg	Gly	Val	Arg	
225					230					235					240	
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ala	His	Leu	Leu	Ser	Val	Ser	Leu	Tyr	
			245						250					255		
Tyr	Gly	Pro	Leu	Ile	Phe	Met	Tyr	Leu	Arg	Pro	Ala	Ser	Pro	Gln	Ala	
		260					265						270			
Asp	Asp	Gln	Asp	Met	Ile	Asp	Ser	Val	Phe	Tyr	Thr	Ile	Ile	Ile	Pro	
	275					280						285				
Leu	Leu	Asn	Pro	Ile	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Gln	Val	Ile	Asp	
	290					295					300					
Ser	Phe	Thr	Lys	Met	Val	Lys	Arg	Asn	Val							
305					310											

<210> 2156

<211> 320

<212> PRT

<213> Homo sapien (7533967-9-17699-19044)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2156

Gly	Val	Gly	Leu	Xaa	Lys	Leu	Xaa	Trp	Gln	Ile	Ile	Phe	Ser	Gly	Asp	
1			5					10						15		
Ser	Phe	Ser	Thr	Trp	Glu	Met	Phe	Ser	Leu	Ser	Ile	Leu	Gln	Leu	Pro	
		20					25						30			
Xaa	Met	Tyr	Thr	Val	Ala	Leu	Ser	Gly	Thr	Ser	Ile	Leu	Ile	Phe	Leu	
	35					40						45				
Ile	Xaa	Thr	Asp	Phe	Xaa	Val	His	Thr	Ser	Leu	Tyr	Ser	Phe	Xaa	Val	
	50				55						60					
Leu	Ile	Asp	Ile	Ala	Ile	Ser	Val	Val	Lys	Ile	Gly	Ile	Glu	Val	Phe	
65				70					75					80		
Ser	Gly	Lys	Ile	Asn	Phe	Ser	His	Thr	Gly	Cys	Gly	Thr	Gln	Ile	Phe	
			85					90					95			
Phe	Phe	Leu	Thr	Ala	Gly	Ile	Phe	Lys	Tyr	Val	Leu	Leu	Thr	Tyr	Met	
		100					105						110			
Ala	Tyr	Asp	His	Asn	Val	Ala	Ile	Cys	Asp	Leu	Arg	Xaa	Pro	Thr	Phe	
	115					120						125				
Met	Ser	Asp	Gln	Val	Phe	Xaa	Gln	Trp	Ala	Val	Glu	Ser	Trp	Ile	Gly	
	130					135					140					
Gly	Lys	Leu	Ser	Ser	Leu	Ala	His	Thr	Ile	Tyr	Ile	Phe	His	Leu	Phe	
145					150					155						

Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa
 165 170 175
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr
 180 185 190
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser
 195 200 205
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly
 210 215 220
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile
 225 230 235 240
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe
 245 250 255
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu
 260 265 270
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val
 275 280 285
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln
 290 295 300
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser
 305 310 315 320

<210> 2157

<211> 196

<212> PRT

<213> Homo sapien (7534025-1-1-1622)

<400> 2157

Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu Arg Tyr Ser
 1 5 10 15
 Val Leu Met Gly His Gly Val Cys Met Gly Leu Met Ala Ala Ala Cys
 20 25 30
 Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr Ser Leu Val Phe His
 35 40 45
 Leu Pro Phe His Ser Ser Asn Gln Leu His His Phe Phe Cys Asp Ile
 50 55 60
 Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser Gly Phe Ser Gln Leu
 65 70 75 80
 Val Ile Phe Met Leu Gly Val Phe Ala Leu Val Ile Pro Leu Leu Leu
 85 90 95
 Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala Ile Leu Lys Ile Pro
 100 105 110
 Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr Cys Ala Ser His Leu
 115 120 125
 Ile Val Val Thr Val His Tyr Ser Cys Ala Ser Phe Ile Tyr Leu Arg
 130 135 140
 Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr Leu Ile Ser Val Ser
 145 150 155 160
 Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met Ile Tyr Ser Leu Arg
 165 170 175
 Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr Ile Gly Gln Thr Phe
 180 185 190
 Tyr Pro Leu Ser
 195

<210> 2158

<211> 307

<212> PRT

<213> Homo sapien (7534025-11-6732-9742)

<220>

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 2158

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Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
 1           5           10           15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Val Tyr Leu Thr Thr Leu
      20           25           30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35           40           45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
 50           55           60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
65           70           75           80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85           90           95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100          105          110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115          120          125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130          135          140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
145           150           155           160
Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
      165          170          175
Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
      180          185          190
Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
      195          200          205
Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
      210          215          220
Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
225           230           235           240
Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      245          250          255
Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
      260          265          270
Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
      275          280          285
Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
      290          295          300
Lys Thr Val
305

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<210> 2159

<211> 321

<212> PRT

<213> Homo sapien (7534025-12-11728-15143)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2159

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
      20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr

```

35	40	45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu		
50	55	60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro		
65	70	75
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile		
85	90	95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn		
100	105	110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys		
115	120	125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln		
130	135	140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe		
145	150	155
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn		
165	170	175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala		
180	185	190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile		
195	200	205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe		
210	215	220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys		
225	230	235
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr		
245	250	255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser		
260	265	270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr		
275	280	285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys		
290	295	300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro		
305	310	315
Pro		320

<210> 2160

<211> 324

<212> PRT

<213> Homo sapien (7534025-3-4346-5996)

<400> 2160

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg		
1	5	10
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe		
20	25	30
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu		
35	40	45
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met		
50	55	60
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr		
65	70	75
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser		
85	90	95
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe		
100	105	110
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr		
115	120	125
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln		

130 135 140
 Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr
 145 150 155 160
 Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met
 165 170 175
 Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val
 180 185 190
 Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala
 195 200 205
 Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala
 210 215 220
 Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln
 225 230 235 240
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe
 245 250 255
 Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala
 260 265 270
 Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro
 275 280 285
 Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala
 290 295 300
 Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
 305 310 315 320
 Gly Ala Phe Ser

<210> 2161

<211> 305

<212> PRT

<213> Homo sapien (7534103-14-4211-5521)

<400> 2161

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
 1 5 10 15
 Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
 20 25 30
 Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
 35 40 45
 Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
 50 55 60
 Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
 65 70 75 80
 Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
 85 90 95
 Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
 100 105 110
 Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
 130 135 140
 Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
 165 170 175
 Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
 180 185 190
 Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
 195 200 205
 Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
 210 215 220
 Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser

225 230 235 240
 His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
 245 250 255
 Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe
 260 265 270
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val
 290 295 300
 Ile
 305

<210> 2162

<211> 301

<212> PRT

<213> Homo sapien (7534103-16-19899-21252)

<220>

<221> VARIANT

<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 2162

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
 1 5 10 15
 Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
 20 25 30
 Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
 35 40 45
 Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
 50 55 60
 Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
 65 70 75 80
 Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
 85 90 95
 Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro
 100 105 110
 Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr
 115 120 125
 Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe
 130 135 140
 Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val
 145 150 155 160
 Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp
 165 170 175
 Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly
 180 185 190
 Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile
 195 200 205
 Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser
 210 215 220
 Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val
 225 230 235 240
 Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr
 245 250 255
 Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu
 260 265 270
 Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met
 275 280 285
 Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu
 290 295 300

<210> 2163
 <211> 134
 <212> PRT
 <213> Homo sapien (7534103-16-5480-6475)

<220>
 <221> VARIANT
 <222> (1)...(134)
 <223> Xaa = Any Amino Acid

<400> 2163
 Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1 5 10 15
 Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg
 20 25 30
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln
 35 40 45
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser
 50 55 60
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly
 65 70 75 80
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln
 85 90 95
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser
 100 105 110
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Lys Xaa Ser Gly Glu Arg
 115 120 125
 Ser Ser Phe Pro Arg Glu
 130

<210> 2164
 <211> 307
 <212> PRT
 <213> Homo sapien (7547121-7-14093-14713)

<220>
 <221> VARIANT
 <222> (1)...(307)
 <223> Xaa = Any Amino Acid

<400> 2164
 Leu Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu
 1 5 10 15
 Phe Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg
 20 25 30
 Ile Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His
 35 40 45
 Gly Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro
 50 55 60
 Ser Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr
 65 70 75 80
 Asp Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu
 85 90 95
 Cys Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser
 100 105 110
 Lys Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys
 115 120 125
 Lys Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe
 130 135 140
 Leu Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys

145 150 155 160
 Gly Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Pro
 165 170 175
 Leu Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly
 180 185 190
 Lys Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile
 195 200 205
 Phe Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser
 210 215 220
 Ala Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr
 225 230 235 240
 Val Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser
 245 250 255
 Thr Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly
 260 265 270
 Val Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met
 275 280 285
 Glu Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp
 290 295 300
 Cys Trp Lys
 305

<210> 2165

<211> 214

<212> PRT

<213> Homo sapien (7622326-1-2092-6993)

<220>

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 2165

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1 5 10 15
 Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
 20 25 30
 Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
 35 40 45
 Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
 50 55 60
 Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
 65 70 75 80
 Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
 85 90 95
 Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
 100 105 110
 Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
 115 120 125
 Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
 130 135 140
 Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
 145 150 155 160
 Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
 165 170 175
 Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
 180 185 190
 Gly Val Lys Ser Lys His Il Gln Glu Asn Met Val Gln Arg Phe Cys
 195 200 205
 Gly Lys Ile Ser Cys His
 210

<210> 2166
 <211> 321
 <212> PRT
 <213> Homo sapien (7622326-2-5218-6423)

<400> 2166
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1 5 10 15
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Phe Ile Tyr Leu Thr Val Ile Leu Gly Asn Leu Thr Ile Leu
 35 40 45
 His Val Ile Cys Thr Asp Ala Thr Leu His Gly Pro Met Tyr Tyr Phe
 50 55 60
 Leu Gly Met Leu Ala Val Thr Asp Leu Gly Leu Cys Leu Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Gly Ile Phe Trp Phe Asp Thr Arg Glu Ile Gly Ile
 85 90 95
 Pro Ala Cys Phe Thr Gln Leu Phe Phe Ile His Thr Leu Ser Ser Met
 100 105 110
 Glu Ser Ser Val Leu Leu Ser Met Ser Ile Asp Arg Ser Val Ala Val
 115 120 125
 Cys Asn Pro Leu His Asp Ser Thr Val Leu Thr Pro Ala Cys Ile Val
 130 135 140
 Lys Met Gly Leu Ser Ser Val Leu Arg Ser Ala Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Phe Gln Tyr Cys His Ser His Val Leu
 165 170 175
 Ala His Ala Tyr Cys Leu His Leu Glu Ile Met Lys Leu Ala Cys Ser
 180 185 190
 Ser Ile Ile Val Asn His Ile Tyr Gly Leu Phe Val Val Ala Cys Thr
 195 200 205
 Val Gly Val Asp Ser Leu Leu Ile Phe Leu Ser Tyr Ala Leu Ile Leu
 210 215 220
 Arg Thr Val Leu Ser Ile Ala Ser His Gln Glu Arg Leu Arg Ala Leu
 225 230 235 240
 Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Ile Pro
 245 250 255
 Met Ile Gly Leu Ser Leu Val His Arg Phe Gly Glu His Leu Pro Arg
 260 265 270
 Val Val His Leu Phe Met Ser Tyr Val Tyr Leu Leu Val Pro Pro Leu
 275 280 285
 Met Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Arg Gln Arg
 290 295 300
 Ile Ile Lys Lys Phe Gln Phe Ile Lys Ser Leu Arg Cys Phe Trp Lys
 305 310 315 320
 Asp

<210> 2167
 <211> 345
 <212> PRT
 <213> Homo sapien (7622326-3-3672-5330)

<220>
 <221> VARIANT
 <222> (1)...(345)
 <223> Xaa = Any Amino Acid

<400> 2167

Met His Leu Pro Asn Ser Ser Glu Ile Ala Il Thr Thr Phe Phe Leu
 1 5 10 15
 Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
 20 25 30
 Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
 35 40 45
 Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
 65 70 75 80
 Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
 85 90 95
 Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
 100 105 110
 Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
 115 120 125
 Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
 130 135 140
 Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
 145 150 155 160
 Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
 165 170 175
 Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
 180 185 190
 Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
 195 200 205
 Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
 210 215 220
 Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
 225 230 235 240
 Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
 245 250 255
 Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
 260 265 270
 Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
 275 280 285
 Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
 290 295 300
 Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
 305 310 315 320
 Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
 325 330 335
 Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
 340 345

<210> 2168

<211> 325

<212> PRT

<213> Homo sapien (7622326-4-1-4013)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2168

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
 1 5 10 15
 Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
 20 25 30
 Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met

<400> 2169																
Met	Ser	Pro	Leu	Asn	Asp	Thr	Lys	Met	Glu	Val	Leu	Arg	Phe	Leu	Leu	
1				5					10					15		
Ile	Gly	Ile	Thr	Gly	Leu	Glu	Lys	Ser	Arg	Thr	Trp	Ile	Ser	Ile	Pro	
			20					25					30			
Phe	Leu	Ser	Val	Tyr	Leu	Leu	Ser	Trp	Met	Gly	Asn	Phe	Thr	Val	Leu	
		35					40				45					
Phe	Phe	Ile	Lys	Thr	Glu	Gln	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Leu	
	50					55					60					
Leu	Ser	Met	Leu	Ser	Ile	Ser	Asp	Leu	Gly	Leu	Ser	Leu	Ser	Ser	Leu	
65					70					75					80	
Pro	Ile	Thr	Leu	Gly	Leu	Phe	Leu	Phe	Asp	Val	His	Glu	Ile	His	Ala	
				85					90					95		

Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
 100 105 110
 Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
 115 120 125
 His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
 130 135 140
 Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser
 180 185 190
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr
 195 200 205
 Met Leu Asp Leu Val Phe Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Met
 245 250 255
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met
 260 265 270
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu
 275 280 285
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val
 290 295 300
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu
 305 310 315

<210> 2170

<211> 323

<212> PRT

<213> Homo sapien (7622326-8-11210-13439)

<400> 2170

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1 5 10 15
 Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
 20 25 30
 Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
 35 40 45
 Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
 50 55 60
 Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
 65 70 75 80
 Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
 85 90 95
 Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
 100 105 110
 His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
 115 120 125
 Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
 130 135 140
 Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
 145 150 155 160
 Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
 165 170 175
 Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
 180 185 190
 Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
 195 200 205

Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
 210 215 220
 Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu S r Arg Glu Asp
 225 230 235 240
 Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
 245 250 255
 Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
 260 265 270
 Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
 275 280 285
 Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
 290 295 300
 Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
 305 310 315 320
 Gly Ala Gln

<210> 2171

<211> 328

<212> PRT

<213> Homo sapien (7631097-4-2553-4836)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2171

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1 5 10 15
 Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
 20 25 30
 Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
 35 40 45
 Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
 50 55 60
 Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
 65 70 75 80
 Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
 85 90 95
 Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
 100 105 110
 Ser Val Val Glu Ser Ser Val Leu Ala Ile Ser Phe Asp His Phe
 115 120 125
 Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
 130 135 140
 Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
 145 150 155 160
 Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
 165 170 175
 Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
 180 185 190
 Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
 195 200 205
 Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
 210 215 220
 Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
 225 230 235 240
 Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
 245 250 255
 Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg

<400> 2173
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20 25 30
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50 55 60
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65 70 75 80
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85 90 95
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
 100 105 110
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
 130 135 140
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met
 145 150 155 160
 Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
 165 170 175
 Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
 180 185 190
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
 195 200 205
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
 210 215 220
 Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
 225 230 235 240
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
 245 250 255
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
 260 265 270
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
 275 280 285
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
 290 295 300
 Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
 305 310 315

<210> 2174

<211> 311

<212> PRT

<213> Homo sapien (7637231-2-1-2470)

<220>

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 2174

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
 35 40 45
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu

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<210> 2175
<211> 117
<212> PRT
<213> Homo sapien (7637231-7-1-1398)
```

```
<210> 2176
<211> 227
<212> PRT
<213> Homo sapien (7637775-10-2645-3375)
```

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<220>  
<221> VARIANT  
<222> (1) ... (227)
```


<223> Xaa = Any Amino Acid

<400> 2176

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
 1          5          10          15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
          20          25          30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
          35          40          45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
          50          55          60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
          65          70          75          80
Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
          85          90          95
Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
          100          105          110
Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly
          115          120          125
Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
          130          135          140
Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
          145          150          155          160
Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
          165          170          175
Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
          180          185          190
Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
          195          200          205
Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
          210          215          220
Lys Val Lys
          225

```

<210> 2177

<211> 316

<212> PRT

<213> Homo sapien (7655430-8-26100-29590)

<220>

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 2177

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
 1          5          10          15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
          20          25          30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
          35          40          45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
          50          55          60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
          65          70          75          80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
          85          90          95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
          100          105          110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
          115          120          125

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Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
 130          135          140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
145          150          155          160
Leu Pro Gly Pr  Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
          165          170          175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
          180          185          190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
          195          200          205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
          210          215          220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
225          230          235          240
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
          245          250          255
Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp
          260          265          270
Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro
          275          280          285
Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg
          290          295          300
Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile
305          310          315

```

<210> 2178

<211> 154

<212> PRT

<213> Homo sapien (7657777-15-1-798)

<220>

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 2178

```

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
 1          5          10          15
His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
          20          25          30
Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
          35          40          45
Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
          50          55          60
Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
          65          70          75          80
Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
          85          90          95
Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe
          100          105          110
Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
          115          120          125
Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
          130          135          140
Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
145          150

```

<210> 2179

<211> 170

<212> PRT

<213> Homo sapien (7657777-22-544-1713)

<220>

<221> VARIANT

<222> (1)...(170)

<223> Xaa = Any Amino Acid

<400> 2179

His	Thr	Gln	Pro	Arg	Gly	Leu	Thr	Arg	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Gln	Asp	Pro	Gln	Leu	Gln	Pro	Val	Leu	Ser	Gly	Leu	Ser
			20					25					30		
Leu	Cys	Met	Cys	Leu	Gly	Thr	Gln	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Gly	Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Ser	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Gly	Ala	Asp	Ile	Ser	Phe	Thr	Ser	Thr	Thr	Gly	Pro
65					70					75					80
Lys	Leu	Ile	Val	Asp	Ile	His	Ser	Tyr	Thr	Arg	Asp	Ile	Ser	Tyr	Ala
				85					90					95	
Arg	Cys	Leu	Thr	His	Thr	Pro	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Val	Glu
			100					105					110		
Arg	Asp	Met	Leu	Leu	Arg	Val	Met	Gly	Tyr	Asp	Arg	Val	Val	Asp	Ile
		115					120					125			
Cys	Asp	Pro	Leu	Tyr	His	Ser	His	Ala	Met	Asn	Pro	Cys	Val	Cys	Gly
	130					135					140				
Ser	Leu	Asp	Leu	Trp	Ser	Leu	Phe	Phe	Leu	Thr	Leu	Leu	Tyr	Thr	His
145					150					155					160
Leu	His	Asn	Ser	Ile	Ala	Leu	His	Met	Thr						
				165					170						

<210> 2180

<211> 198

<212> PRT

<213> Homo sapien (7657777-42-1-597)

<220>

<221> VARIANT

<222> (1)...(198)

<223> Xaa = Any Amino Acid

<400> 2180

Met	Asn	Pro	Cys	Leu	Cys	Gly	Phe	Arg	Val	Val	Val	Ser	Phe	Phe	Phe
1				5					10					15	
His	Ser	Leu	Leu	Gly	Ala	Gln	Val	His	Asn	Leu	Ser	Ala	Ser	Gln	Met
		20						25					30		
Thr	Cys	Phe	Glu	Tyr	Val	Glu	Ile	His	Asn	Phe	Leu	Trp	Ala	Leu	Ser
		35				40						45			
Gln	Leu	Pro	His	Arg	Ala	Trp	Cys	Asp	Thr	Phe	Pro	Asn	Asn	Ile	Ile
	50					55					60				
Val	Tyr	Phe	Pro	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ala	Gly	Thr
65				70					75						80
Leu	Phe	Ser	Xaa	Tyr	Glu	Ser	Val	Ser	Ser	Ile	Glu	Arg	Val	Ser	Ser
			85					90						95	
Xaa	Gly	Gly	Glu	Tyr	Lys	Ala	Phe	Pro	Thr	Cys	Gly	Ser	His	Leu	Ser
			100					105					110		
Val	Val	Cys	Xaa	Leu	Tyr	Gly	Thr	Gly	Val	Gly	Gly	His	Leu	Ser	Ser
		115				120						125			
Asp	Val	Ser	Ser	Ser	Pro	Arg	Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr
	130					135					140				
Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Met	Arg	Asn
145					150					155					160

Arg Asp Thr Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
 165 170 175
 Phe Xaa Tyr Leu Leu Ile Cys Pro Ile Pro Phe Val Val Trp Val Lys
 180 185 190
 Lys Gly Arg Lys Val Lys
 195

<210> 2181
 <211> 199
 <212> PRT
 <213> Homo sapien (7657788-15-11714-13012)

<220>
 <221> VARIANT
 <222> (1)...(199)
 <223> Xaa = Any Amino Acid

<400> 2181
 Leu Glu Met Xaa Leu Lys Ile Leu Tyr Leu Lys Asn Cys Ser Phe Xaa
 1 5 10 15
 Cys Asn Arg Pro Glu His Tyr Asn Xaa Lys Asn Cys Gly Xaa Phe Cys
 20 25 30
 Leu Leu Ile Thr Ile Ile Thr Phe Arg Ser Gly Ile Ile Asp Ile Cys
 35 40 45
 Leu His His His Lys Thr Ile Phe Ile Phe Lys Lys His Ser Gly Phe
 50 55 60
 Glu Gly Xaa Leu Trp Leu Arg Ile Xaa Asn Gln Ser Pro Lys Ser Trp
 65 70 75 80
 Ile Ser Ile Ala Cys Asp Cys Cys Val Ala Xaa Asn Met Lys Gln Val
 85 90 95
 Ala Ile Ser Cys His Ser Phe Ser Ser Val Lys Xaa Ser Pro Tyr Val
 100 105 110
 Ile Trp Lys Tyr Phe Cys Lys Xaa Tyr Lys His Ile Lys Asn Gly Arg
 115 120 125
 Asp Xaa Ile Xaa Leu Leu Thr Leu Lys Xaa Ile Lys His Leu Phe Val
 130 135 140
 Val Cys Ile Ile Tyr Thr Pro Cys Met Phe His Pro Phe Gln Asn Lys
 145 150 155 160
 Tyr Met Val Thr Glu Ser Leu Ile Xaa Ser Tyr Xaa Val Asp Pro Val
 165 170 175
 Ser Asn Pro Ala Leu Ile Thr Ala Arg Ser His Xaa Asn His Leu Val
 180 185 190
 Ile Ser Gln His Asn Asn Asn
 195

<210> 2182
 <211> 324
 <212> PRT
 <213> Homo sapien (7658481-16-11475-15098)

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 2182
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
 1 5 10 15
 Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile
 20 25 30
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu

```

      35      40      45
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
  50      55      60
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
  65      70      75      80
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
      85      90      95
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
      100      105      110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
      115      120      125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
      130      135      140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
      145      150      155      160
Pro Phe Ile Phe Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val
      165      170      175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
      180      185      190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
      210      215      220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
      225      230      235      240
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
      260      265      270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
      275      280      285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
      290      295      300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile Xaa Met
      305      310      315      320
Leu Ser Arg Ser

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<210> 2183

<211> 317

<212> PRT

<213> Homo sapien (7658481-18-4217-6941)

<400> 2183

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
  1      5      10      15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
      20      25      30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
      35      40      45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
      50      55      60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
      65      70      75      80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
      85      90      95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
      100      105      110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
      115      120      125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly

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130	135	140
Arg Thr Gly Leu Ala Il	Ile Cys Cys Cys Val	Leu Ala Val Leu Pro
145	150	155
Ser Leu Phe Leu Leu Lys	Arg Leu Pro Phe Cys	His Ser His Leu Leu
165	170	175
Ser Arg Ser Tyr Cys Leu	His Gln Asp Met Ile	Arg Leu Val Cys Ala
180	185	190
Asp Ile Arg Leu Asn Ser	Trp Tyr Gly Phe Ala	Leu Ala Leu Leu Ile
195	200	205
Ile Ile Val Asp Pro Leu	Leu Ile Val Ile Ser	Tyr Thr Leu Ile Leu
210	215	220
Lys Asn Ile Leu Gly Thr	Ala Thr Trp Ala Glu	Arg Leu Arg Ala Leu
225	230	235
Asn Asn Cys Leu Ser His	Ile Leu Ala Val Leu	Val Leu Tyr Ile Pro
245	250	255
Met Val Gly Val Ser Met	Thr His Arg Phe Ala	Lys His Ala Ser Pro
260	265	270
Leu Val His Val Ile Met	Ala Asn Ile Tyr Leu	Leu Ala Pro Pro Val
275	280	285
Met Asn Pro Ile Ile Tyr	Ser Val Lys Asn Lys	Gln Ile Gln Trp Gly
290	295	300
Met Leu Asn Phe Leu Ser	Leu Lys Asn Met His	Ser Arg
305	310	315

<210> 2184

<211> 315

<212> PRT

<213> Homo sapien (7658481-19-24037-28136)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 2184

Phe Ser Gln Asn Leu Leu Ile	Ser Gly Ser Gly Ser Phe	Val Leu Leu
1	5	10
Gly Met Pro Gly Leu Glu Ala	Leu His Ala Trp Leu Ser	Val Leu Val
20	25	30
Cys Leu Leu Tyr Met Ala Ala	Leu Val Gly Asn Ala Leu	Leu Val Gly
35	40	45
Leu Val Val Thr Asp Lys Ala	Leu Trp Ala Pro Met Tyr	Gln Leu Leu
50	55	60
Trp Leu Leu Ala Ala Ala Asp	Phe Val Leu Ala Thr Ser	Thr Val Pro
65	70	75
Lys Ala Leu Ala Val Leu Trp	Gly Leu Ser Ser Glu Ile Ser	Phe Gly
85	90	95
Gly Cys Leu Ala Gln Leu Phe	Val Ala His Ser Val Asn	His Cys His
100	105	110
Ile Ala Glu Ser Ser Val Leu	Leu Ser Thr Ala Val Asp	Cys Gln Pro
115	120	125
Leu Arg Tyr Gly Ala Leu Leu	Ala Gln Phe Val Val Gly	Leu Val Ala
130	135	140
Leu Thr Thr Met Thr Arg Asp	Val Cys Val Met Tyr Thr	Leu Xaa Phe
145	150	155
Leu Phe Lys Lys Leu Pro Tyr	Cys Gly Gln Trp Ala Leu	Thr His Thr
165	170	175
Tyr Cys Glu His Met Gly Val	Ala Cys Leu Ala Cys Gly	Asp Thr Cys
180	185	190
Pro Ile Ile Arg Tyr Gly Leu	Ala Thr Thr Leu Leu Ser	Pro Ala Leu
195	200	205

Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val
 210 215 220
 Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys
 225 230 235 240
 Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe
 245 250 255
 Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile
 260 265 270
 His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn
 275 280 285
 Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu
 290 295 300
 Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu
 305 310 315

<210> 2185

<211> 320

<212> PRT

<213> Homo sapien (7658481-19-6742-9039)

<400> 2185

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1 5 10 15
 Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
 20 25 30
 Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
 35 40 45
 Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
 50 55 60
 Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
 65 70 75 80
 Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
 85 90 95
 Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
 100 105 110
 His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
 115 120 125
 Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
 130 135 140
 Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
 145 150 155 160
 Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
 165 170 175
 Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
 180 185 190
 Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
 195 200 205
 Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
 210 215 220
 Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Asp
 225 230 235 240
 Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
 245 250 255
 Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
 260 265 270
 Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
 275 280 285
 Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
 290 295 300
 Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
 305 310 315 320

<210> 2186
 <211> 315
 <212> PRT
 <213> Homo sapien (7658481-2-1-1440)

<220>
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 2186
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu
 1 5 10 15
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu
 20 25 30
 Leu Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu
 35 40 45
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe
 85 90 95
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr
 100 105 110
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala
 130 135 140
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val
 165 170 175
 Leu Ser His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys
 180 185 190
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser
 195 200 205
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile
 210 215 220
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr
 225 230 235 240
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val
 245 250 255
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro
 260 265 270
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His
 290 295 300
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys
 305 310 315

<210> 2187
 <211> 124
 <212> PRT
 <213> Homo sapien (7658497-19-2333-3610)

<220>
 <221> VARIANT
 <222> (1)...(124)

<223> Xaa = Any Amino Acid

<400> 2187

```

Leu Ile Leu Ser Ala Gln Ile Cys Arg Ala Leu Xaa Leu Ser Ile Phe
 1           5           10           15
Leu Val Arg Leu His Phe Lys Lys Leu Gly Pro Lys Ser Leu Asp Leu
          20           25           30
Tyr Phe Pro Gly Leu Gly Leu Lys Tyr Lys Ile Asn Ser Thr Asn Asn
          35           40           45
Tyr Arg Thr Ala Leu Glu Phe Xaa Val Phe Arg Gln Ala Val Xaa Leu
          50           55           60
Xaa Phe Thr Phe Phe Leu Phe Lys Tyr Ser Cys Leu Ser Lys Pro Gln
65          70          75          80
Xaa Glu Xaa Gly Ser Ser Asp Xaa Val Pro Cys Gln Tyr Ser Arg Cys
          85          90          95
Ser Glu His Asn Val Ala Leu Leu Ser Pro Gly Phe Ile Val Met Xaa
          100         105         110
Val Leu Val Gln Leu Pro Leu Phe Ser Phe Thr Ser
          115         120

```

<210> 2188

<211> 278

<212> PRT

<213> Homo sapien (7670214-14-2036-3224)

<400> 2188

```

Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser
 1           5           10           15
Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met
          20           25           30
Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu
          35           40           45
Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser
          50           55           60
Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val
65          70          75          80
Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro
          85          90          95
Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp
          100         105         110
Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg
          115         120         125
Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser
130         135         140
Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg
145         150         155         160
Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu
          165         170         175
Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro
          180         185         190
Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu
          195         200         205
Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg
          210         215         220
Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val
225         230         235         240
Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg
          245         250         255
Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
          260         265         270
Leu Gly Asp Pro Ala Ala

```

275

<210> 2189
 <211> 203
 <212> PRT
 <213> Homo sapien (7670214-23-12266-12905)

<220>
 <221> VARIANT
 <222> (1)...(203)
 <223> Xaa = Any Amino Acid

<400> 2189
 Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1 5 10 15
 Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp
 20 25 30
 Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
 35 40 45
 Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
 50 55 60
 Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
 65 70 75 80
 Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
 85 90 95
 Leu Pro His Phe Leu Leu Val Asn Phe Phe His Leu Met Arg Leu
 100 105 110
 Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
 115 120 125
 Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
 130 135 140
 Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
 145 150 155 160
 Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
 165 170 175
 Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
 180 185 190
 Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp
 195 200

<210> 2190
 <211> 321
 <212> PRT
 <213> Homo sapien (7671636-1-417-2747)

<220>
 <221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 2190
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys
 20 25 30
 Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile
 35 40 45
 Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala
 50 55 60
 Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr
 65 70 75 80

```

Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly
      85                      90                      95
Cys L  Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser
      100                      105                      110
Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser
      115                      120                      125
Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met
      130                      135                      140
Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu
      145                      150                      155                      160
Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His
      165                      170                      175
Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr
      180                      185                      190
Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly
      195                      200                      205
Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr
      210                      215                      220
Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr
      225                      230                      235                      240
Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile
      245                      250                      255
Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe
      260                      265                      270
Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn
      275                      280                      285
Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val
      290                      295                      300
Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile
      305                      310                      315                      320
Pro

```

<210> 2191

<211> 295

<212> PRT

<213> Homo sapien (7690091-1-489-1697)

<220>

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 2191

```

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
  1                      5                      10                      15
Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
      20                      25                      30
Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
      35                      40                      45
Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
      50                      55                      60
Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
      65                      70                      75                      80
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
      85                      90                      95
Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
      100                      105                      110
Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
      115                      120                      125
Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe

```

130	135	140
Cys Asp Pro Ser Gln Leu	Pro His Leu Ala Cys	Cys Asp Thr Phe Thr
145	150	155
Asn Asp Ile Val Met Tyr	Phe Leu Ala Ala Ile	Phe Gly Phe Leu Pro
165	170	175
Ile Ser Gly Thr Phe	Phe Ser Tyr Tyr Lys	Ile Val Ser Ser Ile Leu
180	185	190
Arg Val Ser Ser Ser Gly	Gly Lys Tyr Lys Ala Phe	Ser Thr Cys Gly
195	200	205
Ser His Leu Ser Val Val	Cys Leu Phe Tyr Gly Thr	Gly Phe Gly Gly
210	215	220
Asp Leu Ser Ser Asp Met	Ser Ser Tyr Pro Arg	Lys Gly Ala Val Ala
225	230	235
Ser Val Met Tyr Thr Val	Val Thr Pro Met Leu	Asn Pro Phe Ile Tyr
245	250	255
Ser Arg Asn Arg Glu Ile	Lys Ser Ala Leu Arg	Gln Leu His Cys Arg
260	265	270
Ile Val Xaa Ser His Phe	Leu Ile Cys Ser Ile	Pro Ser Val Val
275	280	285
Xaa Val Arg Lys Gly Ser	Lys	
290	295	

<210> 2192

<211> 197

<212> PRT

<213> Homo sapien (7705148-11-94-972)

<220>

<221> VARIANT

<222> (1)...(197)

<223> Xaa = Any Amino Acid

<400> 2192

Ala Ala Met Ala Xaa	Asp Arg Tyr Ile Ala	Ile Cys Asn Pro Leu Leu
1	5	10
Tyr Thr Val Ile Met	Ser Lys Lys Val Cys	Cys Gln Leu Ala Ile Gly
20	25	30
Ala Phe Leu Gly Gly	Thr Met Ser Ser Ile	Ile His Thr Thr Asn Thr
35	40	45
Phe His Leu Ser Phe	Cys Ser Arg Asp Ile	Asn His Phe Phe Cys Asp
50	55	60
Ile Ser Pro Leu Phe	Ser Leu Ser Cys Thr	Asp Thr Tyr Met His Asp
65	70	75
Ile Ile Leu Val Val	Phe Ala Ser Phe Val	Glu Ala Ile Cys Leu Leu
85	90	95
Ser Val Leu Leu Ser	Tyr Val Phe Ile Met	Ala Ala Ile Leu Arg Thr
100	105	110
Gly Ser Val Glu Gly	Arg Arg Arg Gly Phe	Ser Thr Cys Ala Ser His
115	120	125
Leu Thr Val Val Thr	Met Tyr His Gly Thr	Leu Ile Phe Ile Tyr Leu
130	135	140
Arg Pro Ser Thr Gly	His Ser Leu Asp Ile	Asp Lys Val Thr Ser Val
145	150	155
Phe Tyr Thr Leu Ile	Ile Pro Met Leu Asn	Pro Leu Ile Tyr Ser Leu
165	170	175
Arg Asn Lys Asp Val	Lys Asn Ala Phe Arg	Lys Val Ile Gly Arg Lys
180	185	190
Leu Leu Pro Xaa Gly		
195		

<210> 2193

<211> 128
 <212> PRT
 <213> Homo sapien (7705148-13-12855-13510)

<220>
 <221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 2193
 Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1 5 10 15
 Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
 20 25 30
 Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
 35 40 45
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
 50 55 60
 Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
 65 70 75 80
 Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
 85 90 95
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
 100 105 110
 Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
 115 120 125

<210> 2194
 <211> 208
 <212> PRT
 <213> Homo sapien (7705148-18-30183-31440)

<220>
 <221> VARIANT
 <222> (1)...(208)
 <223> Xaa = Any Amino Acid

<400> 2194
 Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
 20 25 30
 Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
 35 40 45
 Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
 65 70 75 80
 Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
 130 135 140
 Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
 145 150 155 160
 Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
 165 170 175
 Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr

180	185	190
Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile		
195	200	205

<210> 2195
 <211> 188
 <212> PRT
 <213> Homo sapien (7705148-8-1-2633)

<400> 2195
 Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
 1 5 10 15
 Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
 20 25 30
 Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
 35 40 45
 Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
 85 90 95
 Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
 100 105 110
 Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
 130 135 140
 Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
 145 150 155 160
 Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Ser
 180 185

<210> 2196
 <211> 210
 <212> PRT
 <213> Homo sapien (7705159-18-2705-3893)

<220>
 <221> VARIANT
 <222> (1)...(210)
 <223> Xaa = Any Amino Acid

<400> 2196
 Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
 1 5 10 15
 Gly Leu Ala Leu Ser Ser Arg Xaa Phe Phe Phe Leu Ser Val Leu
 20 25 30
 Asp Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln
 35 40 45
 Asp Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His
 50 55 60
 Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro
 65 70 75 80
 Ala Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr
 85 90 95
 Tyr Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln
 100 105 110
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa

```

      115      120      125
Phe Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser
 130      135      140
Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr
145      150      155      160
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys
      165      170      175
Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu
      180      185      190
Leu Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys
      195      200      205
Val Lys
 210

```

<210> 2197
 <211> 186
 <212> PRT
 <213> Homo sapien (7708872-11-1-1518)

<220>
 <221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

```

<400> 2197
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
 1      5      10      15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
      20      25      30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Thr Pro Asn Ile Phe
      35      40      45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
      50      55      60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
      65      70      75      80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
      85      90      95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
      100      105      110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
      115      120      125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
      130      135      140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145      150      155      160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
      165      170      175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
      180      185

```

<210> 2198
 <211> 323
 <212> PRT
 <213> Homo sapien (7708872-16-23686-24654)

<220>
 <221> VARIANT
 <222> (1)...(323)
 <223> Xaa = Any Amino Acid

<400> 2198

```

Val Ala Cys Tyr Leu Pr  Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
 1          5          10          15
Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
          20          25          30
Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
          35          40          45
Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
          50          55          60
Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
65          70          75          80
Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
          85          90          95
His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
          100          105          110
Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
          115          120          125
Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu
          130          135          140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val
145          150          155          160
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile
          165          170          175
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr
          180          185          190
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn
          195          200          205
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala
          210          215          220
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ala Ile Leu Arg Ile
225          230          235          240
Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His
          245          250          255
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile
          260          265          270
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met
          275          280          285
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met
          290          295          300
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser
305          310          315          320
His Ser Ser

```

<210> 2199

<211> 328

<212> PRT

<213> Homo sapien (7715624-11-1-3301)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2199

```

Leu Ser Ile Cys Phe Phe Leu Cys Ile Phe Ser Ala Asp Ile Xaa Ser
 1          5          10          15
Met Leu Ala Met Glu Gln Asn Asn Gly Thr Glu Val Thr Glu Phe Ile
          20          25          30
Leu Leu Gly Phe Ala Gly Gln His Lys Ser Trp His Ile Leu Ser Ile
          35          40          45
Ala Phe Leu Ala Ile Tyr Val Val Thr Pro Val Gly Asn Ile Gly Met

```



```

      50              55              60
Ile Leu Leu Ile Lys Ile Asp Ala Ser Leu His Ile Pro Met Xaa Ile
65              70              75              80
Phe Leu Gln His Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Ala Ile
      85              90              95
Thr Pro Lys Met Leu Lys Asn Phe Val Glu Thr Lys Lys Ser Ile Ser
      100              105              110
Cys Ile Gly Cys Met Val Gln Leu Leu Val Tyr Gly Thr Phe Ala Thr
      115              120              125
Ser Asp Cys Tyr Ile Leu Ala Ala Met Ala Val Asp Arg Tyr Val Ala
      130              135              140
Phe Cys Asn Pro Leu His Tyr Pro Gly Val Met Ser Gln Arg Leu Cys
145              150              155              160
Ile Lys Leu Leu Val Ser Ser Tyr Val Met Gly Phe Leu Asn Ala Ser
      165              170              175
Ile Asn Ile Ser Phe Thr Phe Ser Leu Asn Phe Cys Lys Ser Lys Thr
      180              185              190
Ile Asn His Phe Phe Cys Asp Glu Pro Pro Ile Ile Ala Leu Pro Cys
      195              200              205
Ser Asn Ile Asp Leu Asn Ile Met Leu Leu Thr Val Phe Val Gly Leu
      210              215              220
Asn Leu Met Cys Thr Val Met Val Val Ile Ile Ser Cys Ile Tyr Val
225              230              235              240
Leu Val Ala Ile Leu Arg Ile Ser Ser Ala Ala Gly Lys Lys Lys Ser
      245              250              255
Leu Ser Thr Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly
      260              265              270
Val Leu Ser Tyr Met Tyr Leu Cys His Arg Ile Asn Glu Ser Gln Lys
      275              280              285
Gln Glu Lys Val Ala Ser Val Phe Tyr Gly Ile Ile Ile Pro Met Leu
      290              295              300
Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Ile
305              310              315              320
Lys Leu Thr Glu Lys Lys Tyr Phe
      325

```

<210> 2200

<211> 193

<212> PRT

<213> Homo sapien (7768677-1-106933-108798)

<220>

<221> VARIANT

<222> (1)...(193)

<223> Xaa = Any Amino Acid

<400> 2200

```

Phe Phe Asn Ile Thr Xaa Phe Val Pro Glu Val Met Lys Ser Leu Ser
1              5              10              15
Arg Ser Lys Asp Ile Ser Phe Asn Phe Cys Phe Xaa Phe Phe Phe
      20              25              30
Ser Cys Gly Cys Thr Gly Leu Thr Glu Asp Ile Phe Val Val Phe Lys
      35              40              45
Ser Phe Val Leu Phe Gly Val Leu Ser Xaa Ala His Leu Pro Val Lys
      50              55              60
Lys Lys Lys Lys Arg Phe Cys Ser Leu Leu Tyr Xaa Thr Thr Ile Leu
65              70              75              80
Ile Cys Lys Trp Pro Lys Thr Ser Pro Phe Phe Thr Glu Phe Leu Ser
      85              90              95
Leu Ser Arg Lys Asn Leu Lys Phe Gln Lys Asn Ile Glu Cys Glu Tyr
      100              105              110

```

Met Ile Ser Val Xaa Ala Thr Cys Ile Gly Asn Lys Tyr Leu Asn Cys
 115 120 125
 Glu Ile Tyr Leu Arg Ser Leu Thr Phe Pro Asn Il Ser Ser Ile Val
 130 135 140
 Phe Phe Leu Leu Gln Ser Lys Tyr Met Phe Thr Phe Xaa Lys Tyr Arg
 145 150 155 160
 Glu Ala Gln Asn Trp Gly Lys Lys Pro Xaa Xaa Ile Pro Pro Ser Arg
 165 170 175
 Lys Lys Ala Ile Asn Leu Xaa Arg Ile Ser Ser Xaa Ser Leu Phe Cys
 180 185 190
 Val

<210> 2201

<211> 291

<212> PRT

<213> Homo sapien (7770649-26-5915-7266)

<400> 2201

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
 35 40 45
 Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe
 130 135 140
 Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu
 145 150 155 160
 Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser
 180 185 190
 Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
 195 200 205
 Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr
 210 215 220
 Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
 245 250 255
 Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Tyr Thr
 275 280 285
 Phe Arg Asn
 290

<210> 2202

<211> 92

<212> PRT

<213> Homo sapien (7939486-13-581-990)

<220>

<221> VARIANT

<222> (1)...(92)

<223> Xaa = Any Amino Acid

<400> 2202

Cys	His	Pro	Ser	His	Tyr	Phe	Ser	Ile	Leu	Ile	Arg	Phe	Leu	Cys	Leu
1				5					10				15		
Tyr	Leu	Ser	Leu	Glu	Met	Gln	Ala	Ala	Cys	Ser	Ser	Ser	Xaa	Leu	Thr
			20				25						30		
His	Thr	Ile	His	Phe	Met	Lys	His	Lys	Pro	Val	Leu	Thr	Asn	Ser	Leu
		35					40					45			
Ser	Ser	Leu	Phe	Asn	Leu	Ser	Asn	Cys	Asp	Lys	Asn	His	Thr	Ala	Leu
		50				55					60				
Tyr	Pro	Val	Xaa	Pro	Pro	Met	Ile	Phe	Asp	Gln	Lys	Pro	Asn	Leu	Phe
65					70					75					80
Phe	Val	Val	Phe	Thr	Tyr	Gly	Gln	Leu	Gly	Ser	Thr				
				85					90						

<210> 2203

<211> 168

<212> PRT

<213> Homo sapien (7996320-1-1-801)

<400> 2203

Lys	Gln	Ser	Ser	Gly	Asp	Ser	Gly	Asn	Gln	Thr	Thr	Trp	Leu	Ile	Leu
1				5					10				15		
Val	Gly	Phe	Gly	Glu	Leu	Gln	Tyr	Leu	Gly	Phe	Leu	Pro	Phe	Thr	Leu
			20				25						30		
Phe	Leu	Ala	Ile	Tyr	Val	Val	Thr	Val	Val	Gly	Asn	Ala	Leu	Ile	Met
		35					40					45			
Leu	Ala	Val	Ala	Ser	Ser	Arg	Thr	Leu	His	Pro	Pro	Met	Tyr	Phe	Phe
		50				55					60				
Leu	Cys	His	Phe	Ser	Leu	Glu	Ile	Gly	Tyr	Thr	Ser	Asn	Val	Ile	
65					70				75					80	
Leu	Trp	Leu	Leu	Gln	Ser	Phe	Leu	Glu	Gly	Lys	Glu	Val	Ile	Ser	Leu
			85						90					95	
Val	Ser	Cys	Leu	Ala	Gln	Phe	Tyr	Val	Phe	Ser	Ser	Leu	Ala	Ala	Ala
			100				105						110		
Glu	Cys	Leu	Leu	Ser	Ala	Val	Ser	Tyr	Asp	Cys	Tyr	Leu	Ala	Ile	
		115				120					125				
Cys	Cys	Pro	Leu	His	Tyr	Pro	Ala	Leu	Met	Ser	Thr	Trp	Phe	Cys	His
		130				135					140				
Cys	Leu	Ala	Ala	Gly	Ala	Trp	Phe	Ser	Gly	Phe	Phe	Ser	Ser	Ala	Phe
145					150					155					160
Thr	Met	Ala	Leu	Ala	Ala	Pro	Leu								
					165										

<210> 2204

<211> 167

<212> PRT

<213> Homo sapien (7996320-11-500-1042)

<220>

<221> VARIANT

<222> (1)...(167)

<223> Xaa = Any Amino Acid

<400> 2204

Gly Leu Gly Gly Gly Gln Ser Cys Ala Asn Lys Lys Trp Gly Thr Gly
 1 5 10 15
 Leu Asn Leu Thr Pro Ser Phe His Gly Ser Arg Ser Asn Phe Cys Gly
 20 25 30
 Pr Xaa Ile Ser Ile His Ser Tyr Ser Leu Gln Ser Phe Leu Pro Val
 35 40 45
 Leu Ile Met Asn Leu Tyr Xaa Thr His Cys Ser Xaa Gln Ser Ser Pro
 50 55 60
 Ile Leu His Tyr Pro Val Gln Val Leu Gly Leu Gly Thr Leu Val Leu
 65 70 75 80
 Leu Leu Gly Ser Tyr Ser Cys Ile Ile Met Thr Ala Pro Gly Asp Gln
 85 90 95
 Leu Cys Xaa Gln Gly Arg Ser Lys Ile Leu Ser Thr Cys Ser Ser His
 100 105 110
 Tyr Leu Val Val Thr Ile Phe Tyr Thr Ser Gly Phe Leu Arg Tyr Val
 115 120 125
 Ile Leu Tyr Pro Xaa Ile Xaa Met Arg Asp Ile Pro Tyr Pro Lys Trp
 130 135 140
 Ser Pro Leu Ala Glu Glu Ser Ile Thr Lys Xaa Gln Asp Ile Gln Lys
 145 150 155 160
 Ala Xaa Ala Leu Val Leu Leu
 165

<210> 2205

<211> 294

<212> PRT

<213> Homo sapien (8052042-13-4893-7590)

<400> 2205

Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
 1 5 10 15
 Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu
 20 25 30
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
 35 40 45
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
 50 55 60
 Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
 65 70 75 80
 Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe
 85 90 95
 Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser Ser
 100 105 110
 Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile
 115 120 125
 Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp
 130 135 140
 Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala
 145 150 155 160
 Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro
 165 170 175
 Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser
 180 185 190
 Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val
 195 200 205
 Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile
 210 215 220
 Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala
 225 230 235 240
 Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Ile
 245 250 255

Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro
 260 265 270
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys
 275 280 285
 Leu Leu Gln Ala Leu Pro
 290

<210> 2206
 <211> 175
 <212> PRT
 <213> Homo sapien (8052042-5-3342-10968)

<220>
 <221> VARIANT
 <222> (1)...(175)
 <223> Xaa = Any Amino Acid

<400> 2206
 Leu Leu Met Ala Ala Asp Asn His Thr Arg Val Glu Ala Phe Val Leu
 1 5 10 15
 Gln Gly Phe Ser Glu Asp Leu Pro Leu Gln Gly Cys Cys Phe Ala Phe
 20 25 30
 Phe Leu Leu Tyr Leu Met Ala Leu Val Gly Asn Ile Leu Met Val Met
 35 40 45
 Ala Ile Ser Leu Asn Pro Gly Leu His Thr Pro Val Tyr Phe Phe Leu
 50 55 60
 Thr Asn Leu Ala Leu Leu Asp Ile Val Cys Thr Ser Met Asp Asn Ser
 65 70 75 80
 Arg Val Val Ala Val Leu Tyr Thr Val Val Ser Pro Thr Leu Asn Pro
 85 90 95
 Ser Pro Thr Pro Cys Gly Thr Arg Thr Tyr Gln Xaa His Xaa Gly Glu
 100 105 110
 Cys Phe Leu Ala Ser Gly Lys Arg Lys Gly Ser Phe Xaa Cys Glu Met
 115 120 125
 Phe Gln Val Leu Thr Asn Xaa Phe Gln His Met Thr Leu Arg Ile Ser
 130 135 140
 Cys Lys Gln Gln Gly Thr Arg Lys Xaa Leu Met Pro His Ile Tyr Lys
 145 150 155 160
 Xaa Cys Ala Pro Ala Arg Gly Cys His His Ser Met Trp Asn Ser
 165 170 175

<210> 2207
 <211> 275
 <212> PRT
 <213> Homo sapien (8072456-16-39461-40850)

<400> 2207
 Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser
 1 5 10 15
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp
 20 25 30
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu
 35 40 45
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe
 50 55 60
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met
 65 70 75 80
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn
 85 90 95
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Val Val Ala Met Ile
 100 105 110

Gly Gly Phe Val His Ser Val Val Gln Ile Val Ph Leu Tyr Ser Leu
 115 120 125
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr
 130 135 140
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr
 145 150 155 160
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu
 165 170 175
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln
 180 185 190
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val
 195 200 205
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val
 210 215 220
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile
 225 230 235 240
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met
 245 250 255
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg
 260 265 270
 Lys Arg Val
 275

<210> 2208

<211> 316

<212> PRT

<213> Homo sapien (8077072-13-9613-11523)

<220>

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 2208

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val
 1 5 10 15
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met
 20 25 30
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile
 35 40 45
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile
 65 70 75 80
 Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser
 85 90 95
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala
 100 105 110
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys
 130 135 140
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala
 145 150 155 160
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu
 165 170 175
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys
 180 185 190
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
 195 200 205
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val

210	215	220
Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala		
225	230	235
Phe Ser Thr Cys S r Ser His Leu Thr Val Val Ile Val Phe Tyr Gly		240
	245	250
Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu		255
	260	265
Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe		270
	275	280
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu		285
	290	295
Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu		300
305	310	315

<210> 2209

<211> 309

<212> PRT

<213> Homo sapien (8081198-24-6628-8036)

<400> 2209

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr	
1	5
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met	
	20
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile	
	35
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu	
	50
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile	
65	70
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu	
	85
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu	
	100
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu	
	115
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly	
	130
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe	
145	150
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile	
	165
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile	
	180
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile	
	195
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys	
	210
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser	
225	230
His Leu Thr Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr	
	245
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser	
	260
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
	275
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu	
	290
Ala Leu Ala Gly Lys	
305	

<210> 2210
 <211> 270
 <212> PRT
 <213> H mo sapien (8086488-18-2452-4090)

<400> 2210
 Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
 1 5 10 15
 Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
 20 25 30
 Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
 35 40 45
 Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
 65 70 75 80
 Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
 85 90 95
 Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
 100 105 110
 Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
 115 120 125
 Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
 130 135 140
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
 145 150 155 160
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
 165 170 175
 His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
 180 185 190
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
 195 200 205
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
 210 215 220
 Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
 245 250 255
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
 260 265 270

<210> 2211
 <211> 161
 <212> PRT
 <213> Homo sapien (8096828-10-670-2127)

<220>
 <221> VARIANT
 <222> (1)...(161)
 <223> Xaa = Any Amino Acid

<400> 2211
 Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu
 1 5 10 15
 Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro
 20 25 30
 Leu Val Phe Leu Phe Val Thr Ile Ile Ser Ala Asn Ala Leu Val Ile
 35 40 45
 His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu
 50 55 60
 Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met

65					70					75				80
Pro	Lys	Met	Leu	Glu	Gly	Phe	Val	Tyr	Tyr	Ala	Asn	Pro	Ile	Ser
				85					90				95	
His	Gly	Arg	Leu	Ala	Xaa	Val	Phe	Phe	Ile	Tyr	Phe	Thr	Leu	Leu
			100					105					110	
Asp	Tyr	Asn	Phe	Leu	Trp	Pro	Trp	Pro	Trp	Thr	Gly	Tyr	Phe	Ala
		115					120					125		
Cys	His	Pro	Leu	Cys	Phe	Ser	Asp	Leu	Met	Thr	Ser	Gln	Leu	Gly
	130					135					140			
Leu	Leu	Ala	Ile	Leu	Ala	Phe	Glu	Gln	Ser	Pro	Gly	Ser	Asp	Pro
145					150					155				160
Pro														

<210> 2212

<211> 198

<212> PRT

<213> Homo sapien (8096828-22-1-1563)

<220>

<221> VARIANT

<222> (1)...(198)

<223> Xaa = Any Amino Acid

<400> 2212

Val	Ala	Ile	Cys	His	Pro	Leu	Cys	Phe	Gln	Thr	Glu	Xaa	Leu	Pro	Ser
1				5					10					15	
Trp	Leu	Gly	Leu	Leu	Ala	Ile	Leu	Ala	Leu	Thr	Gln	Ser	Trp	Gly	Val
			20					25					30		
Thr	Val	Pro	Leu	Val	Val	Leu	Thr	Ala	Lys	Ala	Asp	Phe	Cys	Arg	Thr
		35				40						45			
Ala	Val	Ile	Arg	His	Phe	Thr	Cys	Glu	Cys	Ile	Ala	Leu	Leu	Ser	Ile
	50					55					60				
Ala	Cys	Gly	Asp	Leu	Thr	Phe	Asn	Asn	Trp	Leu	Gly	Leu	Ala	Met	Cys
65					70				75					80	
Leu	Val	Thr	Val	Ile	Ser	Asp	Met	Ala	Leu	Leu	Gly	Thr	Ser	Tyr	Thr
			85					90					95		
His	Ile	Ile	Tyr	Ala	Ala	Phe	Arg	Ile	Ser	Ser	Trp	Gly	Ala	Gln	Ala
		100					105						110		
Lys	Ala	Leu	His	Thr	Cys	Gly	Ser	His	Leu	Leu	Val	Ile	Leu	Ser	Ile
		115					120					125			
Tyr	Val	Ser	Gly	Leu	Ser	Thr	Ser	Ile	Thr	Phe	Xaa	Val	Ala	Lys	Thr
	130					135					140				
Val	Ser	Gln	Asn	Val	Gln	Asn	Leu	Leu	Ser	Ala	Ile	Tyr	Leu	Leu	Leu
145				150					155					160	
Pro	Gly	Ala	Leu	Asn	Pro	Val	Ile	Tyr	Gly	Val	Arg	Thr	Arg	Glu	Ile
			165						170					175	
Gln	Gln	His	Val	Glu	Lys	Met	Leu	Cys	Glu	Lys	Glu	Thr	Ala	Gln	Lys
		180						185					190		
Ala	Gly	Glu	Lys	Pro	Lys										
		195													

<210> 2213

<211> 323

<212> PRT

<213> Homo sapien (8096945-19-338-2509)

<220>

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 2213

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Ph Ile Leu Leu
 1 5 10 15
 Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser
 20 25 30
 Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr
 35 40 45
 Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu
 50 55 60
 Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro
 65 70 75 80
 Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro
 85 90 95
 Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe
 100 105 110
 Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met
 115 120 125
 Thr Ile Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr
 130 135 140
 Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu
 145 150 155 160
 Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile
 165 170 175
 Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr
 180 185 190
 Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met
 195 200 205
 Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr
 210 215 220
 Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala
 225 230 235 240
 Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr
 245 250 255
 Pro Thr Met Leu Ser Ala Leu Thr His Phe Gly Gln Ser Ile Ser
 260 265 270
 Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro
 275 280 285
 Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn
 290 295 300
 Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp
 305 310 315 320
 Glu Asn Met

<210> 2214

<211> 130

<212> PRT

<213> Homo sapien (8099799-17-8549-9091)

<220>

<221> VARIANT

<222> (1)...(130)

<223> Xaa = Any Amino Acid

<400> 2214

Phe Xaa Ser Ser Ser Gly Gln Thr Arg His Phe Lys Ala Tyr Glu Xaa
 1 5 10 15
 His Leu Val Thr Gln Cys Ser Met Leu Trp Val Xaa Asp Xaa Tyr Phe
 20 25 30
 Leu Cys Ala Leu Leu Gln Pro Leu His His Gly Ser Lys Ser Xaa Thr

35 40 45
 Gln Gly Ser Ser Phe Trp Ala Lys Gly Phe Val Leu Glu Val Ile Leu
 50 55 60
 Ser Phe Ser Xaa Xaa Val Ala His Ile Cys Ser Xaa Leu Val Leu Ser
 65 70 75 80
 Ala Phe Ser Cys Leu Xaa Asn Phe Met Ser Leu Thr Ala Phe Phe His
 85 90 95
 Phe Val Leu Ser Leu Ser Leu Xaa His Lys Leu Val Val Phe Leu Lys
 100 105 110
 Leu Tyr His Phe Xaa Lys Pro Gly Ser Pro Met Tyr Val Met Thr Ile
 115 120 125
 His Ile
 130

<210> 2215

<211> 188

<212> PRT

<213> Homo sapien (8102357-9-3785-4449)

<220>

<221> VARIANT

<222> (1)...(188)

<223> Xaa = Any Amino Acid

<400> 2215

His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile
 1 5 10 15
 Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile
 20 25 30
 Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe
 35 40 45
 Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu
 50 55 60
 Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro
 65 70 75 80
 Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys
 85 90 95
 Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val
 100 105 110
 Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu
 115 120 125
 Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala
 130 135 140
 Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu
 145 150 155 160
 Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg
 165 170 175
 Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala
 180 185

<210> 2216

<211> 318

<212> PRT

<213> Homo sapien (8102369-26-1-1971)

<400> 2216

Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
 20 25 30
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu

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      35      40      45
Thr  Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
  50      55      60
Gln  Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
  65      70      75      80
Thr  Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
      85      90      95
Gly  Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
      100     105     110
Cys  Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115     120     125
Gln  Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
      130     135     140
Met  Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
  145     150     155     160
Ala  Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
      165     170     175
His  Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
      180     185     190
Lys  His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
      195     200     205
Met  Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
      210     215     220
Ala  Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser
  225     230     235     240
Thr  Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala
      245     250     255
Ser  Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp
      260     265     270
Arg  Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro
      275     280     285
Ile  Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr
      290     295     300
Leu  Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly
  305     310     315

```

<210> 2217

<211> 109

<212> PRT

<213> Homo sapien (8102369-32-1554-1892)

<220>

<221> VARIANT

<222> (1)...(109)

<223> Xaa = Any Amino Acid

<400> 2217

```

Tyr Met Val Val Thr Leu Val Leu Val Ile Leu Ser Tyr Ala Phe Ile
  1      5      10      15
Ile Lys Thr Ile Leu Lys Leu Pro Ser Ala Gln Gln Arg Thr Lys Ala
      20      25      30
Phe Pro Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser Tyr Gly
      35      40      45
Ser Cys Met Phe Met Tyr Ile Asn Pro Ser Ala Lys Asp Arg Asp Thr
      50      55      60
Phe Asn Lys Gly Val Ala Leu Leu Ile Thr Ser Val Ala Pro Leu Leu
      65      70      75      80
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Gln Gln Val Arg Gln Pro Phe
      85      90      95
Lys Asp Met Val Lys Lys Leu Leu Asn Leu Xaa Arg Il
      100     105

```

<210> 2218
 <211> 131
 <212> PRT
 <213> Homo sapien (8102369-33-1-1370)

<400> 2218
 Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala
 20 25 30
 Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu
 35 40 45
 Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
 50 55 60
 Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu
 65 70 75 80
 Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe
 85 90 95
 Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu
 100 105 110
 Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met
 115 120 125
 Thr Met His
 130

<210> 2219
 <211> 313
 <212> PRT
 <213> Homo sapien (8102369-49-1-1012)

<220>
 <221> VARIANT
 <222> (1)...(313)
 <223> Xaa = Any Amino Acid

<400> 2219
 Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp
 1 5 10 15
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala
 20 25 30
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Thr Met
 35 40 45
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln
 50 55 60
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly
 85 90 95
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe
 100 105 110
 Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Tyr Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Pro Met Leu Ile Ser Ser Arg Val Cys Thr Gln Leu
 130 135 140
 Ile Leu Thr Cys Trp Leu Leu Gly Phe Ser Phe Ile Ile Met Pro Val
 145 150 155 160
 Ile Leu Thr Ser Gln Leu Pro Phe Cys Asp Thr His Ile Lys His Phe
 165 170 175
 Phe Cys Asp Tyr Thr Pro Leu Met Glu Val Val Cys Ser Gly Pro Lys
 180 185 190

Val Leu Glu Met Val Asp Phe Thr Leu Ala Leu Val Ala Leu Phe Gly
 195 200 205
 Thr Leu Val Leu Ile Thr Leu Ser Tyr Val Gln Ile Ile Gln Thr Ile
 210 215 220
 Val Arg Ile Pro Ala Val Gln Glu Arg Lys Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Val Ile Met Val Thr Met Cys Tyr Asp Ser Cys Phe Phe
 245 250 255
 Met Tyr Val Lys Pro Ser Pro Gly Lys Trp Val Asp Val Asn Lys Gly
 260 265 270
 Val Ser Leu Ile Asn Thr Ile Ile Ala Pro Leu Leu Asn Pro Phe Ile
 275 280 285
 Cys Thr Leu Arg Asn Gln Gln Val Lys Gln Val Met Lys Asp Leu Val
 290 295 300
 Arg Lys Met Thr Leu Ser Glu Asn Lys
 305 310

<210> 2220

<211> 96

<212> PRT

<213> Homo sapien (8117362-7-1589-1951)

<220>

<221> VARIANT

<222> (1)...(96)

<223> Xaa = Any Amino Acid

<400> 2220

Pro Leu Xaa Leu Met Val Val Ile Phe Ser Gln Val Tyr Thr Leu Ala
 1 5 10 15
 Ala Ile Pro Lys Met Ser Ser Thr Ala Gly Arg Thr Gln Gly Phe Phe
 20 25 30
 Met Xaa Ala Ser His Leu Thr Ala Val Val Ile Phe Tyr Gly Thr Pro
 35 40 45
 Ser Tyr Met Tyr Leu His His Gly Asn Asn Gly Ser Pro Lys Gln Gly
 50 55 60
 Lys Val Ser Ser Val Phe Tyr Gly Ile Val Ile Asp Leu Ser Leu Arg
 65 70 75 80
 Val Gln Asp Ala Arg Glu Ala Leu Lys Glu Lys Gly Lys Lys Gln Phe
 85 90 95

<210> 2221

<211> 195

<212> PRT

<213> Homo sapien (8117365-9-1-1453)

<220>

<221> VARIANT

<222> (1)...(195)

<223> Xaa = Any Amino Acid

<400> 2221

Arg Met Phe Xaa Thr Xaa Phe Phe Ser Ser Leu Thr Leu Arg Leu Gln
 1 5 10 15
 Leu Ser His Leu Phe Pro Cys Leu Gly Tyr Val Phe Ser Leu Leu Gly
 20 25 30
 Xaa His Asp Lys Arg Tyr Met Ile Gln Leu Asn Pro Ser Leu Ala Val
 35 40 45
 Leu Lys Cys Val Ile Phe Trp Cys Val Cys Val Leu Val Cys Met Ser
 50 55 60
 Tyr Glu Glu Gly Glu Arg Leu Ser Thr Ser Phe Leu Ala Pro Cys Val

65		70		75		80									
Ser	Xaa	Leu	Trp	Val	Phe	Ile	Thr	Cys	Arg	Val	Gly	Glu	Val	Phe	Gly
		85							90					95	
Phe	Xaa	Gly	Phe	Xaa	Ala	Ser	Gln	Xaa	Ser	His	Lys	Ile	Asn	Tyr	Cys
		100						105					110		
Val	Asn	Ile	Val	Leu	Leu	Gly	Gly	Cys	Ile	Leu	Gln	His	Thr	Xaa	Asp
		115						120					125		
Thr	Ser	Gln	Leu	Lys	Glu	Met	Ser	Ser	Glu	Met	Leu	Ala	Arg	Arg	Lys
		130						135					140		
Arg	Arg	Ile	Thr	Leu	Arg	Ser	Leu	Met	Gly	His	Pro	Ser	Ile	Phe	Leu
		145						150					155		160
Leu	Arg	Arg	Ser	Lys	Ala	Gly	Ser	Ile	Ser	Xaa	Thr	Asp	Lys	Ser	Arg
				165						170				175	
Leu	Ser	His	Arg	His	Ser	Arg	Val	Arg	Leu	Tyr	Ile	Ile	Thr	Gly	Thr
			180						185					190	
Asn	Met	Val													
		195													

<210> 2222

<211> 318

<212> PRT

<213> Homo sapien (8117535-2-10765-15227)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2222

Cys	Val	Asp	Ser	Ser	Leu	Lys	Xaa	Glu	Ile	Thr	Gln	Xaa	Cys	Leu	Ser
1				5					10					15	
Leu	Leu	Leu	Xaa	Met	Ala	Glu	Gly	Trp	Arg	Leu	Tyr	Phe	Ile	Ile	Leu
			20					25					30		
Ile	Ile	Ser	Tyr	Lys	Phe	Cys	Thr	Leu	Leu	Gly	Asn	Val	Ile	Phe	Arg
		35					40					45			
Thr	Leu	Val	Cys	Ser	Leu	Gly	Phe	His	Thr	Ser	Cys	Met	Tyr	Phe	Phe
		50				55					60				
Pro	Xaa	Lys	Ile	Ser	Leu	Xaa	Leu	Ala	Xaa	Val	Cys	His	Ser	Ile	Ile
		65			70				75					80	
Ala	Leu	Pro	Ser	Thr	Gln	Lys	Xaa	Ala	Ile	Asn	Val	Gln	Gly	Ala	Ala
				85					90					95	
Val	His	Val	Phe	Ser	Phe	Pro	Cys	Leu	Tyr	Cys	Pro	Glu	Ile	Phe	Leu
			100					105					110		
His	Ser	Leu	Thr	Gln	Cys	His	Pro	Phe	Ile	Ala	Ile	Gly	Tyr	Pro	Leu
		115					120					125			
Gln	Gly	Met	His	Thr	Ile	Thr	His	Lys	Leu	Tyr	Ile	Leu	Leu	Thr	Thr
		130				135					140				
Gly	Pro	Trp	Arg	Gly	Cys	Xaa	Leu	His	Val	Asn	Leu	Leu	Thr	Ala	Leu
		145			150					155				160	
Leu	Gly	Ser	Tyr	Pro	Asn	Pro	Val	Pro	Thr	Lys	Leu	Trp	Leu	Ser	Phe
			165					170					175		
Pro	Ser	Ile	Pro	Glu	Val	Lys	Leu	Xaa	Pro	Met	Gln	Ala	Tyr	Thr	Lys
			180					185					190		
Pro	Tyr	Ala	Gly	Leu	Ser	Leu	Cys	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser
		195					200					205			
Phe	Ser	Leu	Phe	Ser	Ile	Ile	Ser	Ile	Ser	Tyr	Ile	Cys	Asn	Glu	Ile
		210				215					220				
Asp	Ile	Pro	Lys	Ile	Ile	Ser	Ala	Asp	Ser	Val	His	Gly	Ala	Phe	Ser
		225			230					235				240	
Thr	Cys	Leu	Ala	His	Leu	Phe	Ala	Phe	Ser	Thr	Cys	Ile	Ala	Gln	Pro
			245						250					255	

Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser
 260 265 270
 Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser
 275 280 285
 Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala
 290 295 300
 Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile
 305 310 315

<210> 2223

<211> 304

<212> PRT

<213> Homo sapien (8117535-5-1968-4011)

<220>

<221> VARIANT

<222> (1)...(304)

<223> Xaa = Any Amino Acid

<400> 2223

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro
 1 5 10 15
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile
 20 25 30
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe
 35 40 45
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp
 50 55 60
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser
 65 70 75 80
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe
 85 90 95
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met
 100 105 110
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu
 115 120 125
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu
 130 135 140
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu
 145 150 155 160
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro
 165 170 175
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val
 180 185 190
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val
 195 200 205
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser
 210 215 220
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val
 225 230 235 240
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser
 245 250 255
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val
 260 265 270
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val
 290 295 300

<210> 2224

<211> 268

<212> PRT

<213> Homo sapien (8117653-5-5695-6912)

<400> 2224

```

Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr
1           5           10           15
Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val
20           25           30
Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile
35           40           45
Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val
50           55           60
Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu
65           70           75           80
Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr
85           90           95
Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser
100          105          110
Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn
115          120          125
Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala
130          135          140
Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala
145          150          155          160
Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu
165          170          175
Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys
180          185          190
Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr
195          200          205
Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn
210          215          220
Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met
225          230          235          240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
245          250          255
Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly
260          265

```

<210> 2225

<211> 184

<212> PRT

<213> Homo sapien (8117705-18-1061-1646)

<220>

<221> VARIANT

<222> (1)...(184)

<223> Xaa = Any Amino Acid

<400> 2225

```

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
1           5           10           15
His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
20           25           30
Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
35           40           45
His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
50           55           60
Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
65           70           75           80
Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His

```


65		70		75		80									
Thr	Thr	Val	Ile	Pro	Met	Leu	Asn	Pro	Met	Ile	Tyr	Ser	Leu	Arg	Asn
			85						90					95	
Lys	Asp	Val	Lys	Glu	Ala	Leu	Cys	Lys	Glu	Leu	Phe	Lys	Arg	Lys	Leu
			100					105					110		
Phe	Ser	Lys													
		115													

<210> 2228

<211> 157

<212> PRT

<213> Homo sapien (8118143-4-5591-10363)

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 2228

Ile	Cys	His	Asn	Arg	Lys	Val	Ile	Pro	Ala	Ser	Met	Xaa	Asn	Met	Cys
1			5						10					15	
Xaa	Phe	Leu	Leu	Lys	Val	Ala	Xaa	Asp	Asn	Phe	Leu	His	Val	Leu	Phe
			20					25					30		
Ile	Leu	Ala	Lys	Thr	Ala	Pro	Pro	Leu	Leu	Phe	Leu	Xaa	Glu	Ile	Pro
		35				40						45			
Ser	Tyr	Phe	Ser	Ser	Pro	Ser	Xaa	Ile	Ile	Val	Leu	Xaa	Cys	Leu	Pro
		50				55					60				
Xaa	Phe	Leu	Lys	Gln	Leu	Val	Ile	Leu	Phe	Val	Phe	Leu	Leu	Leu	Asn
65				70					75					80	
Xaa	Ser	Tyr	Leu	Thr	Leu	Ile	Phe	Met	Leu	Leu	Thr	Met	Lys	Ile	Thr
			85					90					95		
Ser	Ser	Phe	Lys	Ala	Ser	Thr	Val	Ile	Ser	Cys	Leu	Gln	Phe	Pro	Ser
			100					105					110		
Lys	Ala	Thr	Cys	Met	His	Gly	Val	Phe	Ser	Ala	Val	Cys	Ala	Gln	Met
		115				120						125			
Xaa	Pro	Tyr	Tyr	Asn	Gly	Xaa	Ile	Ile	Xaa	His	Pro	Glu	Ser	Ile	Thr
		130				135					140				
Glu	Ser	Lys	Xaa	Leu	Thr	Cys	Val	Asn	Pro	Xaa	Phe	Asn			
145					150					155					

<210> 2229

<211> 320

<212> PRT

<213> Homo sapien (8118143-4-617-5265)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2229

Met	Leu	Val	Pro	Lys	Lys	Met	Val	Arg	Gly	Asn	Ser	Thr	Leu	Val	Thr
1				5					10					15	
Glu	Phe	Ile	Leu	Leu	Gly	Leu	Lys	Asp	Leu	Pro	Glu	Leu	Gln	Pro	Ile
			20					25					30		
Leu	Phe	Val	Leu	Phe	Leu	Leu	Ile	Tyr	Leu	Ile	Thr	Val	Gly	Gly	Asn
		35				40						45			
Leu	Gly	Met	Leu	Val	Leu	Ile	Arg	Ile	Asp	Ser	Arg	Leu	His	Thr	Pro
		50				55					60				
Met	Tyr	Phe	Phe	Leu	Ala	Ser	Leu	Ser	Cys	Leu	Asp	Leu	Tyr	Tyr	Ser
65					70					75				80	

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Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85      90      95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100      105      110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115      120      125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130      135      140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
      145      150      155
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165      170      175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180      185      190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195      200      205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210      215      220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
      225      230      235
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245      250      255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260      265      270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275      280      285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290      295      300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
      305      310      315      320

```

<210> 2230

<211> 312

<212> PRT

<213> Homo sapien (8118750-5-4885-6910)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 2230

```

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser
  1      5      10      15
Asn Val Pro Glu Leu Gln Val Pro Phe Phe Ile Met Phe Val Leu Ile
      20      25      30
Tyr Leu Ile Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
      35      40      45
Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu
      50      55      60
Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met
      65      70      75      80
Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala
      85      90      95
Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu
      100      105      110
Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu
      115      120      125
His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile
      130      135      140
Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu

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145 150 155 160
 Thr Ph Ser Leu Phe Cys Met S r Ser Glu Val His His Phe Phe Cys
 165 170 175
 Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn
 180 185 190
 Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu
 195 200 205
 Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys
 210 215 220
 Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser
 225 230 235 240
 His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His
 245 250 255
 Ile Gln Pro Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala
 260 265 270
 Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg
 275 280 285
 Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val
 290 295 300
 Lys Leu Ser Leu Gly Leu Xaa Val
 305 310

<210> 2231

<211> 267

<212> PRT

<213> Homo sapien (8118750-8-1-2827)

<400> 2231

Ile Ile Leu Cys Phe Phe Ile Ile Gly Asn Ser Gln Asp Asn Ser Gln
 1 5 10 15
 Met Thr Leu Met Asp Asn Ile Ser Glu Val Thr Glu Phe Val Leu Val
 20 25 30
 Gly Leu Thr Asp Val Leu Glu Leu Gln Val Pro Leu Phe Ile Ile Phe
 35 40 45
 Thr Val Ile Tyr Leu Thr Thr Leu Val Gly Asn Phe Gly Met Ile Met
 50 55 60
 Leu Ile Leu Leu Asp Ser Arg Leu His Ile Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Gly Lys Leu Ser Leu Val Asp Ser Val Cys Ala Cys Leu Val Thr Gly
 85 90 95
 Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His Val Ala Phe Thr
 100 105 110
 Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn His Phe Phe Cys
 115 120 125
 Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Ile Tyr Ala His
 130 135 140
 Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile Phe Phe Thr Leu
 145 150 155 160
 Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile Ala Ile Leu Arg
 165 170 175
 Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser Thr Cys Ala Tyr
 180 185 190
 His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile Thr Phe Met Tyr
 195 200 205
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Ile Ser Ser
 210 215 220
 Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr Ser
 225 230 235 240
 Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val Val Ile Gly Lys
 245 250 255
 Ala Lys Ser Ser Leu Gly Leu Ala Tyr Tyr Leu

260

265

<210> 2232
 <211> 309
 <212> PRT
 <213> Homo sapien (8118822-9-5564-7217)

<220>
 <221> VARIANT
 <222> (1)...(309)
 <223> Xaa = Any Amino Acid

<400> 2232

Glu	Xaa	Met	Gly	Thr	Ser	Asn	Asn	Val	Thr	Glu	Phe	Val	Leu	Pro	Gly
1				5				10						15	
Leu	Ser	Gln	Asp	Pro	Asp	Val	Gln	Lys	Ala	Leu	Phe	Val	Met	Phe	Leu
			20					25					30		
Leu	Thr	Tyr	Asn	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Val	Val	Thr
		35					40					45			
Ile	Ile	Ala	Ile	Ala	Ser	Leu	Asp	Ser	Pro	Val	Ser	Phe	Phe	Leu	Ala
	50					55					60				
Cys	Leu	Ser	Phe	Ile	Asp	Ala	Val	Tyr	Ser	Thr	Ser	Phe	Ser	Pro	Lys
65					70					75				80	
Leu	Met	Ile	Asp	Leu	Leu	Cys	Asp	Lys	Lys	Thr	Val	Ser	Phe	Leu	Ala
				85					90					95	
Cys	Met	Gly	Gln	Leu	Phe	Ile	Asn	Tyr	Pro	Phe	Gly	Gly	Ile	Glu	Val
			100					105					110		
Phe	Leu	Leu	Val	Gly	Met	Ala	Cys	Asp	His	Tyr	Val	Asp	Ile	Cys	Lys
		115					120					125			
Leu	Leu	His	Tyr	Leu	Thr	Ile	Met	Asn	Trp	Gln	Val	Cys	Ile	Leu	Leu
	130					135					140				
Phe	Met	Val	Ala	Val	Thr	Gly	Gly	Phe	Leu	His	Ser	Met	Phe	Gln	Ile
145					150					155					160
Val	Val	Val	Tyr	Ser	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His
				165					170					175	
Phe	Cys	Asp	Met	Tyr	Pro	Leu	Leu	Glu	Met	Val	Cys	Thr	Asp	Thr	Tyr
			180					185					190		
Phe	Ile	Gly	Leu	Thr	Val	Ile	Ala	Asn	Gly	Gly	Ala	Val	Cys	Met	Val
		195					200					205			
Ile	Phe	Ile	Leu	Leu	Leu	Ile	Ser	Tyr	Gly	Val	Ile	Leu	Asn	Ser	Leu
	210					215					220				
Lys	Thr	Tyr	Ser	Gln	Glu	Gly	Gly	His	Lys	Ala	Leu	Ser	Thr	Cys	Ser
225				230						235					240
Ser	Asn	Ile	Thr	Val	Val	Ser	Leu	Phe	Phe	Asp	Pro	Cys	Ile	Phe	Ile
				245					250					255	
Tyr	Val	Arg	Pro	Asp	Ser	Asn	Phe	Pro	Ile	Asp	Lys	Phe	Met	Thr	Val
			260					265					270		
Phe	Tyr	Thr	Ile	Ile	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu
		275					280					285			
Arg	Asn	Leu	Glu	Val	Arg	Ile	Ala	Val	Lys	Asn	Leu	Trp	Cys	Lys	Asn
	290					295					300				
Xaa	Thr	Ile	Val	Arg											
305															

<210> 2233
 <211> 257
 <212> PRT
 <213> Homo sapien (8118832-14-2647-3682)

<220>
 <221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2233

```

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr
 1           5           10           15
Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly
          20           25           30
Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe
          35           40           45
Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe
          50           55           60
Asp Trp Phe Val Ala Ile Cys Cys Pro Leu Cys Tyr Gly Leu Ile Met
65           70           75           80
Ser Trp Arg Leu Cys Val Gln Leu Thr Leu Gly Ser Leu Leu Leu Gly
          85           90           95
Phe Phe Leu Ala Met Gln Leu Thr Val Leu Ile Phe Gln Leu Pro Leu
          100          105          110
Cys Ser Ser Lys Glu Ile Ser Thr Phe Tyr Cys Asp Val Leu Pro Val
          115          120          125
Met Arg Leu Ala Cys Ala Asp Thr Trp Val His Glu Ala Thr Met Ser
          130          135          140
Met Val Ser Thr Thr Phe Leu Thr Val Pro Phe Leu Leu Ile Thr Leu
145          150          155          160
Ser Tyr Val Ser Ile Met Ala Ala Ile Leu Lys Ile Cys Ser Ala Glu
          165          170          175
Gly Arg His Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val
          180          185          190
Leu Leu Gln Asp Xaa Cys Thr Arg Leu Ala Phe Leu Cys Pro Ser Ser
          195          200          205
Ser Tyr Tyr Pro Glu Arg Gly Gln Ala Val Ser Val Val Tyr Thr Phe
210          215          220
Ile Thr Pro Val Leu Asn Pro Leu Ile Tyr Ser Met Arg Asn Thr Glu
225          230          235          240
Leu Lys Asp Ala Leu Lys Arg Ala Met Thr Arg Val Pro Leu Leu Xaa
          245          250          255
Thr

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<210> 2234

<211> 327

<212> PRT

<213> Homo sapien (8118892-3-16899-18792)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2234

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
 1           5           10           15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
          20           25           30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
          35           40           45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
          50           55           60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
65           70           75           80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile

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```
<210> 2235
<211> 125
<212> PRT
<213> Homo sapien (8118970-10-4947-6912)
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<210> 2236
<211> 112
<212> PRT
<213> Homo sapien (8118970-16-561-1769)
```

1328


```

Met Glu Val Lys Asn Cys Cys Met Val Thr Glu Ph Ile Leu Leu Gly
 1          5          10          15
Ile Pro His Thr Glu Gly Leu Glu Met Thr Leu Phe Val Leu Phe Leu
          20          25          30
Pro Phe Tyr Ala Cys Thr Leu Leu Gly Asn Val Ser Ile Leu Val Ala
          35          40          45
Val Met Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
          50          55          60
Asn Leu Ser Val Phe Asp Met Gly Phe Ser Ser Val Thr Val Pro Lys
          65          70          75          80
Met Leu Leu Tyr Leu Met Gly Leu Ser Arg Leu Ile Ser Tyr Lys Asp
          85          90          95
Cys Val Cys Gln Leu Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys
          100          105          110

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<210> 2237

<211> 287

<212> PRT

<213> Homo sapien (8119016-6-4856-7402)

<220>

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 2237

```

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu
 1          5          10          15
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu
          20          25          30
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr
          35          40          45
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys
          50          55          60
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe
          65          70          75          80
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys
          85          90          95
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys
          100          105          110
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe
          115          120          125
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys
          130          135          140
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln
          145          150          155          160
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa
          165          170          175
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr
          180          185          190
Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys
          195          200          205
Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile
          210          215          220
Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr
          225          230          235          240
Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr
          245          250          255
Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu
          260          265          270
Gly Ser Xaa Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr

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275

280

285

<210> 2238
 <211> 210
 <212> PRT
 <213> Homo sapien (8119057-10-2407-4064)

<220>
 <221> VARIANT
 <222> (1)...(210)
 <223> Xaa = Any Amino Acid

<400> 2238
 Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1 5 10 15
 Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu
 20 25 30
 Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu
 35 40 45
 Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
 50 55 60
 Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
 65 70 75 80
 Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
 85 90 95
 Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
 100 105 110
 Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
 115 120 125
 Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
 130 135 140
 Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
 145 150 155 160
 Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
 165 170 175
 Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
 180 185 190
 Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
 195 200 205
 Ala Phe
 210

<210> 2239
 <211> 228
 <212> PRT
 <213> Homo sapien (8119057-15-786-3116)

<220>
 <221> VARIANT
 <222> (1)...(228)
 <223> Xaa = Any Amino Acid

<400> 2239
 Met Leu Ile Pro Ser Ser Thr Arg Lys Met Ala Ala Glu Ser His Ser
 1 5 10 15
 Thr Val Thr Glu Phe Ile Leu Arg Lys Lys Pro Ala Arg Ala Pro Ala
 20 25 30
 Pro Pro Leu Leu Gly Ile Cys Leu Lys Thr Val Val Gly Ala Leu Ile
 35 40 45
 Leu Ile Thr Leu Val Phe Leu Asn Ser Gln Leu His Pro Pro Met Tyr
 50 55 60

Tyr Val Ile Arg Asn Leu Ser Phe Met Asp His Cys Asn Cys Ser Ile
 65 70 75 80
 Ser Thr Pro Lys Ile Leu Val Lys Phe Val Leu Glu Lys Thr Ile Ile
 85 90 95
 Ser Tyr Glu Asp Gly Met Ser Gln Leu Cys Ser Ala Ser Cys Tyr Il
 100 105 110
 Leu Ser Trp Pro Ser Val Thr Cys Gly Pro Ala Thr Ala Val Ile Thr
 115 120 125
 Phe His Gln Val Ser Ser Leu Leu Val Val Val Val Tyr Tyr Met Glu
 130 135 140
 Leu Thr Gly Thr Thr Ile Glu Phe Cys Leu Val Leu Lys Xaa Tyr Xaa
 145 150 155 160
 Cys Glu Leu Phe Ile Ser His Tyr Phe Cys Ser Cys Thr Ser Ile Tyr
 165 170 175
 Asp Ile Asp Arg Thr Ile Phe Phe Phe Thr Xaa Cys Asn Ile Val Val
 180 185 190
 Thr Arg Leu Thr Val Val Ser Tyr Ser Phe Leu Ser Ser Ile Leu His
 195 200 205
 Ile Ser Phe Thr Arg Ala Ala Leu Gly Phe Ser Arg Arg Ser Asp Ala
 210 215 220
 Phe Met Leu Cys
 225

<210> 2240

<211> 277

<212> PRT

<213> Homo sapien (8119057-2-10436-11711)

<220>

<221> VARIANT

<222> (1)...(277)

<223> Xaa = Any Amino Acid

<400> 2240

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu
 1 5 10 15
 Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa
 20 25 30
 Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr
 35 40 45
 Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser
 50 55 60
 Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr
 65 70 75 80
 Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser
 85 90 95
 Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met
 100 105 110
 Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa
 115 120 125
 Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln
 130 135 140
 Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile
 145 150 155 160
 Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val
 165 170 175
 Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe
 180 185 190
 Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Ph His Xaa Pro Ser Gly
 195 200 205
 Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly

210 215 220
 Leu Gly Thr Phe Met Tyr Leu Arg Ser Pr Glu Ala Met Gly Xaa Cys
 225 230 235 240
 Lys Phe Thr Val Ser Phe Thr Lys Met Gly Pr Val Met Asn Gly Leu
 245 250 255
 Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro
 260 265 270
 Leu Ser Phe Ser Ser
 275

<210> 2241
 <211> 125
 <212> PRT
 <213> Homo sapien (8119057-22-209-1834)

<220>
 <221> VARIANT
 <222> (1)...(125)
 <223> Xaa = Any Amino Acid

<400> 2241
 Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys
 1 5 10 15
 Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe Phe
 20 25 30
 Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu
 35 40 45
 Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met
 50 55 60
 Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala
 65 70 75 80
 Leu Arg Arg Thr Phe Cys Arg Lys Leu Val Ser Xaa Lys Xaa Met Arg
 85 90 95
 Lys Gly Ile Gln Thr Phe Val Asn Gln Gly Val Ser Phe Leu Phe Phe
 100 105 110
 Ser Glu Gly Thr Asn Ala Thr Ala Phe Ser Pro Ile Leu
 115 120 125

<210> 2242
 <211> 164
 <212> PRT
 <213> Homo sapien (8119071-15-1-1473)

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

<400> 2242
 Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg
 1 5 10 15
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys
 20 25 30
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His
 35 40 45
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu
 50 55 60
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu
 65 70 75 80
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile
 85 90 95

Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser
 100 105 110
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys
 115 120 125
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu
 130 135 140
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu
 145 150 155 160
 Leu Arg Thr His

<210> 2243
 <211> 131
 <212> PRT
 <213> Homo sapien (8131609-2-31657-32554)

<220>
 <221> VARIANT
 <222> (1)...(131)
 <223> Xaa = Any Amino Acid

<400> 2243
 Ile Ile Tyr Leu Leu Cys Xaa Asp Pro Ala Ile Cys Glu Ser Val Ile
 1 5 10 15
 Phe Phe Pro Met Gly Phe Ser Asp Cys Leu Pro Ile Leu Ser Ile Met
 20 25 30
 Ile Thr Tyr Leu Phe Thr Phe Ile Asp Leu Leu Ile Pro Leu Pro His
 35 40 45
 Val Xaa Leu Gln Lys Asp Tyr Val Cys Ala Ser Asn Leu Thr Val
 50 55 60
 Val Ser Thr Phe Ser Xaa Asp His Leu Phe Ser Cys Leu His Ser Ser
 65 70 75 80
 Asp Ala Ala Leu Leu Trp Thr Gln Thr Lys Leu His Ser Tyr Phe Ala
 85 90 95
 Ile Val Ile Pro Thr Leu Tyr Pro Leu Val His Ser Leu Lys Asn Arg
 100 105 110
 Gly Gly Gln Ser Ala Leu Arg Lys Val Leu Val Lys Ala Lys Ser Gln
 115 120 125
 Leu Ser Leu
 130

<210> 2244
 <211> 312
 <212> PRT
 <213> Homo sapien (8131609-3-27134-29103)

<220>
 <221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 2244
 Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu
 1 5 10 15
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe
 20 25 30
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu
 35 40 45
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro

65					70					75				80
Lys	Met	Met	Ala	Gly	Leu	Leu	Ile	Ala	His	Lys	Val	Ile	Ser	Tyr Asn
				85					90					95
Val	Cys	Ala	Ala	Gln	Met	Phe	Phe	Phe	Ala	Val	Phe	Ala	Thr	Val Glu
			100					105					110	
Ser	Tyr	Phe	Leu	Thr	Ser	Val	Ala	Tyr	Asp	Cys	Tyr	Arg	Val	Met Cys
		115					120					125		
Lys	Pro	Leu	His	Tyr	Thr	Thr	Thr	Met	Thr	Thr	Asn	Val	Cys	Ala Ser
		130				135					140			
Leu	Ala	Ile	Ala	Cys	Tyr	Val	Leu	Gly	Leu	Leu	Thr	Ala	Ala	Val Asp
145					150					155				160
Ile	Gly	Asp	Ile	Cys	Met	Ser	Asn	Glu	Ile	His	His	Phe	Phe	Cys Asp
			165					170					175	
Ile	Leu	Ala	Val	Met	Thr	Leu	Thr	Cys	Ser	Asn	Lys	His	Ile	Asn Glu
		180						185					190	
Leu	Ile	Leu	Val	Leu	Leu	Gln	Ala	Ile	Phe	Phe	Thr	Leu	Leu	Val Ile
		195				200						205		
Leu	Ile	Ser	Cys	Leu	Phe	Val	Phe	Val	Phe	Val	Thr	Ile	Leu	Lys Met
210					215						220			
His	Leu	Phe	Lys	Ser	Tyr	Lys	Lys	Val	Leu	Ser	Thr	Tyr	Gly	Ser His
225				230					235					240
Leu	Thr	Ala	Val	Pro	Leu	Phe	Tyr	Glu	Thr	Val	Leu	Ile	Thr	Tyr Val
			245					250					255	
Gln	Pro	Ser	Ser	Ser	His	Phe	Met	Asn	Thr	Glu	Lys	Ile	Val	Ser Val
		260					265						270	
Phe	His	Ile	Met	Val	Ile	Pro	Met	Leu	Ile	Pro	Val	Val	Tyr	Ser Leu
		275				280					285			
Arg	Asn	Asn	Glu	Val	Lys	Ser	Ala	Phe	Lys	Thr	Val	Val	Glu	Glu Thr
290					295						300			
Lys	Tyr	Phe	Leu	Gly	Leu	Val	Phe							
305					310									

<210> 2245

<211> 189

<212> PRT

<213> Homo sapien (8131615-11-1-272)

<220>

<221> VARIANT

<222> (1)...(189)

<223> Xaa = Any Amino Acid

<400> 2245

Ala	Thr	Lys	Glu	Leu	Cys	Phe	Leu	Gly	Val	Tyr	Ile	Pro	Lys	Gly Asp
1				5				10						15
Ala	Cys	Trp	Lys	Xaa	Leu	Xaa	Leu	Gly	Leu	His	Leu	Leu	Leu	Gly
		20					25						30	
Xaa	Gln	Val	Val	Ser	Met	Val	Gly	Asn	Leu	Ala	Leu	Ile	Ala	Leu Ile
		35				40						45		
Gly	Xaa	Asn	Ser	Tyr	Leu	His	His	Pro	Gln	Ala	Leu	Phe	Ser	Phe Thr
	50				55						60			
Gln	Ser	Phe	Pro	Asp	Leu	Tyr	Cys	Pro	Val	Cys	Thr	Pro	Arg	Met Leu
65				70					75					80
Met	Thr	Phe	Val	Ser	Lys	Lys	Asn	Ile	Phe	Tyr	Val	Arg	Cys	Met Thr
			85					90					95	
Gln	Leu	Ser	Gln	Leu	Phe	Phe	Leu	Phe	Ile	Val	Leu	Ser	Ile	Lys Tyr
		100					105						110	
His	Val	Leu	Met	Phe	Ile	Ala	Cys	Gly	Cys	Leu	Val	Ala	Ile	Tyr Asn
		115				120					125			
Pro	Ser	Leu	His	Glu	Val	Thr	Met	Ser	Pro	Gln	Val	Arg	Glu	Met Arg
		130				135					140			

Glu Ser Gly Phe Ala Gly Thr Thr Ala His Thr Gly His Il Leu Arg
 145 150 155 160
 Pro Asn Leu Cys Asn Ile Asp Val Ile Asn His His Leu Thr Asp Ser
 165 170 175
 Leu Leu Val Leu Xaa Val Ser Cys Thr Ser Thr Cys Ala
 180 185

<210> 2246

<211> 207

<212> PRT

<213> Homo sapien (8131622-1-12991-13959)

<220>

<221> VARIANT

<222> (1)...(207)

<223> Xaa = Any Amino Acid

<400> 2246

Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
 1 5 10 15
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
 20 25 30
 Asn Met Arg Leu Pro Ser Asp Phe Leu Ser Gln Ala Ile Tyr Tyr
 35 40 45
 Xaa Trp Ala Leu Met Cys Val Leu Glu Asn Lys Thr Tyr Ala Ser Val
 50 55 60
 Arg Leu Val Xaa Arg Phe Gly Trp Xaa Lys Leu Ala Asn Xaa Met Ser
 65 70 75 80
 Val Leu Tyr Leu Glu Ala Asn Leu Gly Asn Met Asp Asn Ala Leu Leu
 85 90 95
 Lys Xaa Leu Lys Arg Asn Tyr Phe Val Phe Val Phe Thr Ser Phe Leu
 100 105 110
 Phe Gly Cys Ile Ala Phe Lys Xaa Lys Glu Ile Phe Tyr Pro Tyr Thr
 115 120 125
 Ser Ile Cys Ile Tyr His Leu Leu Met Met Glu Arg Lys Val Ser Cys
 130 135 140
 Leu Thr Leu Ile Cys Leu Ala Xaa Asp Leu Xaa His Phe Xaa Cys Ser
 145 150 155 160
 Leu Val Thr Val Leu Ser Leu Glu Cys Xaa Gln Leu Asp Ile Cys Asn
 165 170 175
 Val Val Thr Tyr Phe Asn Thr Met Val Xaa Ser Thr Thr Gly Ser Asn
 180 185 190
 Ser Xaa Thr Pro Asn His Ser Val Leu Ile Cys Asn Met Leu Lys
 195 200 205

<210> 2247

<211> 311

<212> PRT

<213> Homo sapien (8131622-11-1950-4442)

<400> 2247

Met Thr Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
 20 25 30
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
 35 40 45
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
 65 70 75 80

Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val
 85 90 95
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
 100 105 110
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp
 130 135 140
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln
 145 150 155 160
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg
 165 170 175
 His Phe Phe Cys Asp Met Pro Gln Leu Ile Leu Ser Cys Thr Asp
 180 185 190
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly
 195 200 205
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile
 210 215 220
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Ser Pro Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly
 245 250 255
 Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp
 260 265 270
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg
 290 295 300
 Leu Gln Lys Arg Lys Cys Cys
 305 310

<210> 2248

<211> 444

<212> PRT

<213> Homo sapien (8131622-13-5638-8129)

<220>

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 2248

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe
 20 25 30
 Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala
 35 40 45
 Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu
 50 55 60
 Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro
 65 70 75 80
 Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
 85 90 95
 Gly Cys Thr Met Gln Tyr Phe Ser Ser Leu Asn Val Thr Glu Cys Cys
 100 105 110
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pro
 115 120 125
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val
 130 135 140
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys

145 150 155 160
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe
 165 170 175
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe
 180 185 190
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His
 195 200 205
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His
 210 215 220
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp
 225 230 235 240
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met
 245 250 255
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr
 260 265 270
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Leu Ser Leu Ala
 275 280 285
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln
 290 295 300
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser
 305 310 315 320
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val
 325 330 335
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr
 340 345 350
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys
 355 360 365
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr
 370 375 380
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu
 385 390 395 400
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg
 405 410 415
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala
 420 425 430
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro
 435 440

<210> 2249

<211> 312

<212> PRT

<213> Homo sapien (8131671-12-1836-3192)

<400> 2249

Met Gly Val Lys Asn His Ser Thr Val Thr Glu Phe Leu Leu Ser Gly
 1 5 10 15
 Leu Thr Glu Gln Ala Glu Leu Gln Leu Pro Leu Phe Cys Leu Phe Leu
 20 25 30
 Gly Ile Tyr Thr Val Thr Val Val Gly Asn Leu Ser Met Ile Ser Ile
 35 40 45
 Ile Arg Leu Asn Arg Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ser Gly Phe Leu Cys Arg Asp Arg Ser Ile Ser Tyr Ser Gly
 85 90 95
 Cys Met Ile Gln Leu Phe Phe Phe Cys Val Cys Val Ile Ser Glu Cys
 100 105 110
 Tyr Met Leu Ala Ala Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Arg Val Ile Met Ser Pro Arg Val Cys Ser Leu Leu

130	135	140
Val Ala Ala Val Phe Ser	Val Gly Phe Thr Asp	Ala Val Ile His Gly
145	150	155
Gly Cys Ile Leu Arg Leu Ser Phe Cys Gly Ser Asn Ile Ile Lys His		160
	165	170
Tyr Phe Cys Asp Ile Val Pro Leu Ile Lys Leu Ser Cys Ser Ser Thr		175
	180	185
Tyr Ile Asp Glu Leu Leu Ile Phe Val Ile Gly Gly Phe Asn Met Val		190
	195	200
Ala Thr Ser Leu Thr Ile Ile Ile Ser Tyr Ala Phe Ile Leu Thr Ser		205
	210	215
Ile Leu Arg Ile His Ser Lys Lys Gly Arg Cys Lys Ala Phe Ser Thr		220
225	230	235
Cys Ser Ser His Leu Thr Ala Val Leu Met Phe Tyr Gly Ser Leu Met		240
	245	250
Ser Met Tyr Leu Lys Pro Ala Ser Ser Ser Ser Leu Thr Gln Glu Lys		255
	260	265
Val Ser Ser Val Phe Tyr Thr Thr Val Ile Leu Met Leu Asn Pro Leu		270
	275	280
Ile Tyr Ser Leu Arg Asn Asn Glu Val Arg Asn Ala Leu Met Lys Leu		285
	290	295
Leu Arg Arg Lys Ile Ser Leu Ser		300
305	310	

<210> 2250

<211> 305

<212> PRT

<213> Homo sapien (8131682-2-1-1878)

<400> 2250

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe	
1	5
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly	10
	15
	20
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile	25
	30
	35
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Val Gly Asn	40
	45
	50
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile	55
65	60
	65
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys	70
	75
	80
	85
Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr	90
	95
	100
Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro	105
	110
	115
Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val	120
	125
	130
Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys	135
145	140
	145
Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe	150
	155
	160
	165
Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly	170
	175
	180
Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys	185
	190
	195
Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val	200
	205
	210
Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys	215
225	220
	225
Ser Ser His Leu Thr S r Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr	230
	235
	240

245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pr Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300

Pro
305

<210> 2251

<211> 306

<212> PRT

<213> Homo sapien (8131682-3-415-2331)

<400> 2251

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20 25 30
 Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35 40 45
 Cys Asn Asp Ser Arg Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val His Thr Pro Lys Ile
 65 70 75 80
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
 100 105 110
 Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
 115 120 125
 Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
 130 135 140
 Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
 145 150 155 160
 Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
 165 170 175
 Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Val Arg Glu Ser
 180 185 190
 Tyr Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro
 195 200 205
 Thr Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu
 210 215 220
 Arg Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser
 225 230 235 240
 Ser His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn
 245 250 255
 Tyr Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val
 260 265 270
 Ser Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Ser Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys
 290 295 300
 Ser Ala
 305

<210> 2252

<211> 324

<212> PRT

<213> Homo sapien (8152118-1-59952-61847)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 2252

His	Thr	Glu	Pro	Arg	Asn	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Leu	Leu	Ser
			20					25					30		
Leu	Ser	Leu	Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ser
	35					40						45			
Ile	Leu	Ala	Val	Arg	Ser	Glu	Ser	Pro	Leu	His	Thr	Thr	Met	Tyr	Phe
	50					55				60					
Phe	Leu	Ser	Ile	Leu	Cys	Trp	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Ala	Thr
65					70					75					80
Val	Pro	Lys	Met	Ile	Val	Asp	Met	Gln	Trp	Tyr	Ser	Lys	Val	Ile	Ser
			85					90						95	
His	Ala	Gly	Cys	Leu	Thr	Gln	Met	Ser	Phe	Leu	Val	Leu	Phe	Ala	Cys
			100					105						110	
Ile	Glu	Gly	Met	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Gly
		115				120						125			
Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His	Leu	Cys
	130					135					140				
Val	Phe	Phe	Val	Leu	Val	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln
145					150					155					160
Leu	His	Ser	Trp	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn	Val	Glu
				165					170					175	
Ile	Ser	Asn	Phe	Val	Cys	Asp	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys
		180						185						190	
Ser	Asp	Ser	Val	Ile	Asn	Ser	Ile	Phe	Ile	Tyr	Phe	Gly	Ser	Thr	Met
		195					200					205			
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile
	210					215					220				
Val	Pro	Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala
225					230					235					240
Phe	Ser	Thr	Tyr	Gly	Ser	His	Leu	Ala	Val	Phe	Cys	Xaa	Phe	Asp	Gly
				245					250					255	
Thr	Gly	Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Val	Ala	Pro	Pro	Pro	Arg
			260					265						270	
Asn	Gly	Val	Val	Val	Ser	Val	Lys	Xaa	Ala	Val	Val	Thr	Pro	Met	Pro
		275					280					285			
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu
	290					295					300				
Arg	Arg	Leu	Pro	Asn	Lys	Thr	Val	Glu	Ser	Pro	Xaa	Ser	Val	Pro	Ser
305					310					315					320
Phe	Phe	Trp	Cys												

<210> 2253

<211> 212

<212> PRT

<213> Homo sapien (8247820-10-10207-11695)

<220>

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 2253

```

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Xaa Cys Ile Thr
 1          5          10          15
Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr
          20          25          30
Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys
          35          40          45
Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys
          50          55          60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
          65          70          75          80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
          85          90          95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Xaa Glu
          100          105          110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
          115          120          125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
          130          135          140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
          145          150          155          160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
          165          170          175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
          180          185          190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
          195          200          205
Ala Leu Phe Cys
          210

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<210> 2254

<211> 314

<212> PRT

<213> Homo sapien (8247820-11-34143-40656)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2254

```

Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu
 1          5          10          15
Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu
          20          25          30
Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile
          35          40          45
Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe
          50          55          60
Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile
          65          70          75          80
Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr
          85          90          95
His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr
          100          105          110
Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val
          115          120          125
Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile
          130          135          140
Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr
          145          150          155          160
His Leu Ser Ser Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile

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<400>	2255														
Met	Ser	Xaa	Xaa	Ile	Phe	Cys	Leu	Pro	Lys	Ile	Ile	Ile	Thr	Leu	Leu
1				5					10					15	
Gln	Xaa	Glu	Trp	Asp	Ala	Leu	Asn	Leu	Glu	Thr	Arg	Val	Phe	Leu	Glu
			20					25					30		
Glu	Asp	Phe	Pro	Cys	Gly	Phe	Ser	Leu	Trp	Ile	Val	Arg	Gln	Leu	Ser
		35					40					45			
Phe	Phe	Leu	Glu	Ile	Asn	Xaa	Phe	Ala	His	Leu	Lys	Lys	Xaa	Cys	Arg
	50					55					60				
Lys	His	Thr	Ser	Thr	Phe	Ser	Leu	Ser	Asn	Leu	Ala	Phe	Xaa	Asp	Phe
65					70					75					80
Cys	Tyr	Ala	Ser	Val	Ile	Thr	Ser	Lys	Met	Phe	Gly	Ser	Phe	Leu	Tyr
				85					90					95	
Lys	Gln	Lys	Lys	Leu	Thr	Phe	Asn	Ala	Leu	Gly	Cys	Ser	Leu	Thr	Phe
			100					105					110		
Met	Thr	Thr	Glu	Cys	Leu	Leu	Leu	Ala	Phe	Met	Ala	Cys	Asp	Gln	Tyr
		115					120					125			
Leu	Val	Ile	Cys	Asn	Pro	Pro	Leu	Tyr	Met	Val	Thr	Met	Ser	Pro	Pro
	130					135					140				
Gln	Gly	Val	Cys	Ile	Gln	Leu	Met	Pro	Ala	Ser	Tyr	Ser	Tyr	Ser	Phe
145					150					155					160
Leu	Met	Thr	Leu	Ser	His	Tyr	Leu	Ser	Ala	Phe	Arg	Leu	Pro	Tyr	Cys
				165					170					175	
Pro	Ser	Val	Ser	Leu	Met	Phe	Asn	Gly	Ser	Leu	Phe	Leu	Tyr	Cys	Thr
			180					185					190		
Xaa	Cys	Ser	Glu	Asn	Ser	Leu	Asp	Thr	Asp	Arg	Met	Ala	Ser	Val	Phe
		195					200					205			
Tyr	Thr	Val	Val	Ile	Pro	Met	Leu	Ser	Pro	Leu	Ile	Trp	Ser	Leu	Arg
	210					215					220				
Asn	Lys	Asp	Val	Lys	Asp	Ala	Leu	Arg	Lys	Val	Ile	Val	Asn	Arg	Asn
225					230					235					240

Gln Ala Leu Phe Cys
245

<210> 2256
<211> 302
<212> PRT
<213> Homo sapien (8308370-1-1-2758)

<220>
<221> VARIANT
<222> (1)...(302)
<223> Xaa = Any Amino Acid

<400> 2256
Ile Arg Glu Thr His Ser His Val Pro Tyr Thr Ser Val Phe Leu Pro
1 5 10 15
Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val Leu Gly Asn Leu Val
20 25 30
Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser Arg Arg Leu Ile Asp
35 40 45
Ile Phe Ile Ile Asn Leu Ala Ser Asp Phe Ile Val Ser Cys His
50 55 60
Ile Ala Ser Leu Gly Gly Xaa Arg Thr Ser Leu Gly Leu Trp Arg Thr
65 70 75 80
Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met Ile Ser Val Asn Met
85 90 95
His Cys Ser Val Leu Leu Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
100 105 110
Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe Arg Arg Thr Asp Cys
115 120 125
Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Asn Leu Leu Pro Ala Gly
130 135 140
Val Ala Tyr Ser Ser Val Gln Gly Ala His Ala Val Asp Asp Lys Pro
145 150 155 160
Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys Leu Ile Trp Ser Leu
165 170 175
Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu Leu Ser Ile Val Thr
180 185 190
Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala His Tyr Gln Gln Ser
195 200 205
Gly Lys His Asn Lys Lys Leu Lys Lys Ser Ile Lys Ile Ile Phe Ile
210 215 220
Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro Phe Asn Thr Phe Lys
225 230 235 240
Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu His Tyr Leu Pro Ser
245 250 255
Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly Pro Leu Ala Phe Ala
260 265 270
Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile Phe Asp Ser Tyr Ile
275 280 285
Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys Leu Lys Asn
290 295 300

<210> 2257
<211> 336
<212> PRT
<213> Homo sapien (8318124-7-422-2124)

<220>
<221> VARIANT
<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 2257

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
 35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
 85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100         105         110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115         120         125
His Pro Leu Tyr Arg Ser Ala Thr Leu Asn Pro Cys Phe Cys Gly Phe
 130         135         140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Ser Leu Arg Leu Leu Asp Ser
 145         150         155         160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 165         170         175
Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala
 180         185         190
Cys Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala
 195         200         205
Val Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys
 210         215         220
Met Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
 225         230         235         240
Ala Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr
 245         250         255
Gly Thr Gly Phe Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
 260         265         270
Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ser Val Val Thr Pro Met
 275         280         285
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val
 290         295         300
Leu Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile
 305         310         315         320
Cys Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
 325         330         335

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<210> 2258

<211> 319

<212> PRT

<213> Homo sapien (8348136-100-2086-3409)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2258

```

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
 1          5          10          15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu
 20          25          30

```


Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Il
 35 40 45
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys
 100 105 110
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys
 130 135 140
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu
 145 150 155 160
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315

<210> 2259

<211> 186

<212> PRT

<213> Homo sapien (8389427-13-4913-5701)

<220>

<221> VARIANT

<222> (1)...(186)

<223> Xaa = Any Amino Acid

<400> 2259

Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu
 1 5 10 15
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser
 20 25 30
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn
 35 40 45
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val
 50 55 60
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr
 65 70 75 80
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp
 85 90 95
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly

100 105 110
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His
 115 120 125
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr
 130 135 140
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg
 145 150 155 160
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr
 165 170 175
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu
 180 185

<210> 2260

<211> 304

<212> PRT

<213> Homo sapien (8389428-12-1-2464)

<400> 2260

Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1 5 10 15
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
 20 25 30
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
 35 40 45
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
 50 55 60
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
 65 70 75 80
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
 85 90 95
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
 100 105 110
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
 115 120 125
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
 130 135 140
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
 145 150 155 160
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
 165 170 175
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
 180 185 190
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
 195 200 205
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
 245 250 255
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
 260 265 270
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
 275 280 285
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
 290 295 300

<210> 2261

<211> 275

<212> PRT

<213> Homo sapien (8439748-1-6412-8052)

<220>

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 2261

```

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
 1           5           10           15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
          20           25           30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
          35           40           45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
          50           55           60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
65           70           75           80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
          85           90           95
Ser Pro Ser Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
          100          105          110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
          115          120          125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
          130          135          140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
145          150          155          160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
          165          170          175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
          180          185          190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
          195          200          205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
          210          215          220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
225          230          235          240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
          245          250          255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
          260          265          270
Gln Tyr Ser
          275

```

<210> 2262

<211> 317

<212> PRT

<213> Homo sapien (8439748-5-3942-6516)

<400> 2262

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
          20           25           30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
          35           40           45
Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
          50           55           60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
65           70           75           80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val

```

								85				90				95			
Cys	Cys	Met	Thr	Gln	Met	Tyr	Phe	Val	Phe	Cys	Val	Gly	Val	Ala	Glu				
				100					105				110						
Cys	Ile	Leu	Leu	Ala	Phe	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys				
				115	120				125										
Tyr	Pro	Leu	Asn	Tyr	Val	Pro	Ile	Ile	Ser	Gln	Lys	Val	Cys	Val	Arg				
				130	135				140										
Leu	Val	Gly	Thr	Ala	Trp	Phe	Phe	Gly	Leu	Ile	Asn	Gly	Ile	Phe	Leu				
				145	150				155				160						
Glu	Tyr	Ile	Ser	Phe	Arg	Glu	Pro	Phe	Arg	Arg	Asp	Asn	His	Ile	Glu				
				165	170				175										
Ser	Phe	Phe	Cys	Glu	Ala	Pro	Ile	Val	Ile	Gly	Leu	Ser	Cys	Gly	Asp				
				180	185				190										
Pro	Gln	Phe	Ser	Leu	Trp	Ala	Ile	Phe	Ala	Asp	Ala	Ile	Val	Val	Ile				
				195	200				205										
Leu	Ser	Pro	Met	Val	Leu	Thr	Val	Thr	Ser	Tyr	Val	His	Ile	Leu	Ala				
				210	215				220										
Thr	Ile	Leu	Ser	Lys	Ala	Ser	Ser	Ser	Gly	Arg	Gly	Lys	Thr	Phe	Ser				
				225	230				235				240						
Thr	Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ile	Phe	Leu	Tyr	Thr	Ser	Ala				
				245	250				255										
Met	Phe	Ser	Tyr	Met	Asn	Pro	His	Ser	Thr	His	Gly	Pro	Asp	Lys	Asp				
				260	265				270										
Lys	Pro	Phe	Ser	Leu	Leu	Tyr	Thr	Ile	Ile	Thr	Pro	Met	Cys	Asn	Pro				
				275	280				285										
Ile	Ile	Tyr	Ser	Phe	Arg	Asn	Lys	Glu	Ile	Lys	Glu	Ala	Met	Val	Arg				
				290	295				300										
Ala	Leu	Gly	Arg	Thr	Arg	Leu	Ala	Gln	Pro	Gln	Ser	Val							
				305	310				315										

<210> 2263

<211> 320

<212> PRT

<213> Homo sapien (8439993-14-9565-12410)

<400> 2263

Met	Leu	His	Thr	Asn	Asn	Thr	Gln	Phe	His	Pro	Ser	Thr	Phe	Leu	Val
1				5					10					15	
Val	Gly	Val	Pro	Gly	Leu	Glu	Asp	Val	His	Val	Trp	Ile	Gly	Phe	Pro
			20					25					30		
Phe	Phe	Ala	Val	Tyr	Leu	Thr	Ala	Leu	Leu	Gly	Asn	Ile	Ile	Ile	Leu
		35					40					45			
Phe	Val	Ile	Gln	Thr	Glu	Gln	Ser	Leu	His	Gln	Pro	Met	Phe	Tyr	Phe
	50					55					60				
Leu	Ala	Met	Leu	Ala	Gly	Thr	Asp	Leu	Gly	Leu	Ser	Thr	Ala	Thr	Ile
65					70					75					80
Pro	Lys	Met	Leu	Gly	Ile	Phe	Trp	Phe	Asn	Leu	Gly	Glu	Ile	Ala	Phe
				85					90					95	
Gly	Ala	Cys	Ile	Thr	Gln	Met	Tyr	Thr	Ile	His	Ile	Cys	Thr	Gly	Leu
			100					105					110		
Glu	Ser	Val	Val	Leu	Thr	Val	Thr	Gly	Ile	Asp	Arg	Tyr	Ile	Ala	Ile
		115					120					125			
Cys	Asn	Pro	Leu	Arg	Tyr	Ser	Met	Ile	Leu	Thr	Asn	Lys	Val	Ile	Ala
	130					135					140				
Ile	Leu	Gly	Ile	Val	Ile	Ile	Val	Arg	Thr	Leu	Val	Phe	Val	Thr	Pro
145					150					155					160
Phe	Thr	Phe	Leu	Thr	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Val	Arg	Ile	Ile
				165					170					175	
Pro	His	Thr	Tyr	Cys	Glu	His	Met	Gly	Leu	Ala	Lys	Leu	Ala	Cys	Ala
			180					185					190		
Ser	Ile	Asn	Val	Ile	Tyr	Gly	Leu	Ile	Ala	Phe	Ser	Val	Gly	Tyr	Ile

195	200	205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val		
210	215	220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys		
225	230	235
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe		
245	250	255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His		
260	265	270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser		
275	280	285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg		
290	295	300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe		
305	310	315
		320

<210> 2264

<211> 329

<212> PRT

<213> Homo sapien (8439993-17-12459-15729)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 2264

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu	
1	5
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro	
20	25
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile	
35	40
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe	
50	55
Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val	
65	70
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe	
85	90
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met	
100	105
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile	
115	120
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr	
130	135
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro	
145	150
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile	
165	170
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly	
180	185
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile	
195	200
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile	
210	215
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe	
225	230
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro	
245	250
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro	
260	265
	270

His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
 275 280 285
 Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
 290 295 300
 Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
 305 310 315 320
 Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
 325

<210> 2265

<211> 324

<212> PRT

<213> Homo sapien (8439993-2-191-1624)

<400> 2265

Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
 1 5 10 15
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His
 20 25 30
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
 35 40 45
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
 50 55 60
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
 65 70 75 80
 Leu Thr Cys Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
 85 90 95
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
 100 105 110
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala
 115 120 125
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg
 145 150 155 160
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn
 275 280 285
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320
 Lys Gly Ala Gly

<210> 2266

<211> 312

<212> PRT

<213> Hom sapien (8516051-13-18887-21998)

<400> 2266

```

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1           5           10           15
Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
 20           25           30
Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35           40           45
Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50           55           60
Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65           70           75           80
Met Leu Ala Asn Leu Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85           90           95
Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
100           105           110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
115           120           125
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
130           135           140
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
145           150           155           160
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
165           170           175
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
180           185           190
Ser Ile Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
195           200           205
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
210           215           220
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
225           230           235           240
Cys Ala Ser His Phe Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
245           250           255
Ser Met Tyr Val Gln Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
260           265           270
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
275           280           285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
290           295           300
Leu Lys Arg Ile Gly Ile Leu Ala
305           310

```

<210> 2267

<211> 289

<212> PRT

<213> Homo sapien (8516051-8-7333-8874)

<220>

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 2267

```

Leu Leu Phe Phe Ile Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
 20           25           30
Ser Ser Leu Tyr Phe Ph Ile Ser Val Leu Ser Phe Leu Glu Il Trp
 35           40           45

```

Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
 50 55 60
 Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Ph
 65 70 75 80
 Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
 85 90 95
 Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
 100 105 110
 Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
 115 120 125
 Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
 130 135 140
 Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
 145 150 155 160
 Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
 165 170 175
 Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
 180 185 190
 Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
 195 200 205
 Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
 210 215 220
 Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
 225 230 235 240
 Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
 245 250 255
 Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
 260 265 270
 Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
 275 280 285
 His

<210> 2268

<211> 166

<212> PRT

<213> Homo sapien (8516144-1-909-1747)

<220>

<221> VARIANT

<222> (1)...(166)

<223> Xaa = Any Amino Acid

<400> 2268

Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn
 1 5 10 15
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala
 20 25 30
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly
 35 40 45
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg
 50 55 60
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys
 65 70 75 80
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 85 90 95
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr
 100 105 110
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 115 120 125
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala

130 135 140
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa
 145 150 155 160
 Xaa His Leu Glu Leu Leu
 165

<210> 2269
 <211> 540
 <212> PRT
 <213> Homo sapien (8516144-24-10674-13726)

<220>
 <221> VARIANT
 <222> (1)...(540)
 <223> Xaa = Any Amino Acid

<400> 2269
 Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val
 1 5 10 15
 Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val
 20 25 30
 Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile
 35 40 45
 Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe
 50 55 60
 Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr
 65 70 75 80
 Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro
 85 90 95
 Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe His Leu Leu Ala Gly
 100 105 110
 Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln
 130 135 140
 Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu
 145 150 155 160
 Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val
 165 170 175
 Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys
 180 185 190
 Ser Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe
 195 200 205
 Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val
 210 215 220
 Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
 245 250 255
 Thr Gly Val Phe Ser Tyr Thr Arg Leu Gly Ser Val Glu Ser Ser Asp
 260 265 270
 Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Val Ile Ser Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Trp Thr Ser Leu Leu Asp Val Gly Cys Ile Ser
 290 295 300
 His Cys Ser Ser Asp Ala Gly Val Ser Pro Gly Pro Pro Val Gln Ser
 305 310 315 320
 Pro Tyr Ala Ala Cys Ser Ser Gln Leu Phe Phe Pro His Leu Leu Ala
 325 330 335
 Gly Val Asp Cys His Leu Leu Ile Ala Met Ala Tyr Asp Arg Tyr Leu
 340 345 350

Ala Ile Cys Gln Leu Leu Thr Asn Ser Thr Arg Met Ser Cys Glu Val
 355 360 365
 Gln Gly Ala Leu Val Gly Ile Cys Cys Thr Val Ser Phe Ile Asn Ala
 370 375 380
 Leu Thr His Thr Val Ala Val Ser Ala Leu Asp Phe Cys Gly Pro Asn
 385 390 395 400
 Val Val Asn His Phe Tyr Cys Asp Leu Pro Pro Leu Phe Gln Leu Ser
 405 410 415
 Cys Ser Ser Ile His Leu Asn Gly Gln Leu Leu Leu Val Gly Ala Thr
 420 425 430
 Phe Ile Gly Val Ile Pro Met Ile Phe Ile Ser Val Ser Tyr Ala His
 435 440 445
 Val Thr Ala Ala Ile Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys
 450 455 460
 Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Xaa Ile Phe Tyr
 465 470 475 480
 Gly Thr Gly Phe Phe Ser Tyr Met Cys Leu Gly Ser Val Ser Ala Ser
 485 490 495
 Asp Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Ile Leu Ser Pro Met
 500 505 510
 Leu Asn Pro Val Ile Tyr Ser Leu Gln Asn Pro Asp Val Gln Gly Thr
 515 520 525
 Leu Lys Arg Val Leu Thr Gly Lys Arg Pro Pro Ala
 530 535 540

<210> 2270

<211> 106

<212> PRT

<213> Homo sapien (8518017-12-460-1010)

<220>

<221> VARIANT

<222> (1)...(106)

<223> Xaa = Any Amino Acid

<400> 2270

Gln Leu Leu Ile Leu Ala Cys Ser Glu Ser Ser Leu Asn Ser Leu Tyr
 1 5 10 15
 Ser Phe Ile His Ser Phe Phe Cys Ser Phe Leu Pro Asn Ser Gly Tyr
 20 25 30
 Leu Val Ser Gln Thr Asp Leu Val Pro Asp Leu Arg Glu Phe Arg Ile
 35 40 45
 Xaa Ser Arg Arg His Ile Arg Asn Trp Asn Val Met Gly Ala Met Ile
 50 55 60
 Leu Asn Val Cys Glu Ala Thr Gly Asn Gly Val Ala Leu Pro Ile Ser
 65 70 75 80
 Lys Ala Ala Thr Pro Glu Ala Met Thr Gly Val Xaa Ser Glu His Asp
 85 90 95
 Ile Ala Leu Leu Phe Trp Leu Leu Arg Leu
 100 105

<210> 2271

<211> 223

<212> PRT

<213> Homo sapien (8546599-5-2194-2867)

<220>

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 2271

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pr
 1           5           10           15
Pr Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
 20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
 35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
 50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
 65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
 85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
 100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
 115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
 165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
 180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
 195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 210          215          220

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<210> 2272

<211> 120

<212> PRT

<213> Homo sapien (8546616-1-110163-110999)

<220>

<221> VARIANT

<222> (1)...(120)

<223> Xaa = Any Amino Acid

<400> 2272

```

Val Cys Ile Asn Ile Ser Xaa His His Xaa His Met Tyr Phe Xaa Leu
 1           5           10           15
Ser Tyr Gly Ser Phe Xaa Glu Leu Leu Val His Ser Ala Glu Leu Pro
 20           25           30
Ser Arg Ile Trp Arg Leu Lys Ser Ser Xaa Ser Cys Lys Ile Leu Ser
 35           40           45
Gly Tyr Ser Asn Glu Val Trp Phe His Cys Ile Phe Leu Cys Leu Leu
 50           55           60
Ser Lys Arg Leu Lys Xaa Ala His Ser Asp Lys Cys Gly Gln Val Ser
 65           70           75           80
Leu Pro Leu His Pro Ser Leu Cys Leu Leu Leu Ser Leu Gly Asn Trp
 85           90           95
Cys Gly Lys Ser Leu Cys Pro Gly Met Ala Thr Leu Leu Val Ser Arg
 100          105          110
Leu Ile Gln Ser Ser Leu Cys Ser
 115          120

```

<210> 2273

<211> 260

<212> PRT

<213> Homo sapien (8547576-2-9950-11981)

<220>

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 2273

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1           5           10           15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
          20           25           30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
          35           40           45
Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Ile Pro Leu Met Trp Met
          50           55           60
Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn
          65           70           75           80
Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe
          85           90           95
Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr
          100          105          110
Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu
          115          120          125
Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala
          130          135          140
Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val
          145          150          155          160
Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu
          165          170          175
Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile
          180          185          190
Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu
          195          200          205
Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro
          210          215          220
Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser
          225          230          235          240
Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn
          245          250          255
Leu Asn Ile Arg
          260

```

<210> 2274

<211> 328

<212> PRT

<213> Homo sapien (8567470-5-1-1337)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2274

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
          20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
          35           40           45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys

```

50	55	60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys		
65	70	75
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly		30
	85	90
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu		95
	100	105
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys		110
	115	120
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe		125
	130	135
Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu		140
145	150	155
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile		160
	165	170
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys		175
	180	185
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe		190
	195	200
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		205
	210	215
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe		220
225	230	235
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr		240
	245	250
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys		255
	260	265
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn		270
	275	280
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp		285
	290	295
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His		300
305	310	315
Leu Phe His Ser Phe Cys Arg Met		320
	325	

<210> 2275

<211> 310

<212> PRT

<213> Homo sapien (8567878-9-2833-5012)

<220>

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 2275

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly	
1	5
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu	10
	15
	20
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu	25
	30
	35
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser	40
	45
	50
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn	55
65	60
	65
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr	70
	75
	80
	85
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met	90
	95
	100
	105
	110

Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
 130 135 140
 Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
 145 150 155 160
 Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
 165 170 175
 Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
 180 185 190
 His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe
 195 200 205
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly
 245 250 255
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp
 260 265 270
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile
 275 280 285
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met
 290 295 300
 Glu Asn Leu Cys Leu Thr
 305 310

<210> 2276

<211> 358

<212> PRT

<213> Homo sapien (8567902-2-5416-6914)

<220>

<221> VARIANT

<222> (1)...(358)

<223> Xaa = Any Amino Acid

<400> 2276

Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro
 1 5 10 15
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala
 20 25 30
 Thr Asn Ala Thr Pro Pro Met Leu Val Asn Phe Val Phe Ser Lys Arg
 35 40 45
 Lys Thr Val Ser Phe Ile Gly Cys Phe Ile Gln Phe His Leu Phe Ile
 50 55 60
 Ala Leu Val Ile Thr Asp Tyr His Met Leu Thr Val Met Val Tyr Asp
 65 70 75 80
 His Tyr Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Ser
 85 90 95
 Arg Cys Val Cys Leu Cys Leu Thr Ala Ala Pro Tyr Ile Tyr Gly Ser
 100 105 110
 Ala Asn Gly Leu Val Gln Val Ile Leu Met Leu Cys Leu Phe Phe Cys
 115 120 125
 Glu Pro His Glu Ile Asn His Phe Phe Phe Phe Gly Glu Asn Ala Leu
 130 135 140
 Tyr Ala His Leu Ile Pro Leu Xaa Ile Phe Glu Trp Thr Val Gly Glu
 145 150 155 160
 Glu Gly Arg Asn Asn Ile Asn Gly Glu Asn Thr Thr Gln Lys Val Tyr
 165 170 175
 Thr Met Gly Glu Arg Asn Leu Leu Ile Gln Val Ser Ile Phe Leu Leu

180	185	190
Trp His Ile Arg Ser Xaa Leu Phe Ser Gln Tyr Glu Ala Ser Pro Arg		
195	200	205
Ala Asp Ser Asp Val Lys Leu Glu Ile Asn His Phe Tyr Tyr Ala Glu		
210	215	220
Pro Pro Leu Leu Val Leu Ala Cys Leu Asp Thr Tyr Val Lys Glu Thr		
225	230	235
Ala Met Phe Met Val Ala Gly Ser Asn Leu Ile Cys Pro Leu Thr Ile		
245	250	255
Ile Phe Ile Ser Tyr Thr Phe Ile Phe Thr Asp Ile Leu His Ile Cys		
260	265	270
Thr Ala Glu Gly Arg Tyr Asn Ala Phe Ser Thr Cys Gly Ser Leu Val		
275	280	285
Thr Ala Val Thr Val Phe Gln Gly Thr Leu Phe His Met Cys Leu Arg		
290	295	300
Pro Pro Ser Glu Ala Ser Val Glu Gln Gly Lys Ile Val Ala Ala Phe		
305	310	315
Tyr Ile Phe Val Ser Pro Thr Leu Asn Pro Leu Ile Tyr Arg Leu Arg		
325	330	335
Asn Lys Asn Val Lys Arg Thr Ile Arg Glu Val Ile Gln Lys Lys Leu		
340	345	350
Phe Ala Lys Xaa Gly Arg		
355		

<210> 2277

<211> 305

<212> PRT

<213> Homo sapien (8567902-4-4497-6890)

<400> 2277

Met Ser Asn Thr Asn Gly Ser Ala Ile Thr Glu Phe Ile Leu Leu Gly	
1	5
Leu Thr Asp Cys Pro Glu Leu Gln Ser Leu Leu Phe Val Leu Phe Leu	
20	25
Val Val Tyr Leu Val Thr Leu Leu Gly Asn Leu Gly Met Ile Met Leu	
35	40
Met Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr	
50	55
Asn Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Asn Ala Thr Pro Gln	
65	70
Met Ser Thr Asn Ile Val Ser Glu Lys Thr Ile Ser Phe Ala Gly Cys	
85	90
Phe Thr Gln Cys Tyr Ile Phe Ile Ala Leu Leu Thr Glu Phe Tyr	
100	105
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr Asp Pro	
115	120
Leu Arg Tyr Ser Val Lys Thr Ser Arg Arg Val Cys Ile Cys Leu Ala	
130	135
Thr Phe Pro Tyr Val Tyr Gly Phe Ser Asp Gly Leu Phe Gln Ala Ile	
145	150
Leu Thr Phe Arg Leu Thr Phe Cys Arg Ser Ser Val Ile Asn His Phe	
165	170
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ser Cys Ser Asp Thr Tyr	
180	185
Val Lys Glu His Ala Met Phe Ile Ser Ala Gly Phe Asn Leu Ser Ser	
195	200
Ser Leu Thr Ile Val Leu Val Ser Tyr Ala Phe Ile Leu Ala Ala Ile	
210	215
Leu Arg Ile Lys Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys	
225	230
Gly Ser His Met Met Ala Val Thr Leu Phe Tyr Gly Thr Leu Phe Cys	
	235
	240

				245					250					255	
Met	Tyr	Ile	Arg	Pro	Pro	Thr	Asp	Lys	Thr	Val	Glu	Glu	Ser	Lys	Ile
			260					265					270		
Ile	Ala	Val	Phe	Tyr	Thr	Phe	Val	Ser	Pro	Val	Leu	Asn	Pro	Leu	Ile
			275				280					285			
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gln	Ala	Leu	Lys	Asn	Val	Leu
	290					295					300				

Arg
305

<210> 2278

<211> 319

<212> PRT

<213> Homo sapien (8567954-21-10804-13693)

<220>

<221> VARIANT

<222> (1) ... (319)

<223> Xaa = Any Amino Acid

<400> 2278

Met	Gly	Val	His	Asn	Leu	Phe	Thr	Val	Thr	Gln	Phe	Ile	Leu	Ile	Gly
1				5					10					15	
Leu	Ser	Tyr	Phe	Ser	Asn	Glu	His	Tyr	Leu	Leu	Phe	Val	Ala	Leu	Ala
			20					25					30		
Ile	Ile	Cys	Gln	Val	Phe	Leu	Val	Arg	Ser	Gly	Asp	Ile	Leu	Leu	Ala
		35					40					45			
Ile	Gly	Thr	Val	Ile	Lys	Leu	His	Thr	Thr	Met	Tyr	Tyr	Phe	Leu	Ala
	50					55					60				
Asn	Val	Ser	Ile	Leu	Asp	Ile	Leu	Cys	Ser	Ser	Ala	Thr	Ile	Pro	Lys
65					70					75					80
Met	Pro	Lys	Ile	Leu	Xaa	Thr	Glu	Asp	His	Ser	Ile	Ser	Phe	Val	Arg
				85					90					95	
Xaa	Ala	Leu	Gln	Pro	Tyr	Phe	Leu	Val	Ala	Trp	Ala	Gly	Lys	Lys	Cys
			100					105					110		
Phe	Leu	Thr	Val	Thr	Ala	Tyr	Asp	Trp	Cys	Val	Val	Thr	Cys	Phe	Ser
			115				120					125			
Leu	Cys	Tyr	Ile	Leu	Ile	Met	Asn	Lys	Leu	Val	Ser	Val	Gln	Leu	Val
		130				135					140				
Tyr	Gly	Thr	Xaa	Ala	Ala	Gly	Phe	Leu	Asn	Phe	Leu	Leu	Leu	His	Val
145					150					155					160
Val	Ser	Thr	Leu	Cys	Leu	Ser	Phe	Cys	Lys	Pro	Asp	Arg	Val	Asn	Gln
				165					170					175	
Tyr	Tyr	Cys	Asp	Ile	Ser	Pro	Met	Gly	Ala	Leu	Leu	Cys	Gln	Ser	Met
			180					185					190		
His	Leu	Ala	Asn	Met	Leu	Val	Leu	Val	Glu	Ser	Val	Ile	Leu	Gly	Ile
		195					200					205			
Ser	Ala	Phe	Leu	Ala	Ala	Phe	Asn	Phe	Tyr	Ile	Tyr	Ile	Ile	Ser	Thr
		210				215					220				
Ile	Leu	Lys	Ile	Gln	Cys	Val	Glu	Trp	Ser	Ala	Lys	Cys	Phe	Ser	Thr
225					230					235					240
Cys	Thr	Ser	His	Leu	Leu	Thr	Val	Cys	Leu	Phe	Tyr	Gly	Ile	Leu	Thr
				245					250					255	
Phe	Thr	Tyr	Ile	Tyr	Ser	Phe	Ser	Ser	His	Thr	His	Met	Ser	Lys	Ala
			260					265					270		
Ser	Pro	Asp	Leu	Ala	Thr	Asp	Arg	Leu	Ile	Ser	Met	Leu	Tyr	Arg	Val
		275					280					285			
Ile	Thr	Leu	Met	Phe	Asn	Phe	Ile	Thr	Asp	Asn	Leu	Arg	Asn	Thr	Glu
		290				295					300				
Val	Lys	Gly	Ala	Ser	Glu	Arg	Phe	Tyr	Val	Ile	Glu	His	Val	Tyr	
305					310					315					

<210> 2279

<211> 307

<212> PRT

<213> Homo sapien (8567954-21-4824-8043)

<400> 2279

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1          5          10          15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
          20          25          30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr
          35          40          45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
          50          55          60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
65          70          75          80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
          85          90          95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
          100          105          110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          115          120          125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
          130          135          140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
145          150          155          160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
          165          170          175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
          180          185          190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
          195          200          205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
          210          215          220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
225          230          235          240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
          245          250          255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
          260          265          270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
          275          280          285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
290          295          300
Leu Lys His
305

```

<210> 2280

<211> 104

<212> PRT

<213> Homo sapien (8568141-22-12851-13662)

<220>

<221> VARIANT

<222> (1)...(104)

<223> Xaa = Any Amino Acid

<400> 2280

```

Leu Pro Pro Asn Il Leu Cys Val Ile Ile Ser Tyr Ser Arg His Phe
 1          5          10          15

```

S r Lys Leu Leu Lys Ile Pro Asn Ile Arg Thr Gln Ile Gln Lys Phe
 20 25 30
 Ser His Ile Ser Xaa Asn Leu Lys Val Ser Val Leu Arg Leu Thr
 35 40 45
 Trp Thr Arg Tyr Pro Ser Xaa Met Leu Pro Xaa Tyr Pro Ala Pro Thr
 50 55 60
 Leu Thr Lys His Ile Pro Cys Gly Leu Val Thr Cys Leu Leu Gln Pro
 65 70 75 80
 Arg Met Ser Cys Trp Arg Ala Arg Asn Ala Pro Ser Thr Cys Leu Ala
 85 90 95
 Leu Thr Ala Lys His Ile Ser Ala
 100

<210> 2281

<211> 333

<212> PRT

<213> Homo sapien (8568143-10-1394-2684)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2281

Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His
 1 5 10 15
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa
 20 25 30
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa
 35 40 45
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser
 50 55 60
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val
 65 70 75 80
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys
 85 90 95
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Ile
 100 105 110
 Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr
 115 120 125
 Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Val
 130 135 140
 Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr
 145 150 155 160
 Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val
 165 170 175
 Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser
 180 185 190
 Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala
 195 200 205
 Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile
 210 215 220
 Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln
 225 230 235 240
 Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr
 245 250 255
 Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro
 260 265 270
 Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met
 275 280 285
 Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr

290 295 300
 Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr
 305 310 315 320
 Pr Leu Trp Ser Val Val Arg Lys Asn Ser Lys Leu Lys
 325 330

<210> 2282
 <211> 157
 <212> PRT
 <213> Homo sapien (8568247-23-1134-2556)

<220>
 <221> VARIANT
 <222> (1)...(157)
 <223> Xaa = Any Amino Acid

<400> 2282
 Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
 1 5 10 15
 Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
 20 25 30
 Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
 35 40 45
 Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
 50 55 60
 Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
 65 70 75 80
 Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
 85 90 95
 Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
 100 105 110
 Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
 115 120 125
 Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
 130 135 140
 Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
 145 150 155

<210> 2283
 <211> 91
 <212> PRT
 <213> Homo sapien (8568259-4-1499-2114)

<220>
 <221> VARIANT
 <222> (1)...(91)
 <223> Xaa = Any Amino Acid

<400> 2283
 Gln Glu Ile Ser Ala Ala Arg Glu Arg Lys Ala Thr Lys Ile Leu Gly
 1 5 10 15
 Ile Ile Leu Gly Ala Phe Ile Ile Cys Trp Leu Pro Phe Phe Val Val
 20 25 30
 Ser Leu Val Leu Pro Ile Cys Arg Asp Ser Cys Trp Ile His Pro Ala
 35 40 45
 Leu Phe Asp Phe Phe Thr Trp Leu Gly Tyr Leu Asn Ser Leu Ile Asn
 50 55 60
 Pro Ile Ile Tyr Thr Val Phe Asn Glu Glu Phe Arg Gln Ala Phe Gln
 65 70 75 80
 Lys Ile Val Pro Phe Arg Lys Ala Ser Xaa Ser
 85 90

<210> 2284

<211> 320

<212> PRT

<213> Homo sapien (8569904-8-5520-7957)

<400> 2284

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1          5          10          15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu Leu
      20          25          30
Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
      35          40          45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
      50          55          60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
      65          70          75          80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
      85          90          95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
      100          105          110
Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val
      115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
      130          135          140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
      145          150          155          160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
      165          170          175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
      180          185          190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
      195          200          205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
      210          215          220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
      225          230          235          240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
      245          250          255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
      260          265          270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
      275          280          285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
      290          295          300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
      305          310          315          320

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<210> 2285

<211> 130

<212> PRT

<213> Homo sapien (8569934-12-21632-22280)

<220>

<221> VARIANT

<222> (1)...(130)

<223> Xaa = Any Amino Acid

<400> 2285

```

Lys Val Cys Leu Phe Gln Ala Leu Met Cys Trp Leu Ser Leu Xaa Gln
 1          5          10          15

```

Gln Pro Phe Thr Gln Ser Ala S r Thr Leu Leu Leu Pro Leu Cys Ile
 20 25 30
 Pro Arg Gln Ala Pro Gln Cys Pro Gly Asr Leu Arg Thr Ala Leu Arg
 35 40 45
 Ala Val Met Cys Thr Arg Gly Cys Val Phe Xaa Ala Trp Glu Trp Val
 50 55 60
 Ala Ser Tyr Ile His Leu Ile Pro Leu Cys Ile Pro Val Arg Ser Ala
 65 70 75 80
 Tyr Asn Leu Gly Arg Val Leu Asn Gly Val Lys Trp Cys Ser Xaa Gly
 85 90 95
 Gln Gln Val Glu Phe Cys Ser Cys Lys Ala Lys Leu Met Leu Leu Ala
 100 105 110
 Ser Val Asp Val Val Leu Val Ser Thr Gln Pro Xaa Asn Pro Arg Pro
 115 120 125
 His Glu
 130

<210> 2286

<211> 318

<212> PRT

<213> Homo sapien (8569993-13-6018-8083)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2286

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1 5 10 15
 Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
 20 25 30
 Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
 35 40 45
 Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
 50 55 60
 Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
 65 70 75 80
 Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
 85 90 95
 Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
 100 105 110
 Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
 115 120 125
 Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
 130 135 140
 Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
 145 150 155 160
 Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
 165 170 175
 Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
 180 185 190
 Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
 195 200 205
 Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
 210 215 220
 Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
 225 230 235 240
 Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
 245 250 255
 Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala

	260		265		270										
Pro	His	Ile	Val	His	Val	Leu	Met	Ala	Asn	Val	Tyr	Leu	Met	Gly	Pro
	275					280						285			
Pro	Leu	Met	Asn	Pro	Val	Phe	Tyr	Ser	Val	Lys	Thr	Arg	Gln	Ile	Arg
	290					295					300				
Asp	Arg	Ile	Phe	Gln	Ile	Lys	Phe	Arg	Asn	Met	Lys	Cys	Arg		
305				310						315					

<210> 2287

<211> 235

<212> PRT

<213> Homo sapien (8570235-22-3034-4808)

<220>

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 2287

Met	Leu	Phe	Ile	Ser	Gln	Trp	Gly	Glu	Arg	Xaa	Arg	Val	Arg	Arg	Asn
1				5				10						15	
Val	Gln	Leu	Met	Thr	Ala	Phe	Ile	Leu	Met	Asp	Leu	Pro	His	Val	Pro
		20						25					30		
Ala	Leu	Asp	Ala	Pro	Leu	Phe	Gly	Val	Phe	Leu	Val	Val	Tyr	Val	Leu
		35					40					45			
Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Val	Ile	Arg	Val	Tyr	Ser
	50				55						60				
His	Leu	His	Thr	Pro	Lys	Tyr	Tyr	Phe	Leu	Thr	Asn	Leu	Ser	Phe	Ile
65					70					75				80	
Asp	Leu	Trp	Phe	Phe	Thr	Val	Met	Val	Pro	Lys	Met	Pro	Arg	Thr	Leu
			85						90					95	
Leu	Ser	Leu	Cys	Gly	Lys	Ala	Val	Ser	Phe	His	Ser	Cys	Met	Thr	Gln
		100						105					110		
Leu	Tyr	Phe	Phe	Tyr	Phe	Leu	Gly	Ser	Thr	Glu	Cys	Leu	Leu	Tyr	Thr
	115						120					125			
Val	Met	Ser	Tyr	Asp	Arg	Tyr	Arg	Gly	Asn	Thr	Gln	His	Phe	Pro	Gly
	130					135					140				
Ser	Glu	Asn	Leu	Pro	Thr	Lys	Xaa	Ala	Lys	Cys	Xaa	Trp	Pro	Gly	Gly
145					150					155				160	
His	Thr	Gly	Xaa	Pro	Leu	Ile	Ile	Leu	Ala	Asp	Leu	Ser	Gly	Xaa	Leu
			165						170					175	
Arg	Val	Asp	Ser	Ser	Xaa	Trp	Ala	Ile	Gln	Asn	Xaa	Xaa	Tyr	Asn	Leu
		180					185						190		
Val	Ile	Gln	Val	Lys	Phe	Ile	Thr	Cys	Ile	Gly	Leu	Ser	Ile	Lys	His
	195						200					205			
Tyr	Ser	Lys	Gln	Leu	Ala	Gln	Leu	Xaa	Phe	Phe	His	Arg	Leu	Ser	Lys
	210					215					220				
Thr	Phe	Leu	Asn	Ser	Gln	Leu	Asp	Phe	Tyr	Leu					
225					230					235					

<210> 2288

<211> 325

<212> PRT

<213> Homo sapien (8570522-1-103735-108559)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2288

```

Met Lys Ile Asn Gln Thr Ile Leu Lys Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Ser Val Tyr Pro His Val Gln Thr Phe Leu Phe Val Val Phe Phe Cys
          20           25           30
Leu Tyr Leu Leu Thr Leu Ala Gly Asn Leu Thr Ile Met Gly Leu Thr
          35           40           45
Xaa Val Asp Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Ser Ala
          50           55           60
Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Thr Ile Val Pro Lys Met
65           70           75           80
Leu Glu Asp Leu Leu Ala Lys Asp Arg Ser Ile Ser Val Thr Gly Cys
          85           90           95
Ser Leu Gln Met Cys Phe Phe Leu Gly Leu Gly Gly Thr Asn Cys Ile
          100          105          110
Ile Leu Thr Leu Met Gly Tyr Asp Arg Phe Leu Ala Ile Cys Asn Pro
          115          120          125
Leu Arg Tyr Pro Leu Leu Met Thr Asn Ile Val Cys Gly Gln Leu Val
          130          135          140
Ala Ser Ala Cys Thr Ala Gly Phe Phe Ile Ser Leu Thr Glu Thr Ala
145          150          155          160
Leu Ile Phe Arg Asp Ser Phe Cys Arg Pro Asn Leu Val Lys His Phe
          165          170          175
Phe Cys His Met Leu Ala Val Ile Arg Leu Ser Cys Ile Asp Ser Asn
          180          185          190
His Thr Glu Phe Ile Ile Thr Leu Ile Ser Val Ser Gly Leu Leu Gly
          195          200          205
Thr Leu Leu Leu Ile Ile Leu Thr Asp Val Phe Ile Ile Ser Thr Val
          210          215          220
Leu Arg Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Thr Thr Cys
225          230          235          240
Ala Ser His Leu Thr Val Val Ile Ile His Phe Gly Phe Ala Ser Ile
          245          250          255
Val Tyr Leu Lys Pro Glu Ala Ser Gly Asp Asp Thr Leu Ile Ala Val
          260          265          270
Pro Tyr Thr Val Ile Thr Pro Phe Leu Ser Pro Ile Ile Phe Ser Leu
          275          280          285
Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
          290          295          300
Val Ala Leu Lys Lys Xaa Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
305          310          315          320
Gly Leu Asn Val Pro
          325

```

<210> 2289

<211> 151

<212> PRT

<213> Homo sapien (8570523-1-20584-21124)

<220>

<221> VARIANT

<222> (1)...(151)

<223> Xaa = Any Amino Acid

<400> 2289

```

Cys Val Ser Xaa Gln Arg Ser Pro His Phe Leu Cys Ser Gly Asp Ser
 1           5           10           15
Val Phe Cys Leu Val His Ser Val Gly Cys Cys Thr Leu Leu Leu Ser
          20           25           30
Gln Ser Leu Arg Leu Leu Ser Val Phe Leu Leu Ser Ser Cys Ala Ala
          35           40           45
Ser Trp Lys Lys Val His Ser Met Asn Leu Tyr Thr Pro Phe Cys Leu

```

```

      50              55              60
Ser Lys Trp Xaa Asn His Val Asn Asn Ala Phe Asn Leu Pro Ser Trp
65              70              75              80
Lys Lys Ser Lys Ser Val Val Thr Met Phe Xaa Gly Pro Ala Met Ile
      85              90              95
Thr Tyr Leu Arg Ser Asp Ser Xaa Tyr Asn Pro Thr Val Gly Lys Gln
      100              105              110
Leu Val Leu Phe Tyr Ser Ile Val Ser Ala Phe Ile Lys Pro Ile Ile
      115              120              125
Ser Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Ser Trp Lys Val Leu
      130              135              140
Arg Val Lys Gly Thr Ala Gln
145              150

```

<210> 2290

<211> 96

<212> PRT

<213> Homo sapien (8570526-1-82280-82723)

<220>

<221> VARIANT

<222> (1)...(96)

<223> Xaa = Any Amino Acid

<400> 2290

```

Ile Val Val Asp Tyr Leu Ile Ile Lys Ser Ser Ile Phe Pro Pro Ala
1              5              10              15
Asn Ser Asn Leu Phe Lys Leu Ile Arg Lys Ser Ile Pro Ile Leu Ala
      20              25              30
Cys Xaa Arg Val Met Met Asp Leu Gly Xaa Thr Gln Asn Val Ser Thr
      35              40              45
Ser Lys Xaa Gly Cys Val Asp Lys Glu Tyr Asn Cys Phe Ile Pro Phe
      50              55              60
Leu Ile Ala Trp His Leu Xaa His Arg Glu Xaa Arg Ile Ile Xaa Asp
65              70              75              80
Arg Ile Ser Ile Leu Val Xaa Lys Ala Leu Trp Met Lys Asn Lys Gly
      85              90              95

```

<210> 2291

<211> 162

<212> PRT

<213> Homo sapien (8575931-7-5387-5879)

<220>

<221> VARIANT

<222> (1)...(162)

<223> Xaa = Any Amino Acid

<400> 2291

```

Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
1              5              10              15
Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
      20              25              30
Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
      35              40              45
Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
      50              55              60
Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
65              70              75              80
Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
      85              90              95

```


Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr
 100 105 110
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu
 115 120 125
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser
 130 135 140
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr
 145 150 155 160
 Val Gln

<210> 2292

<211> 264

<212> PRT

<213> Homo sapien (8648586-17-1126-4850)

<220>

<221> VARIANT

<222> (1)...(264)

<223> Xaa = Any Amino Acid

<400> 2292

Ala Cys Val Thr Phe Leu Val Glu Val Thr Val Met Pro Phe Ser Thr
 1 5 10 15
 Val Arg Phe Val Lys Ser Cys Trp Tyr Phe Gly Asp Ser Ser Cys Lys
 20 25 30
 Phe Asn Thr Trp Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His
 35 40 45
 Xaa Gly Cys Ile Ser Val Asp Arg Tyr Met Leu Val Ser Asp Leu Leu
 50 55 60
 Thr Tyr Pro Thr Lys Phe Thr Val Ser Val Leu Gly Ile Cys Met Val
 65 70 75 80
 Leu Cys Trp Phe Leu Phe Cys Pro Tyr Ser Phe Ser Ile Phe Asn Thr
 85 90 95
 Gly Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys
 100 105 110
 Val Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys
 115 120 125
 Phe Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser
 130 135 140
 Lys Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr
 145 150 155 160
 Ala Ser Gln Ala Gln Ser Ser Ser Glu Ser Tyr Lys Glu Arg Val Ala
 165 170 175
 Lys Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala
 180 185 190
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala
 195 200 205
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp
 210 215 220
 Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe
 225 230 235 240
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val
 245 250 255
 Leu Arg Thr Asp Ser Ser Thr Thr
 260

<210> 2293

<211> 126

<212> PRT

<213> Homo sapien (8648858-36-1-1206)

<220>

<221> VARIANT

<222> (1)...(126)

<223> Xaa = Any Amino Acid

<400> 2293

```

Leu Cys Met Leu Cys Trp Gln Trp Pro Ala Val Met Thr Asp Arg Thr
 1           5           10           15
Ile Ala Thr Cys Lys Ser Arg His Phe Leu Phe Leu Ile Leu Val Leu
      20           25           30
Thr Cys Ser Leu Ile Pro Ala Xaa Ala Trp Phe Thr Tyr Phe Phe Phe
      35           40           45
Asn Ser Lys Ser Cys Val Val Leu Phe Gln His Ile His Phe Cys Leu
      50           55           60
Leu Xaa Ile Pro Ser Asn Phe Tyr Cys Leu Xaa Thr Thr Ala Tyr Leu
      65           70           75           80
Lys Xaa Leu Leu Asn Met Xaa Leu Lys His Xaa Ile Lys Xaa Thr Tyr
      85           90           95
Ile Val Phe Leu Ala Val Arg Ile Leu Xaa Ala Phe Leu Ile Leu Ile
      100           105           110
Cys Ile Met Asn Leu Gln Leu Arg Gln Cys Ala Thr His Phe
      115           120           125

```

<210> 2294

<211> 183

<212> PRT

<213> Homo sapien (8649180-1-4193-6564)

<220>

<221> VARIANT

<222> (1)...(183)

<223> Xaa = Any Amino Acid

<400> 2294

```

Val Ile Met His Lys Lys Glu Cys Xaa Lys Lys Thr His Asn Ile Val
 1           5           10           15
Phe Leu Leu Met Val Trp Glu Phe Phe Tyr Lys Phe Leu Val Phe Phe
      20           25           30
Phe Phe Ser Leu His Xaa Cys Val Ser Ser Ile Ile Met Ser Val Tyr
      35           40           45
Tyr Xaa Lys Ile Asn Ile Phe Ile Xaa Ile Glu Thr Lys Leu Leu Phe
      50           55           60
His Ile Ser Arg Xaa Asp Arg Met Ile Arg Cys Ser Phe Gln Lys Asn
      65           70           75           80
Tyr Leu Leu Asn His Asn Gly Leu Met Cys Arg Ser Lys Cys Gln Leu
      85           90           95
Val Tyr Gln Thr Val Ser Asn Ser Leu Asn Tyr Phe Tyr Ile Thr Pro
      100           105           110
Ile Xaa Leu Phe Gln Ile Val Val Tyr Lys Lys Tyr Lys Phe Leu His
      115           120           125
Cys Ile Val Leu Asp Val Pro Ala Tyr Ile Asn Ile Leu Gly Cys Ile
      130           135           140
Val Ser Phe Leu His Val Ile Cys Asn Val Xaa Leu Tyr Val Ile Asn
      145           150           155           160
Lys Thr Xaa Asn Xaa Tyr Lys Ser Arg Phe Ser Thr Cys Leu Ser His
      165           170           175
Ser Asp Ile Thr Asp Leu Phe
      180

```

<210> 2295

<211> 157

<212> PRT

<213> Homo sapien (902315-1-1-472)

<400> 2295

```

Ile Cys His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys
 1           5           10           15
Val Phe Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile
          20           25           30
Ile Val Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu
          35           40           45
Ile His His Phe Phe Cys Asp Val Ala Ala Leu Leu Pro Leu Ser Cys
          50           55           60
Thr Glu Thr Ser Ala Phe Glu Arg Leu Leu Val Ile Cys Cys Val Val
65          70          75          80
Met Leu Ile Phe Pro Val Ser Val Ile Ile Leu Ser Tyr Ser His Val
          85          90          95
Leu Arg Ala Val Ile His Met Gly Ser Gly Glu Ser Arg Arg Lys Ala
          100         105         110
Phe Thr Thr Cys Ser Ser His Pro Ser Val Val Gly Leu Tyr Tyr Gly
          115         120         125
Ala Ala Met Phe Met Tyr Met Arg Pro Ala Ser Lys His Thr Pro Asp
          130         135         140
Gln Asp Lys Met Val Ser Ala Phe Tyr Thr Asn Pro Ala
145          150          155

```

<210> 2296

<211> 325

<212> PRT

<213> Mus musculus (M1 4726083-1-12568-18197 3361-4335)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2296

```

Thr Met Trp Ser Asn Ile Ser Ala Ala Pro Phe Leu Leu Thr Gly Phe
 1           5           10           15
Pro Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala
          20           25           30
Ile Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile
          35           40           45
Lys Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met
          50           55           60
Leu Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val
65          70          75          80
Met Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys
          85          90          95
Phe Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly
          100         105         110
Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro
          115         120         125
Leu His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly
          130         135         140
Leu Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu
145          150         155         160
Pro Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala
          165         170         175
Phe Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr
          180         185         190

```

Phe Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu
 195 200 205
 Asp Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val
 210 215 220
 Met Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys
 225 230 235 240
 Val Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly
 245 250 255
 Leu Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His
 260 265 270
 Ile Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro
 275 280 285
 Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His
 290 295 300
 Leu Leu Ser Val Xaa Asp Asp Val Asn His Tyr Ile Ile Ile Gln Arg
 305 310 315 320
 Ser Leu Gly Met Phe
 325

<210> 2297

<211> 318

<212> PRT

<213> Mus musculus (M2 4726083-1-175-4296 2476-1523)

<400> 2297

Leu Ser Ala Met Pro Ser Met Trp Leu Asn Ile Ser Ser Ser Pro Phe
 1 5 10 15
 Leu Leu Thr Gly Phe Pro Gly Leu Glu Lys Ala His His Leu Ile Ser
 20 25 30
 Leu Pro Leu Leu Met Ala Tyr Ile Ser Ile Leu Leu Gly Asn Gly Thr
 35 40 45
 Leu Leu Phe Leu Ile Lys Asp Asp His Asn Leu His Glu Pro Met Tyr
 50 55 60
 Tyr Phe Leu Gly Met Leu Ala Ala Thr Asp Leu Gly Val Thr Leu Thr
 65 70 75 80
 Thr Met Pro Thr Val Leu Ser Val Leu Trp Leu Asn His Arg Glu Ile
 85 90 95
 Gly His Gly Ala Cys Phe Ser Gln Ala Tyr Phe Ile His Thr Leu Ser
 100 105 110
 Ile Val Glu Ser Gly Val Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile
 115 120 125
 Ala Ile Arg Asn Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asp Thr Lys
 130 135 140
 Val Ile Lys Ile Gly Ile Gly Leu Val Met Arg Ala Gly Leu Ser Ile
 145 150 155 160
 Met Pro Ile Ile Ile Arg Leu His Trp Phe Pro Tyr Cys Arg Ser His
 165 170 175
 Val Leu Ser His Ala Phe Cys Leu His Gln Asp Val Ile Lys Leu Ala
 180 185 190
 Cys Ala Asp Ile Thr Phe Asn Arg Leu Tyr Pro Val Val Val Val Phe
 195 200 205
 Ala Met Val Leu Leu Asp Phe Leu Ile Ile Phe Phe Ser Tyr Val Leu
 210 215 220
 Ile Leu Lys Thr Val Met Gly Ile Ala Ser Thr Asp Glu Arg Ala Lys
 225 230 235 240
 Ala Leu Asn Thr Cys Val Ser His Ile Cys Cys Ile Leu Val Phe Tyr
 245 250 255
 Val Thr Val Val Gly Leu Thr Phe Ile His Arg Phe Gly Lys Asn Val
 260 265 270
 Pro His Val Val His Ile Thr Met Ser Tyr Ile Tyr Phe Leu Phe Pro
 275 280 285

Pro Phe Met Asn Pro Val Il Tyr Ser Ile Lys Thr Lys Gln Ile Gln
 290 295 300
 Ser Gly Leu Leu Arg Leu Phe Ser Leu Pro Cys Ser Lys Thr
 305 310 315

<210> 2298

<211> 351

<212> PRT

<213> Mus musculus (M3 4726083-1-26023-28273 267-1318)

<220>

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 2298

Leu Ser Pro Ser Leu Lys Pro Ser Cys Asn Cys Asp Pro Thr Met Trp
 1 5 10 15
 Pro Asn Ser Ser Asp Ala Pro Phe Leu Leu Thr Gly Phe Leu Gly Leu
 20 25 30
 Glu Met Ile His His Trp Ile Ser Ile Pro Phe Phe Val Ile Tyr Phe
 35 40 45
 Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp Ser Asp
 50 55 60
 His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu Ala Ser
 65 70 75 80
 Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu Gly Val
 85 90 95
 Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe Ile Gln
 100 105 110
 Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val Leu Leu
 115 120 125
 Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu His Tyr
 130 135 140
 Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu Gly Ala
 145 150 155 160
 Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro Leu Phe
 165 170 175
 Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe Cys Leu
 180 185 190
 His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn Leu
 195 200 205
 Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp Ala Leu
 210 215 220
 Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met Gly Ile
 225 230 235 240
 Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val Ser His
 245 250 255
 Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu Thr Phe
 260 265 270
 Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile Thr Met
 275 280 285
 Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr
 290 295 300
 Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu Leu Ser
 305 310 315 320
 Lys His Ser Arg Thr Xaa Ile Leu Ile Ile Asp Ser Gln Val Leu Tyr
 325 330 335
 Tyr Phe Trp Pro Phe Ile Arg Asn Lys S r Cys Leu Lys Xaa Tyr
 340 345 350

<210> 2299

<211> 339

<212> PRT

<213> Mus musculus (M4 4761596-1-24347-28106 1259-2275)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 2299

Ala	Ser	Ser	Phe	His	Asn	Asp	Thr	Asn	Pro	Gln	Asp	Val	Trp	Tyr	Val
1				5					10					15	
Leu	Ile	Gly	Ile	Pro	Gly	Leu	Glu	Asp	Leu	His	Ser	Trp	Ile	Ala	Ile
			20					25					30		
Pro	Ile	Cys	Ser	Met	Tyr	Ile	Val	Ala	Val	Ile	Gly	Asn	Val	Leu	Leu
		35					40					45			
Ile	Phe	Leu	Ile	Val	Thr	Glu	Arg	Ser	Leu	His	Glu	Pro	Met	Tyr	Phe
	50					55					60				
Phe	Leu	Ser	Met	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Leu	Ser	Thr	Ala	Thr
65				70					75						80
Ala	Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	His	Ser	Arg	Gly	Ile	Ser
			85					90						95	
Phe	Gly	Ser	Cys	Val	Ser	Gln	Met	Phe	Phe	Ile	His	Phe	Ile	Phe	Val
		100						105					110		
Ala	Glu	Ser	Ala	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala
		115						120					125		
Ile	Cys	Tyr	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Ser	Ser	Val	Ile
	130					135					140				
Gly	Lys	Ile	Gly	Thr	Ala	Ala	Val	Val	Arg	Ser	Phe	Leu	Ile	Cys	Phe
145					150					155					160
Pro	Phe	Ile	Phe	Leu	Val	Tyr	Arg	Leu	Leu	Tyr	Cys	Gly	Lys	His	Ile
			165					170						175	
Ile	Pro	His	Ser	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg	Leu	Ala	Cys
		180						185					190		
Asp	Asn	Ile	Thr	Val	Asn	Ile	Ile	Tyr	Gly	Leu	Thr	Met	Ala	Leu	Leu
		195					200					205			
Ser	Thr	Gly	Leu	Asp	Ile	Leu	Leu	Ile	Ile	Ile	Ser	Tyr	Thr	Met	Ile
	210				215						220				
Leu	Arg	Thr	Val	Phe	Gln	Ile	Pro	Ser	Trp	Ala	Ala	Arg	Tyr	Lys	Ala
225					230					235					240
Leu	Asn	Thr	Cys	Gly	Ser	His	Ile	Cys	Val	Ile	Leu	Leu	Phe	Tyr	Thr
			245					250						255	
Pro	Ala	Phe	Phe	Ser	Phe	Phe	Ala	His	Arg	Phe	Gly	Gly	Lys	Thr	Val
		260					265						270		
Pro	Arg	His	Ile	His	Ile	Leu	Val	Ala	Asn	Leu	Tyr	Val	Val	Val	Pro
	275					280						285			
Pro	Met	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys	Gln	Ile	Gln
	290					295					300				
Asp	Arg	Val	Val	Phe	Leu	Phe	Ser	Ser	Val	Ser	Thr	Cys	Gln	His	Asp
305					310					315					320
Ser	Arg	Cys	Xaa	Arg	Xaa	His	Ile	Pro	Lys	Glu	Asn	Ser	Phe	Lys	Cys
			325					330						335	

His Pro Cys

<210> 2300

<211> 344

<212> PRT

<213> Mus musculus (M5 4761596-1-36028-37764 563-1594)

<220>

<221> VARIANT

<222> (1)...(344)

<223> Xaa = Any Amino Acid

<400> 2300

```

Ile Ser Glu Leu Thr Met Ile Lys Phe Ala Gly Ser Val Phe Met Pro
1          5          10          15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
20          25          30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
35          40          45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
50          55          60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65          70          75          80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
85          90          95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
100          105          110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
115          120          125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
130          135          140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ala Phe
145          150          155          160
Ile Leu Val Ser Pro Ser Ile Leu Leu Ile Lys Cys Arg Leu Lys Tyr
165          170          175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
180          185          190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
195          200          205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
210          215          220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225          230          235          240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
245          250          255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
260          265          270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
275          280          285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr
290          295          300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Leu Phe Ser Lys Lys Pro
305          310          315          320
Leu Val Ser Leu Ser Val Glu Lys Leu Cys Gly Phe Xaa Xaa Gln Leu
325          330          335
Xaa Xaa Val Lys Leu Phe Ile Phe
340

```

<210> 2301

<211> 347

<212> PRT

<213> Mus musculus (M6 4761596-1-45918-48570 619-1659)

<220>

<221> VARIANT

<222> (1)...(347)

<223> Xaa = Any Amino Acid

<400> 2301

```

Thr Gly Arg Phe Ser Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro
1      5      10      15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
20      25      30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
35      40      45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
50      55      60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65      70      75      80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
85      90      95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
100     105     110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
115     120     125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
130     135     140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu
145     150     155     160
Ile Thr Thr Phe Pro Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr
165     170     175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
180     185     190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
195     200     205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
210     215     220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225     230     235     240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
245     250     255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
260     265     270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
275     280     285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr
290     295     300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro
305     310     315     320
Leu Xaa Thr Ser Val Thr Arg Ser Val Glu Lys Leu Cys Gly Phe Xaa
325     330     335
Leu Glu Leu Glu Xaa Val Lys Pro Xaa Ile Phe
340     345

```

<210> 2302

<211> 351

<212> PRT

<213> Mus musculus (M7 5051393-1-104482-107691 2444-1393)

<220>

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 2302

```

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Ser Ser Asn Xaa Ile
1      5      10      15
Gln Met Thr Met Val Asn Gln Ser Thr Pro Val Gly Ph Leu Leu Leu
20      25      30

```


Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe Val Val Val
 35 40 45
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu
 50 55 60
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro
 85 90 95
 Gln Met Leu Phe Asn Leu Trp Gly Pro Thr Lys Thr Ile Ser Phe Leu
 100 105 110
 Gly Cys Ser Val Gln Leu Phe Ile Phe Met Leu Leu Gly Thr Thr Glu
 115 120 125
 Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
 130 135 140
 Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Arg Gln
 145 150 155 160
 Leu Ala Gly Val Ala Trp Ala Ile Gly Leu Val Gln Ser Ile Val Gln
 165 170 175
 Ile Pro Pro Thr Leu Thr Leu Pro Phe Cys Ser His Arg Gln Ile Asp
 180 185 190
 Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp
 195 200 205
 Thr Thr Phe Asn Glu Ile Gln Leu Ser Val Ala Gly Val Ile Phe Leu
 210 215 220
 Leu Val Pro Leu Ser Leu Ile Ile Val Ser Tyr Gly Val Ile Ala Arg
 225 230 235 240
 Ala Val Leu Lys Thr Asn Ser Ser Lys Gly Arg Arg Lys Ala Phe Gly
 245 250 255
 Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val
 260 265 270
 Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Ser
 275 280 285
 Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu Asn Pro
 290 295 300
 Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Trp Arg
 305 310 315 320
 Leu Leu Gly Lys Asp Ala Ala Ser Gly Arg Asn Xaa Gly Gln Ile Leu
 325 330 335
 Val Xaa Phe Leu Asn Tyr Lys Val Ser Ser Xaa Tyr Val Tyr Cys
 340 345 350

<210> 2303

<211> 320

<212> PRT

<213> Mus musculus (M8 5051393-1-124150-125858 1430-472)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2303

Arg Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe
 1 5 10 15
 Phe Leu Leu Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe
 20 25 30
 Val Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr

```

65          70          75          80
Cys Val Pro Gln Met Leu Ph Asn Leu Trp Gly Pro Glu Lys Thr Ile
      85          90          95
Ser Phe Leu Gly Cys Phe Val Xaa Leu Phe Ile Phe Met Ser Leu Gly
      100          105          110
Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
      115          120          125
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val Ile Asn Pro Arg Leu
      130          135          140
Cys Gln Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser
145          150          155          160
Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg
      165          170          175
Gln Ile Asp Asn Phe Val Cys Glu Val Pro Ser Leu Ile Gln Leu Ser
      180          185          190
Cys Gly Asp Ile Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile
      195          200          205
Phe Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala
210          215          220
Ile Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys
225          230          235          240
Ala Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr
      245          250          255
Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg
      260          265          270
Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ile
      275          280          285
Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala
290          295          300
Phe Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Trp Arg
305          310          315          320

```

<210> 2304

<211> 317

<212> PRT

<213> Mus musculus (M9 5051393-1-149569-151395 1755-805)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2304

```

Pro Gln Ala Asn His Ser Ser Ala Glu Arg Phe Leu Leu Leu Gly Phe
1          5          10          15
Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val Leu Leu
      20          25          30
Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ala Ala Leu Val Leu Leu Ala
      35          40          45
Ile Arg Asp Pro Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Cys His
50          55          60
Leu Ala Leu Val Asp Val Gly Phe Thr Thr Ser Val Val Pro Pro Leu
65          70          75          80
Leu Ala Ser Leu Arg Gly Ser Met Leu Gln Leu Pro Arg Ala Gly Cys
      85          90          95
Met Ala Gln Leu Cys Ser Ser Leu Ala Leu Gly Ser Ala Glu Cys Val
      100          105          110
Leu Leu Ala Val Met Ala Leu Asp Arg Ala Ala Ala Val Cys Asn Pro
      115          120          125
Leu Arg Tyr Thr Ser Leu Ala Ser Pro Leu Leu Cys Arg Thr Leu Ala
130          135          140

```

Gly Val Ser Trp Leu Gly Gly Leu Ala Asn Ser Ala Ala Gln Thr Ala
 145 150 155 160
 Leu Leu Ala Ala Arg Pr Leu Cys Ala Pro Arg Cys Leu Asp His Phe
 165 170 175
 Ile Cys Glu Leu Pro Ala Leu Leu Gln Leu Ala Cys Arg Gly Gly Arg
 180 185 190
 Ser Ala Thr Glu Arg Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu
 195 200 205
 Val Pro Ser Ala Val Ile Leu Ala Ser Tyr Ile Ala Val Gly Arg Ala
 210 215 220
 Val Trp Gly Met His Ser Ser Ser Gly Trp Arg Lys Ala Ala Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Thr
 245 250 255
 Tyr Thr Tyr Leu Gln Pro Thr His Ser Tyr Asn Gln Gly Arg Gly Lys
 260 265 270
 Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Ala Leu Arg Leu
 290 295 300
 Leu Arg Ser Leu Gly Arg Pro Xaa Val Gly Gln Xaa Lys
 305 310 315

<210> 2305

<211> 348

<212> PRT

<213> Mus musculus (M10 5051393-1-39874-41685 1277-235)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400> 2305

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Pro Ser Asn Xaa Ile
 1 5 10 15
 Gln Met Thr Met Val Asn Gln Ser Ser Pro Val Gly Phe Leu Leu Leu
 20 25 30
 Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Ile Val Val Val
 35 40 45
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu
 50 55 60
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro
 85 90 95
 Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser Phe Leu
 100 105 110
 Gly Cys Phe Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu
 115 120 125
 Cys Ile Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys
 130 135 140
 Gln Pro Leu His Tyr Ala Thr Val Ile His Pro Arg Leu Cys Cys Gln
 145 150 155 160
 Leu Ala Ala Val Ala Cys Thr Ile Gly Leu Val Glu Ser Val Val Gln
 165 170 175
 Thr Pro Ser Thr Leu Arg Leu Pro Phe Cys Pro His His Gln Val Asp
 180 185 190
 Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Gly Asp
 195 200 205
 Thr Thr Tyr Asn Glu Il Gln Met Ala Val Ala Ser Val Phe Ile Leu

210	215	220
Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Ala Arg		
225	230	235
Ala Val Leu Arg Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly		240
	245	250
Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val		255
	260	265
Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu Arg Gly		270
	275	280
Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro		285
	290	295
Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Arg Arg		300
305	310	315
Leu Leu Trp Lys Glu Val Lys Pro Ser Xaa His Thr Leu Ser Lys Leu		320
	325	330
Asn Gly Lys Ser Ala Cys Leu Val Gly Leu Ser Phe		335
	340	345

<210> 2306

<211> 347

<212> PRT

<213> Mus musculus (M11 5051393-1-46409-49345 2458-1419)

<220>

<221> VARIANT

<222> (1)...(347)

<223> Xaa = Any Amino Acid

<400> 2306

Cys Pro Lys Ser Thr Thr Ser Gly His Ile Glu Ser Cys Met Gly Gln	
1 5 10 15	
Tyr Phe Gln Leu Asp Ser Xaa Gln Lys Gln Thr Met Val Asn Gln Ser	
20 25 30	
Ser Pro Val Gly Phe Leu Leu Leu Gly Phe Ser Glu His Pro Gln Leu	
35 40 45	
Glu Lys Val Leu Phe Val Ile Val Leu Cys Ser Tyr Leu Leu Thr Leu	
50 55 60	
Leu Gly Asn Thr Leu Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu	
65 70 75 80	
His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu	
85 90 95	
Cys Phe Thr Thr Thr Cys Val Pro Gln Met Leu Phe Asn Leu Trp Gly	
100 105 110	
Pro Ala Lys Thr Ile Ser Phe Leu Gly Cys Ser Val Gln Leu Phe Ile	
115 120 125	
Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ser	
130 135 140	
Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val	
145 150 155 160	
Ile His Pro Arg Leu Cys Trp Lys Leu Ala Ala Val Ala Trp Met Met	
165 170 175	
Gly Leu Leu Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro	
180 185 190	
Phe Cys Pro His Arg Gln Ile Asp Asp Phe Leu Cys Glu Val Pro Ser	
195 200 205	
Leu Ile Arg Leu Ser Cys Gly Asp Thr Thr Phe Asn Glu Ile Gln Leu	
210 215 220	
Ala Val Ser Ser Val Ile Leu Val Val Val Pro Leu Ser Leu Ile Leu	
225 230 235 240	
Val Ser Tyr Gly Ala Ile Ala Arg Ala Val Met Arg Ile Asn Ser Thr	
	245 250 255

Glu Ala Trp Lys Lys Ala Leu Arg Thr Cys Ser Ser His Leu Il Val
 260 265 270
 Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys
 275 280 285
 Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala
 290 295 300
 Val Gly Thr Pro Thr Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys
 305 310 315 320
 Glu Val Lys Arg Ala Phe Trp Arg Leu Leu Gly Lys Asp Gly Asp Ser
 325 330 335
 Lys Asn Thr Xaa Glu Ile Asn Ser Arg Arg Thr
 340 345

<210> 2307

<211> 326

<212> PRT

<213> Mus musculus (M12 5051393-1-65471-67664 1437-460)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 2307

Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe Phe
 1 5 10 15
 Leu Leu Gly Phe Ser Glu His Pro Gln Leu Lys Lys Val Leu Phe Val
 20 25 30
 Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile
 35 40 45
 Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys
 65 70 75 80
 Val Pro Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser
 85 90 95
 Phe Leu Gly Cys Phe Val Gln Leu Phe Ile Phe Met Ser Leu Gly Thr
 100 105 110
 Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Val Cys Gln Pro Leu His Tyr Ala Thr Lys Ile Asn Pro His Leu Cys
 130 135 140
 Arg Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser Ile
 145 150 155 160
 Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg Gln
 165 170 175
 Ile Asp Asn Phe Leu Cys Glu Val Pro Ser Leu Ile Gln Leu Ser Cys
 180 185 190
 Gly Asp Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile Phe
 195 200 205
 Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile
 210 215 220
 Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala
 225 230 235 240
 Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser
 245 250 255
 Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu
 260 265 270
 Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu
 275 280 285
 Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe

290 295 300
 Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Xaa Arg Arg
 305 310 315 320
 Asn Thr Xaa His Thr Phe
 325

<210> 2308
 <211> 282
 <212> PRT
 <213> Mus musculus (M13 6143913-1-1-2867 848-3)

<400> 2308
 Leu Ile Ile Tyr Cys Leu Phe Leu Ser Phe Pro Gly Ile Met Asp His
 1 5 10 15
 Val Asn Tyr Thr Trp Thr Arg Thr Phe Ile Leu Ala Gly Phe Thr Thr
 20 25 30
 Ser Gly Thr Leu Gln His Leu Ala Val Phe Gly Thr Leu Cys Ile Tyr
 35 40 45
 Leu Leu Thr Leu Ala Gly Asn Leu Phe Ile Ile Val Leu Val Gln Ala
 50 55 60
 Asp Ser Gly Leu Ser Thr Pro Met Tyr Phe Phe Ile Ser Val Leu Ser
 65 70 75 80
 Phe Leu Glu Leu Trp Tyr Val Ser Thr Thr Val Pro Thr Leu Leu His
 85 90 95
 Thr Leu Leu His Gly Pro Ser Pro Ile Pro Ser Ser Ala Cys Phe Val
 100 105 110
 Gln Leu Tyr Val Phe His Ser Leu Gly Met Thr Glu Cys Tyr Leu Leu
 115 120 125
 Gly Val Met Ala Leu Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His
 130 135 140
 Tyr His Ala Leu Met Ser Arg Gln Val Gln Lys Gln Leu Val Gly Val
 145 150 155 160
 Thr Trp Leu Ala Gly Phe Ser Ala Ala Leu Val Pro Ala Gly Leu Thr
 165 170 175
 Ala Ser Leu Pro Tyr Cys Leu Lys Glu Val Ala His Tyr Phe Cys Asp
 180 185 190
 Leu Ala Pro Val Met Gln Leu Ala Cys Val Asp Thr Ser Trp His Ala
 195 200 205
 Arg Leu Tyr Ile Ala Val Ile Gly Met Ile Asn Thr Cys Asn Leu Thr
 210 215 220
 Phe Ile Leu Gly Leu Tyr Gly Gly Ile Val Arg Ala Val Leu Lys Leu
 225 230 235 240
 Pro Ser Ala Ala Ser Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His
 245 250 255
 Ile Thr Val Val Thr Leu Phe Phe Gly Ser Ala Phe Ile Val Tyr Val
 260 265 270
 Gly Pro Pro Glu Ile Arg Ala Glu Gly Arg
 275 280

<210> 2309
 <211> 333
 <212> PRT
 <213> Mus musculus (M14 6143913-1-6180-10825 2950-1952)

<220>
 <221> VARIANT
 <222> (1)...(333)
 <223> Xaa = Any Amino Acid

<400> 2310
 Leu Leu Leu Gly Thr Met Asp His Val Asn Tyr Thr Trp Thr Arg Thr

```

1           5           10           15
Phe Ile Leu Ala Gly Phe Thr Thr Ser Gly Ala L u Arg Pro Leu Ala
20           25           30
Phe Leu Gly Thr Leu Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Leu
35           40           45
Phe Ile Ile Val Leu Val Gln Ala Asp Ser Gly Leu Ser Thr Pro Met
50           55           60
Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Leu Trp Tyr Val Ser
65           70           75           80
Thr Thr Val Pro Thr Leu Leu His Thr Leu Leu His Gly His Ser Pro
85           90           95
Ile Pro Ser Ser Ala Cys Phe Val Gln Leu Tyr Val Phe His Ser Leu
100          105          110
Gly Met Thr Glu Cys Tyr Leu Leu Gly Val Met Ala Leu Asp Arg Tyr
115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr His Ala Leu Met Ser Lys Gln
130          135          140
Val Gln Leu Trp Leu Ala Gly Ala Thr Trp Val Ala Gly Phe Ser Ala
145          150          155          160
Ala Leu Val Pro Ala Cys Leu Thr Ala Ser Leu Pro Tyr Cys Leu Lys
165          170          175
Glu Ile Ala His Tyr Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala
180          185          190
Cys Val Ser Thr Arg Trp His Ala Arg Val His Gly Ala Val Ile Gly
195          200          205
Val Ala Thr Gly Cys Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly
210          215          220
Ile Leu Thr Ala Val Leu Lys Leu Pro Ser Ala Ala Ser Arg Ala Lys
225          230          235          240
Ala Phe Ser Thr Cys Ser Ser His Met Thr Val Val Ala Leu Phe Tyr
245          250          255
Ala Ser Ala Phe Thr Val Tyr Val Gly Ser Pro Gln Ser Arg Pro Glu
260          265          270
Gly Thr Asp Lys Leu Ile Ala Leu Val Tyr Ala Leu Leu Thr Pro Phe
275          280          285
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
290          295          300
Val Lys Arg Val Ser Glu Lys Ile Arg Thr Leu Leu Arg Asp Thr Xaa
305          310          315          320
Leu Ser Leu Leu Thr Leu Pro Thr Phe Arg Val Asn Ala
325          330

```

<210> 2311

<211> 120

<212> PRT

<213> Mus musculus (M15 6143913-1-66312-67763 687-330)

<220>

<221> VARIANT

<222> (1)...(120)

<223> Xaa = Any Amino Acid

<400> 2311

```

Val Thr Val Gly His Cys Leu Gly Gln Met Ser Leu Ser Val Asp Thr
1           5           10           15
Asp Phe Leu Ile Glu Phe Phe Cys Leu Lys Arg Lys Glu Lys Lys Arg
20           25           30
Lys Lys Lys Asp Cys Ser Pro Leu Tyr Leu Asp Ser Xaa Phe Gln Ser
35           40           45
His Glu Ile Thr Gly Ser Phe Ser Phe Ser Val Phe His Arg Ser Leu
50           55           60

```

Leu Ser Asn Ile Ser Leu Gln Met Met Ala Tyr Phe Gln Ile Thr Leu
 65 70 75 80
 Pro Ser Thr Phe Cys Ile Pro Xaa Gln Arg Ser Gln Thr Ser Ala Cys
 85 90 95
 Ile Tyr Val Leu Asn Asn Leu Leu Ser Leu Phe His Ser Leu Ile Ser
 100 105 110
 Ser Leu Xaa Pro Thr Ala Ser Thr
 115 120

<210> 2312

<211> 323

<212> PRT

<213> Mus musculus (M16 6456795-1-106495-108409 847-1815)

<400> 2312

Leu Ser Ser Tyr Gln Phe Leu Leu Glu Lys Lys Arg Pro Ile Met Asn
 1 5 10 15
 Cys Ser Lys Thr Pro Gly Phe Ile Leu Leu Gly Leu Ser Ser Asp Pro
 20 25 30
 Glu Lys Trp Gln Pro Leu Phe Asn Ile Phe Leu Cys Leu Tyr Leu Leu
 35 40 45
 Gly Leu Leu Gly Asn Leu Leu Leu Leu Leu Ala Ile Gly Thr Asp Val
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu Val
 65 70 75 80
 Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala Leu
 85 90 95
 Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln Phe
 100 105 110
 Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Leu Ala Val
 115 120 125
 Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Phe Tyr Pro
 130 135 140
 Phe Leu Met Thr Pro Cys Arg Cys Glu Val Leu Ala Ser Gly Ser Trp
 145 150 155 160
 Gly Ile Ala His Cys Val Ser Leu Phe Tyr Thr Leu Leu Leu Ser Gln
 165 170 175
 Phe Tyr Tyr His Thr Asn Gln Gly Ile Pro His Phe Phe Cys Asp Ser
 180 185 190
 Arg Pro Leu Leu Leu Ser Cys Ser Asp Thr His Leu Ser Glu Gly
 195 200 205
 Leu Met Met Ala Leu Ser Gly Val Leu Gly Met Ser Ser Val Leu Cys
 210 215 220
 Leu Val Ser Ser Tyr Gly Cys Ile Phe Tyr Ala Val Ala Arg Val Pro
 225 230 235 240
 Ser Ala Gln Gly Lys Arg Lys Ser Leu Ala Thr Cys Ser Ser His Leu
 245 250 255
 Ser Val Val Leu Leu Phe Tyr Ser Thr Val Phe Ala Thr Tyr Leu Lys
 260 265 270
 Pro Pro Ser Thr Ser His Ser Ser Ala Glu Val Val Ala Ala Val Met
 275 280 285
 Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Ser Leu Arg
 290 295 300
 Asn Lys Asp Val Lys Ser Ser Leu Arg Lys Ile Leu Asn Met Asp Lys
 305 310 315 320
 Phe Gln Gly

<210> 2313

<211> 284

<212> PRT

<213> Mus musculus (M17 6456795-1-108765-110526 1744-894)

<220>

<221> VARIANT

<222> (1)...(284)

<223> Xaa = Any Amino Acid

<400> 2313

```

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
 1           5           10          15
Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val
          20          25          30
Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val
          35          40          45
Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly
          50          55          60
Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp
65          70          75          80
Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr
          85          90          95
Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly
          100         105         110
Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val
          115         120         125
Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His
          130         135         140
Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr
145         150         155         160
Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr
          165         170         175
Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr
          180         185         190
Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr
          195         200         205
Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met
210         215         220
Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys
225         230         235         240
Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly
          245         250         255
Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His
          260         265         270
Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg
          275         280

```

<210> 2314

<211> 312

<212> PRT

<213> Mus musculus (M18 6456795-1-142088-143512 370-1305)

<400> 2314

```

Ile Ser Pro Arg Met Asn Cys Ser Gln Ala Pro Gly Phe Ile Leu Leu
 1           5           10          15
Gly Leu Pro Arg Glu Pro Glu Lys Trp Gln His Phe Phe Ile Ile Phe
          20          25          30
Leu Gly Leu Tyr Leu Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu Leu
          35          40          45
Ala Ile Gly Ser Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Gln Leu Ser L u Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro
65          70          75          80

```

Lys Thr Leu Glu Thr Trp Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser
 85 90 95
 Gly Cys Leu Thr Gln Leu Tyr Phe Phe Gly Val Phe Ala Asp Met Asp
 100 105 110
 Asn Leu Leu Leu Ala Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 His Pro Leu Leu Tyr Pro Leu Leu Met Thr Pro Cys Arg Cys Glu Val
 130 135 140
 Leu Val Ser Gly Ser Trp Gly Ile Ala His Cys Val Ser Leu Met Tyr
 145 150 155 160
 Thr Leu Leu Leu Ser Gln Leu Tyr Phe His Thr Asn Gln Glu Ile Pro
 165 170 175
 Arg Phe Phe Cys Asp Cys Arg Pro Leu Leu Leu Ser Cys Ser Asp
 180 185 190
 Thr His Leu Asn Glu Val Leu Met Met Ala Leu Ala Gly Val Leu Gly
 195 200 205
 Val Ser Ala Val Leu Cys Ile Val Ser Ser Tyr Gly Cys Ile Phe Tyr
 210 215 220
 Ala Val Ala Arg Val Pro Ser Ala Gln Gly Lys Arg Lys Ala Leu Thr
 225 230 235 240
 Thr Cys Ser Ser His Leu Ser Val Val Leu Leu Phe Tyr Ser Thr Val
 245 250 255
 Phe Ala Thr Tyr Leu Lys Pro Pro Ser Thr Ser His Ser Ser Gly Glu
 260 265 270
 Val Val Ala Ala Val Met Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Ser Leu Arg Arg
 290 295 300
 Val Leu Asn Ile Glu Lys Ser Gln
 305 310

<210> 2315

<211> 325

<212> PRT

<213> Mus musculus (M19 6456795-1-14626-16881 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2315

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe
 1 5 10 15
 Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe
 20 25 30
 Val Ile Phe Phe Thr Ile Tyr Phe Val Asn Ile Thr Gly Asn Gly Ala
 35 40 45
 Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val
 65 70 75 80
 Thr Leu Pro Lys Met Leu Gln Asn Leu Leu Ser Thr Asn Lys Ala Ile
 85 90 95
 Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
 100 105 110
 Ser Thr Glu Ala Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val
 115 120 125
 Ala Il Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu
 130 135 140
 Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala

145 150 155 160
 Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Pro Asn
 165 170 175
 His Val His His Phe Phe Cys Asp Ile Lys Pro Leu Leu Asp Leu Ala
 180 185 190
 Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Glu
 195 200 205
 Thr Ile Ala Leu Thr Pro Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr
 210 215 220
 Ile Ile Thr Tyr Leu Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His
 225 230 235 240
 Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Ile Leu Leu
 245 250 255
 Tyr Val Pro Val Leu Phe Thr Tyr Ile Arg Pro Ala Ser Gly Ser Ser
 260 265 270
 Leu Asp Gln Asp Arg Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
 275 280 285
 Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
 290 295 300
 Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Xaa Phe Glu Glu Ile Xaa
 305 310 315 320
 Ile Thr Leu Leu Trp
 325

<210> 2316

<211> 237

<212> PRT

<213> Mus musculus (M20 6456795-1-147325-149242 1694-983)

<220>

<221> VARIANT

<222> (1)...(237)

<223> Xaa = Any Amino Acid

<400> 2316

Leu Xaa Thr Tyr Ile Pro Thr His Thr His Thr His Thr His
 1 5 10 15
 Thr His Thr His Ile Tyr Ile Cys Asn Tyr Asn Val Gln Arg Asn Asn
 20 25 30
 Gly Tyr Gln Val Asp His Tyr Leu Xaa Ile Cys His Pro Leu His Tyr
 35 40 45
 Pro Leu Leu Met Gly His Gln Trp Cys Leu Gly Phe Val Leu Thr Leu
 50 55 60
 Gln Leu Phe Gly Ile Thr Val Asp Gly Leu Val Val Ile Leu Val Ala
 65 70 75 80
 Gln Met Trp Phe Cys Gly Pro Asn Leu Ile Asp Tyr Phe Xaa Tyr Asn
 85 90 95
 Phe Ser Pro Ile Met Asp Leu Ala Xaa Ser Asp Thr Gln Val Phe Gln
 100 105 110
 Val Ile Thr Phe Val Leu Ser Val Val Phe Leu Thr Val Pro Phe Gly
 115 120 125
 Leu Val Leu Ile Ser Tyr Ile Gln Ile Val Val Thr Val Leu Arg Val
 130 135 140
 Leu Ser Gly Asp Arg Arg Thr Lys Asp Phe Ser Thr Cys Ser Ser His
 145 150 155 160
 Leu Ala Val Val Ser Thr Phe Tyr Arg Ser Leu Met Val Leu Tyr Thr
 165 170 175
 Val Pro Leu Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Lys Val Val
 180 185 190
 Ile Pro Ile Phe Asn His Val Ile Tyr Thr Leu Arg Asn Gln Glu Val
 195 200 205

Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa
 210 215 220
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys
 225 230 235

<210> 2317

<211> 237

<212> PRT

<213> Mus musculus (M21 6456795-1-153518-155435 1694-983)

<220>

<221> VARIANT

<222> (1)...(237)

<223> Xaa = Any Amino Acid

<400> 2317

Leu Xaa Thr Tyr Ile Pro Thr His Thr His Thr His Thr His
 1 5 10 15
 Thr His Thr His Ile Tyr Ile Cys Asn Tyr Asn Val Gln Arg Asn Asn
 20 25 30
 Gly Tyr Gln Val Asp His Tyr Leu Xaa Ile Cys His Pro Leu His Tyr
 35 40 45
 Pro Leu Leu Met Gly His Gln Trp Cys Leu Gly Phe Val Leu Thr Leu
 50 55 60
 Gln Leu Phe Gly Ile Thr Val Asp Gly Leu Val Val Ile Leu Val Ala
 65 70 75 80
 Gln Met Trp Phe Cys Gly Pro Asn Leu Ile Asp Tyr Phe Xaa Tyr Asn
 85 90 95
 Phe Ser Pro Ile Met Asp Leu Ala Xaa Ser Asp Thr Gln Val Phe Gln
 100 105 110
 Val Ile Thr Phe Val Leu Ser Val Val Phe Leu Thr Val Pro Phe Gly
 115 120 125
 Leu Val Leu Ile Ser Tyr Ile Gln Ile Val Val Thr Val Leu Arg Val
 130 135 140
 Leu Ser Gly Asp Arg Arg Thr Lys Asp Phe Ser Thr Cys Ser Ser His
 145 150 155 160
 Leu Ala Val Val Ser Thr Phe Tyr Arg Ser Leu Met Val Leu Tyr Thr
 165 170 175
 Val Pro Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Lys Val Val
 180 185 190
 Ile Pro Ile Phe Asn His Val Ile Tyr Thr Leu Arg Asn Gln Glu Val
 195 200 205
 Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa
 210 215 220
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys
 225 230 235

<210> 2318

<211> 318

<212> PRT

<213> Mus musculus (M22 6456795-1-37464-41929 1501-549)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2318

Cys Val Ile Phe Xaa Val Met Leu Asn Gln Thr Ser Val Thr Glu Phe
 1 5 10 15
 Ile Leu Leu Gly Val Arg Asp Ile Gln Glu Pro Gln Pro Phe Leu Phe

	20		25		30										
Ala	Ile	Phe	Phe	Thr	Ile	Tyr	Phe	Val	Asn	Ile	Thr	Gly	Asn	Gly	Ala
	35						40					45			
Ile	Leu	Met	Ile	Val	Ile	Leu	Asp	Pro	Arg	Leu	His	Ser	Pro	Met	Tyr
	50					55					60				
Phe	Phe	Leu	Gly	Asn	Leu	Ala	Cys	Leu	Asp	Ile	Ser	Tyr	Ser	Thr	Val
65				70					75						80
Thr	Val	Pro	Lys	Met	Leu	Glu	Asn	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Ile
			85					90					95		
Ser	Leu	Leu	Gly	Cys	Ile	Thr	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly
			100				105					110			
Thr	Thr	Glu	Ser	Leu	Leu	Leu	Ala	Val	Met	Ala	Phe	Asp	Arg	Phe	Val
		115					120					125			
Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Ser	Val	Ile	Met	Asn	Trp	Gln	Val
	130					135					140				
Cys	Ile	Leu	Met	Ala	Val	Thr	Ile	Trp	Thr	Ile	Ala	Phe	Leu	His	Ala
145				150					155						160
Leu	Leu	His	Ser	Val	Met	Thr	Ser	Arg	Leu	Ser	Phe	Cys	Gly	Leu	Asn
			165					170						175	
His	Ile	His	His	Phe	Phe	Cys	Asp	Val	Lys	Pro	Leu	Leu	Glu	Leu	Ala
		180					185						190		
Cys	Gly	Asn	Thr	Glu	Leu	Asn	Leu	Trp	Leu	Leu	Asn	Thr	Val	Thr	Gly
	195					200					205				
Thr	Ile	Ala	Ser	Val	Pro	Phe	Phe	Leu	Thr	Phe	Leu	Ser	Tyr	Phe	Tyr
	210					215					220				
Ile	Ile	Thr	Tyr	Leu	Phe	Leu	Lys	Thr	Arg	Ser	Cys	Ser	Met	Leu	His
225				230					235						240
Lys	Ala	Leu	Ser	Thr	Cys	Ala	Ser	His	Phe	Met	Val	Val	Val	Leu	Phe
			245					250						255	
Tyr	Ala	Pro	Val	Leu	Phe	Thr	Tyr	Ile	Arg	Pro	Thr	Ser	Gly	Ser	Ser
		260					265					270			
Leu	Asp	Gln	Asp	Arg	Ile	Ile	Ala	Ile	Met	Tyr	Ser	Val	Val	Thr	Pro
	275					280					285				
Ala	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Arg	Ser
	290				295					300					
Ala	Leu	Asn	Arg	Lys	Val	Arg	Arg	Trp	Leu	Leu	Glu	Glu			
305				310				315							

<210> 2319

<211> 308

<212> PRT

<213> Mus musculus (M23 6456795-1-63066-65167 771-1694)

<400> 2319

Val	Leu	Leu	Asn	His	Thr	Leu	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Val
1				5					10					15	
Thr	Asp	Ile	Gln	Glu	Leu	Asn	Pro	Ile	Leu	Phe	Val	Thr	Val	Leu	Ala
			20				25					30			
Met	Tyr	Phe	Val	Asn	Val	Ala	Gly	Asn	Gly	Ala	Ile	Leu	Met	Ile	Val
	35					40					45				
Ile	Ser	Asp	Pro	Arg	Leu	His	Leu	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn
	50				55					60					
Leu	Ala	Cys	Leu	Asp	Ile	Cys	Phe	Ser	Thr	Val	Thr	Val	Pro	Lys	Met
65				70					75						80
Leu	Glu	Asn	Phe	Phe	Ser	Thr	Ser	Lys	Ala	Ile	Ser	Phe	Leu	Gly	Cys
			85					90					95		
Ile	Thr	Gln	Leu	His	Phe	Phe	Asn	Phe	Leu	Gly	Ser	Thr	Glu	Ala	Leu
	100						105					110			
Leu	Leu	Thr	Val	Met	Ala	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	Arg	Pro
	115					120					125				
Leu	His	Tyr	Pro	Ala	Ile	Met	Asn	Ser	Gln	Val	Cys	Ile	Gln	Val	Ala

130 135 140
 Ile Ser Ile Trp Ala Ile Pr Phe Leu His Ala Leu Val His Ser Il
 145 150 155 160
 Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn His Ile His His Phe
 165 170 175
 Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
 180 185 190
 Leu Asn Arg Trp Leu Leu Asn Thr Leu Thr Gly Thr Val Ala Ile Gly
 195 200 205
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
 210 215 220
 Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
 245 250 255
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
 260 265 270
 Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys
 290 295 300
 Ile Arg Ile Leu
 305

<210> 2320

<211> 325

<212> PRT

<213> Mus musculus (M24 6456795-1-750-2697 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2320

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe
 1 5 10 15
 Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe
 20 25 30
 Val Ile Phe Phe Thr Ile Tyr Phe Ile Asn Ile Thr Gly Asn Gly Ala
 35 40 45
 Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Ser Tyr Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Leu Leu Gln Asn Leu Leu Ser Thr Ser Lys Ala Ile
 85 90 95
 Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
 100 105 110
 Ser Thr Glu Thr Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val
 115 120 125
 Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu
 130 135 140
 Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala
 145 150 155 160
 Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Pro Asn
 165 170 175
 His Val His His Phe Phe Cys Asp Ile Lys Pro Leu Leu Asp Leu Ala
 180 185 190
 Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
 195 200 205

```

Thr Ile Ala Leu Thr Ser Phe Phe Leu Ile Phe Leu Ser Tyr Phe Tyr
 210                215                220
Ile Ile Thr Asn Leu Leu Leu Lys Thr Arg Ser Cys Ser Met Leu His
225                230                235                240
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Val Leu Phe
                245                250                255
Tyr Ala Pro Val Leu Phe Thr Tyr Ile Arg Pro Ala Ser Gly Ser Ser
                260                265                270
Leu Asp Gln Asp Thr Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
                275                280                285
Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
                290                295                300
Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Xaa Pro Glu Glu Ser Lys
305                310                315                320
Glu Val Phe Phe Ser
                325

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<210> 2321

<211> 177

<212> PRT

<213> Mus musculus (M25 6456795-1-78460-79066 2-526)

<220>

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 2321

```

Val Ser Ala His Val Cys Met Gly Cys Xaa Leu Ser Trp Pro Val Arg
 1                5                10                15
Cys Glu Ile Ile Phe Gly Val Met His Thr Thr Val Asn Phe Ser Ile
                20                25                30
Val Leu Cys Gly Thr Ser Val Ile His Xaa Phe Cys Asp Val Leu Leu
                35                40                45
Val Leu Lys Leu Ser Cys Leu Tyr Asp His Val Ser Glu Ile Ala Ile
                50                55                60
Ser Asp Phe Ser Ile Ser Leu Ala Phe Phe Cys Phe Ile Ser Pro Asn
65                70                75                80
Phe Thr Tyr Val His Ile Phe Ser Thr Glu Leu Arg Met Pro Phe Val
                85                90                95
Glu Gly Lys Thr Ser Val Phe Ser Thr Cys Leu Cys His Met Thr Ser
                100                105                110
Ile Leu Phe Ile Pro Thr Gly Ile Phe Glu Phe Leu Arg Ser His Thr
                115                120                125
Glu Ser Ser Thr Ser Leu Asp Phe Ile Leu Asn Phe Ser Tyr Phe Ser
                130                135                140
Leu Ser Thr Leu Asn Pro Gly Ile Tyr Ser Leu Arg Asn Glu Ala Val
145                150                155                160
Asp Thr Val Gln Arg Lys Ile Phe Phe Phe Lys Glu Lys Tyr Leu Phe
                165                170                175
Leu

```

<210> 2322

<211> 308

<212> PRT

<213> Mus musculus (M26 6456795-1-84123-87238 211-1134)

<400> 2322

```

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val
 1                5                10                15

```

Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Ph Val Met Val Leu Ala
 20 25 30
 Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val
 35 40 45
 Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn
 50 55 60
 Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
 65 70 75 80
 Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
 85 90 95
 Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu
 100 105 110
 Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
 115 120 125
 Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala
 130 135 140
 Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
 145 150 155 160
 Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe
 165 170 175
 Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
 180 185 190
 Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly
 195 200 205
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
 210 215 220
 Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
 245 250 255
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
 260 265 270
 Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys
 290 295 300
 Leu Arg Ile Leu
 305

<210> 2323

<211> 314

<212> PRT

<213> Mus musculus (M27 6456795-1-89089-90071 35-969)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2323

Ser Leu Phe Tyr Ser Gln Arg Ser Arg Met Asn Val Ala Asn Phe Thr
 1 5 10 15
 Ala Met Thr Ile Phe Leu Leu Leu Met Gly Phe Ser Arg Asn Ser Gln
 20 25 30
 Val Glu Ile Ile Phe Ser Thr Leu Ala Leu Val Val Leu Ile Gly Thr
 35 40 45
 Ile Ser Ile Val Ala Val Thr Ser Leu Ser Ile Arg Leu Cys Ser Leu
 50 55 60
 Met Pro Phe Leu Leu Ile His Leu Phe Cys Phe Asp Val Cys Tyr Ile
 65 70 75 80
 Ser Val Met Met Pro Lys Ser Val Cys Ser Ser Phe Met Tyr Ser Ala


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<210> 2324
<211> 309
<212> PRT
<213> Mus musculus (M28 6456795-1-95949-101645 434-1360)
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1393

195 200 205
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Il Ile Thr Tyr Leu
 210 215 220
 Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
 245 250 255
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
 260 265 270
 Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys
 290 295 300
 Leu Arg Ile Leu Leu
 305

<210> 2325

<211> 296

<212> PRT

<213> Mus musculus (M29 6691272-106-1-1090 908-19)

<220>

<221> VARIANT

<222> (1)...(296)

<223> Xaa = Any Amino Acid

<400> 2325

Cys Ile Phe Ile Gly Val Phe Leu Ile Ser Ser Ala Ser Gly Ala Met
 1 5 10 15
 Pro Gly Gln Asn Tyr Ser Thr Ile Ser Glu Phe Ile Leu Phe Gly Phe
 20 25 30
 Ser Ala Phe Pro His Gln Met Leu Pro Ala Leu Phe Leu Tyr Leu
 35 40 45
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Val Ile Met Ala Ala
 50 55 60
 Ile Trp Thr Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu Cys
 65 70 75 80
 Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Val Ile Thr Pro Arg
 85 90 95
 Met Leu Ser Asp Met Leu Ser Thr His Arg Ser Ile Thr Phe Ile Ala
 100 105 110
 Cys Ala Asn Gln Leu Phe Phe Ser Phe Thr Phe Gly Tyr Thr His Ser
 115 120 125
 Phe Leu Leu Val Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 130 135 140
 Pro Leu His Tyr His Ala Leu Met Ser Leu Gln Gly Cys Ala Arg Leu
 145 150 155 160
 Val Ala Trp Ser Trp Ala Gly Gly Ser Leu Ile Gly Met Ala Leu Thr
 165 170 175
 Ile Ile Ile Phe His Leu Thr Phe Cys Glu Ser Asn Val Ile His His
 180 185 190
 Ile Leu Cys His Val Phe Ser Leu Leu Lys Leu Ala Cys Gly Glu Arg
 195 200 205
 Thr Ala Phe Val Thr Ile Ala Val Ile Leu Val Cys Val Thr Pro Leu
 210 215 220
 Ile Gly Cys Leu Val Phe Ile Ile Leu Ser Tyr Ile Phe Ile Val Ala
 225 230 235 240
 Ala Ile Leu Arg Ile Pro Ser Thr Glu Gly Arg His Lys Thr Phe Ser
 245 250 255
 Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Phe Ala
 260 265 270

Ser Leu Il Tyr Leu Gln Gly Tyr Pro Leu Glu Ser Asp Xaa Thr Gly
 275 280 285
 Met Ser Ser Trp His Ala Ser Phe
 290 295

<210> 2326

<211> 334

<212> PRT

<213> Mus musculus (M30 6691273-103-1206-2961 586-1585)

<220>

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 2326

Trp Ala Asn Gln Ser Arg Ala Arg Glu Leu Glu Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ala His Val Pro Ser Leu Arg Pro Met Leu Ala Ala Leu Phe Leu
 20 25 30
 Ala Ala Phe Leu Leu Thr Met Ser Gly Asn Ser Leu Ile Val Leu Leu
 35 40 45
 Thr Ser Leu Asp Phe Gly Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Gln Leu Ala Leu Val Glu Ile Cys Phe Ser Leu Asp Val Ala Pro Arg
 65 70 75 80
 Leu Leu Val Thr Leu Leu Gln Pro Gly Arg Gly Val Ser Pro Thr Ser
 85 90 95
 Cys Ala Leu Gln Leu Leu Val Leu Ser Cys Val Thr Ser Glu Cys
 100 105 110
 Phe Leu Leu Met Val Met Ala Trp Asp Arg Phe Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Gly Ala Ile Met Ser Pro Gln Leu Cys Tyr Leu Leu
 130 135 140
 Ala Thr Thr Cys Trp Leu Ala Gly Ile Pro Val Ala Leu Val Phe Thr
 145 150 155 160
 Ile Trp Leu Phe Asn Phe Pro Phe Cys Gly Pro Arg Gly Ile Arg His
 165 170 175
 Phe Phe Cys Asp Ile Ala Pro Leu Leu Ser Leu Val Cys Ala Asp Thr
 180 185 190
 Arg Val Phe Glu Ala Asn Val Phe Val Ala Thr Val Leu Val Ile Met
 195 200 205
 Val Pro Phe Cys Leu Ile Ala Thr Ser Tyr Val Met Ile Leu Val Ala
 210 215 220
 Val Leu Arg Met Pro Ser Ala Ser Gly Arg His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Ile Leu Phe Tyr Gly Thr Thr Gly
 245 250 255
 Val Ile His Leu Arg Pro Lys Ala Ser Tyr Ser Pro Glu Ser Lys Gln
 260 265 270
 Val Val Ser Leu Ser Tyr Thr Met Val Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Phe Gly Arg Val
 290 295 300
 Cys Cys Gly Arg Xaa Glu Ser Arg Leu His Glu Xaa Thr His Leu Leu
 305 310 315 320
 Cys Gln Pro Phe Ser Val Arg Xaa Leu Leu Arg Pro Thr Phe
 325 330

<210> 2327

<211> 330

<212> PRT

<213> Mus musculus (M31 6691273-105-4369-6206 1597-608)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 2327

Val	Leu	Leu	Xaa	Cys	Tyr	Xaa	Arg	Thr	Asp	Asp	Asn	Asn	Trp	Leu	Val
1				5					10					15	
Ser	Leu	Gln	Met	Ala	Arg	Ser	Leu	Glu	Leu	Ala	Asn	Met	Thr	Arg	Val
			20					25					30		
Gln	Lys	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Thr	Arg	Leu	Asp	Ile	Arg	Asp
		35					40					45			
Ala	Leu	Phe	Ala	Val	Phe	Leu	Thr	Leu	Tyr	Leu	Leu	Thr	Leu	Val	Glu
		50				55					60				
Asn	Thr	Leu	Ile	Ile	Tyr	Leu	Ile	Phe	Ser	His	Lys	Glu	Leu	His	Lys
65					70					75					80
Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn	Leu	Ser	Cys	Leu	Glu	Met	Cys	Tyr
			85						90					95	
Val	Ser	Val	Thr	Met	Pro	Thr	Leu	Leu	Val	Gly	Leu	Trp	Thr	Gly	Pro
			100					105					110		
Tyr	His	Ile	Pro	Phe	Thr	Leu	Cys	Met	Thr	Gln	Leu	Phe	Phe	Phe	Ile
		115					120					125			
Val	Leu	Ile	Cys	Thr	Glu	Cys	Thr	Leu	Leu	Ala	Ser	Met	Ala	Tyr	Asp
	130					135					140				
Arg	Tyr	Val	Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Leu	Leu	Met	Arg
145					150					155					160
Pro	Gln	Val	Cys	Leu	Gly	Leu	Ala	Leu	Ser	Ser	Trp	Leu	Gly	Gly	Leu
			165						170					175	
Ile	Val	Ser	Val	Ala	Lys	Thr	Thr	Cys	Ile	Ala	Ser	Leu	Ser	Tyr	Cys
			180					185						190	
Gly	Pro	Asn	Val	Leu	Asn	Gln	Phe	Cys	Asp	Val	Ser	Pro	Leu	Leu	
		195				200					205				
Asn	Leu	Ser	Cys	Thr	His	Val	Ala	Leu	Thr	Glu	Leu	Val	Asp	Phe	Ile
	210					215					220				
Ser	Ala	Ile	Val	Ile	Phe	Cys	Gly	Thr	Leu	Leu	Val	Ser	Leu	Ala	Ser
225					230					235					240
Tyr	Ser	Ala	Ile	Gly	Met	Ala	Val	Leu	Arg	Met	Pro	Ser	Ala	Ala	Ala
			245						250					255	
Arg	Arg	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Val	Val	Val	Gly
			260					265					270		
Ile	Phe	Tyr	Ser	Ala	Ala	Leu	Phe	Ile	Tyr	Cys	Arg	Pro	Ser	Arg	Ile
	275						280					285			
Lys	Ser	Met	Asp	Leu	Asn	Lys	Val	Leu	Ser	Val	Ile	Tyr	Thr	Val	Val
	290					295					300				
Thr	Pro	Leu	Cys	Asn	Pro	Ile	Ile	Tyr	Cys	Leu	Arg	Asn	Lys	Glu	Val
305					310					315					320
His	Thr	Val	Leu	Lys	Lys	Thr	Leu	His	Trp						
			325						330						

<210> 2328

<211> 319

<212> PRT

<213> Mus musculus (M32 6691273-108-10257-11726 1388-432)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2328

```

Leu Val Pro Ser Phe Gln Arg His Thr Met Ala Asn Leu Ser Thr Val
1      5      10      15
Ser Val Phe Ile Leu Gln Gly Phe Ser Ala Val Pro Ala Leu Gln Leu
20     25     30
Leu Ser Met Ala Ile Phe Leu Leu Ile Tyr Leu Ala Ala Val Leu Gly
35     40     45
Asn Val Ser Ile Met Ile Ala Val Thr Leu Asp Ser His Leu His Thr
50     55     60
Pro Met Tyr Phe Phe Ile Lys His Leu Ser Leu Val Asp Leu Cys Ser
65     70     75     80
Thr Ser Thr Thr Leu Pro Arg Ala Leu Val Ala Thr Met Ala Asp Thr
85     90     95
Lys Glu Ile Ser Leu Pro Ala Cys Ala Ser Gln Leu Phe Ala Phe Val
100    105    110
Cys Phe Gly Ser Leu Glu Cys Phe Leu Ile Thr Ala Met Ala Phe Asp
115    120    125
Arg Cys Leu Ala Ile Tyr Arg Pro Leu Thr Tyr Gly Val Thr Met Ser
130    135    140
Ser Gln Thr Cys Val Ser Leu Val Val Val Ala Trp Val Ser Gly Leu
145    150    155    160
Leu Phe Ser Thr Phe His Met Val Asn Thr Phe Ser Leu Pro Phe Cys
165    170    175
Gly Pro Asn Met Ile Asp His Phe Phe Cys Asp Ile Pro Pro Leu Met
180    185    190
His Leu Ala Cys Gly Asp Thr Gln Gly His Glu Ala Ala Gly Phe Ile
195    200    205
Val Ser Gly Cys Val Ile Met Thr Cys Phe Ala Leu Thr Cys Leu Ser
210    215    220
Tyr Val Leu Ile Val Tyr Thr Val Val His Ile Arg Ser Ala Ala Gly
225    230    235    240
Arg Trp Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ala Thr Val Leu
245    250    255
Leu Phe Tyr Gly Thr Gly Ser Ser Ala Tyr Met Gln Pro Thr Ala His
260    265    270
Tyr Ser Pro Leu Gln Gly Arg Met Ala Ala Ile Phe Tyr Ser Ile Leu
275    280    285
Met Pro Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met
290    295    300
Lys Ala Ala Leu Arg Lys Leu Tyr Pro Gln Val Pro Ser Xaa Ile
305    310    315

```

<210> 2329

<211> 133

<212> PRT

<213> Mus musculus (M33 6850399-12-3847-5066 800-1195)

<220>

<221> VARIANT

<222> (1)...(133)

<223> Xaa = Any Amino Acid

<400> 2329

```

Thr Glu Leu Asn Ser Cys Leu Gln Trp Leu Pro Ile Leu His Arg Ser
1      5      10      15
Thr Thr Glu Ala Ser Ser Ala Val Leu Xaa Glu Leu Leu Leu Gln Arg
20     25     30
Pro Ala Ser Ala Leu Xaa Pro Pro Ile Gly S r Ser Asp Leu Ala Gly
35     40     45
Cys Phe Ser Val Tyr Ile Leu Thr Leu Thr Asp Asn Thr Thr Val Arg

```

50 55 60
 11 Asn Ser Phe Leu Asn His Lys Leu His Thr Pro Met Ser Ser Phe
 65 70 75 80
 Cys Phe Gly Leu Ser Ile Leu Asp Leu Cys Phe Thr Pro Ser Thr Val
 85 90 95
 Pro Pro Asp His Gln Ile Leu Gly Asn Pro Xaa Gly Pro Glu Lys Leu
 100 105 110
 Ala Ile Leu Val Xaa Ala Ile Gln Leu Ser Val Ala Leu Gly Phe Gly
 115 120 125
 Ser Thr Val Cys Val
 130

<210> 2330

<211> 191

<212> PRT

<213> Mus musculus (M35 6850399-2-1-641 21-587)

<220>

<221> VARIANT

<222> (1)...(191)

<223> Xaa = Any Amino Acid

<400> 2330

Asp Ala Ile Ser Gln Pro Leu His Tyr Gly Ala Ile Thr His Ser Glu
 1 5 10 15
 Ile Leu Trp Gln Leu Ala Thr Val Ala Gln Ile Ser Gly Phe Val Glu
 20 25 30
 Phe Arg Ser Pro Ser Ile Phe Gln Leu Pro Arg Cys Gly Gly Gly Gly
 35 40 45
 Val Val Cys Lys Ala Xaa Asn Tyr Leu Cys Arg His Asn Phe Pro Gly
 50 55 60
 Lys Xaa Leu Ser Thr Val Thr Ala Leu Cys Val Val Thr Leu Met Gly
 65 70 75 80
 Leu Val Leu Val Ser Tyr Val Ser Ile Val Lys Gly Val Leu Arg Gly
 85 90 95
 Gly Pro Ile Glu Asp Met Gly Lys Ala Phe Gly Thr Cys Gly Tyr His
 100 105 110
 Leu Ile Ala Gly Leu Leu Phe Phe Lys Ala Ile Ile Ser Val Tyr Thr
 115 120 125
 His Pro Arg Asn Glu Phe Thr Gly Ser His Gly Lys Pro Phe Leu Leu
 130 135 140
 Leu Tyr Pro Val Val Met Pro Ser Leu Gly Pro Leu Ile Asp Thr Leu
 145 150 155 160
 Arg Ser Gln Glu Ser Ser Arg Val Ile Lys Arg Leu Val Ala Lys Asp
 165 170 175
 Xaa Lys Leu Ser Arg Lys Asn Thr Xaa Cys Thr Ser Arg Ser Trp
 180 185 190

<210> 2331

<211> 320

<212> PRT

<213> Mus musculus (M36 7263202-1-54100-55962 166-1125)

<400> 2331

Ser Ser Gln Ala Pro Glu Lys Gln Gln Asp Asn Gly Thr Trp Leu Val
 1 5 10 15
 Thr Glu Phe Leu Leu Val Gly Phe Ser Asn Leu Pro Glu Leu Arg Pro
 20 25 30
 Thr Leu Phe Ile Leu Phe Leu Leu Thr Tyr Leu Val Thr Leu Ser Gly
 35 40 45
 Asn Ala Thr Ile Ile Thr Ile Ile Gln Val Asp Arg Thr Leu His Thr

50	55	60
Pro Met Tyr Arg Phe Leu Ala Val Leu Ser Leu Ser Glu Thr Cys Tyr		
65	70	75
Thr Leu Val Thr Il Pr Asn Met Leu Ala His Leu Leu Met Glu Ser		80
	85	90
Gln Ala Ile Ser Ile Ala Gly Cys Arg Ala Gln Met Phe Phe Phe Leu		95
	100	105
Gly Leu Gly Cys Ser His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp		110
	115	120
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ser Val Ile Met Arg		125
	130	135
Pro Thr Val Cys Leu Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe		140
	145	150
Ser Val Ala Leu Ile Glu Thr Cys Met Ile Phe Ser Ser Pro Phe Cys		155
	165	170
Gly Ala Gly His Val Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu		175
	180	185
Lys Leu Ser Cys Asp Glu Ser Ser Leu Lys Gly Leu Gly Ile Phe Phe		190
	195	200
Leu Ser Ile Leu Val Val Leu Val Ser Phe Leu Phe Ile Leu Leu Ser		205
	210	215
Tyr Ala Phe Ile Val Ala Ala Ile Val Arg Ile Pro Ser Ala Ser Gly		220
	225	230
Arg Arg Lys Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile		235
	245	250
Val His Phe Gly Cys Ala Ser Ile Ile Tyr Leu Arg Pro Asp Ser Gly		255
	260	265
Ala Asn Pro Ser Gln Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val		270
	275	280
Thr Pro Leu Leu Asn Pro Val Val Tyr Thr Leu Arg Asn Lys Glu Val		285
	290	295
Arg Val Ala Leu Arg Lys Asn Leu Ala Arg Gly Cys Gly Ala Phe Lys		300
	305	310
		315
		320

<210> 2332

<211> 122

<212> PRT

<213> Mus musculus (M38 7340303-58-1-1344 4-367)

<220>

<221> VARIANT

<222> (1)...(122)

<223> Xaa = Any Amino Acid

<400> 2332

His Leu Ser Glu Glu Val Gly Phe Ala Val Ser Ser Cys Ile Val Met	
1	5
Ser Ser Phe Ala Leu Thr Val Val Ser Tyr Ile Gly Ile Val Ala Thr	
	10
	15
Val Leu Arg Ile Pro Ser Val Glu Gly Arg Trp Lys Ala Phe Ser Thr	
	20
	25
	30
Val Leu Arg Ile Pro Ser Val Glu Gly Arg Trp Lys Ala Phe Ser Thr	
	35
	40
	45
Cys Ser Ser His Leu Thr Thr Val Ile Leu Phe Tyr Gly Thr Gly Ser	
	50
	55
	60
Phe Val Tyr Leu Arg Pro Ala Ser Gln Tyr Ser Pro Thr Leu Gly Pro	
	65
	70
	75
Leu Ala Ser Ile Phe Tyr Ser Val Val Thr Pro Ser Leu Asn Pro Val	
	85
	90
	95
Val Tyr Cys Leu Arg Asn Lys Asp Met Lys Phe Ala Leu Gln Lys Leu	
	100
	105
	110
Tyr Cys Gly Arg Lys Tyr Xaa Asp Leu Glu	
	115
	120

<210> 2333
 <211> 356
 <212> PRT
 <213> Mus musculus (M41 7363372-318-7546-10891 3278-2211)

<220>
 <221> VARIANT
 <222> (1)...(356)
 <223> Xaa = Any Amino Acid

<400> 2333
 Tyr Val Phe Phe Cys Phe Gln Tyr Ser Xaa Glu Trp Lys Thr Glu Leu
 1 5 10 15
 Glu Met Asp Val Ser Asn Gln Thr Thr Val Thr Glu Phe Val Leu Leu
 20 25 30
 Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
 35 40 45
 Leu Ser Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 50 55 60
 Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Pro
 85 90 95
 Leu Val Leu Asp Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser
 100 105 110
 Gly Cys Ala Val Gln Met Phe Leu Thr Ser Phe Ala Met Gly Ala Thr Glu
 115 120 125
 Cys Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 130 135 140
 Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala Tyr Val Pro
 145 150 155 160
 Met Ala Val Ser Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln
 165 170 175
 Ile Ser Leu Ala Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
 180 185 190
 His Phe Ile Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
 195 200 205
 Ile Ser Ile Asn Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu
 210 215 220
 Gly Val Pro Val Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser
 225 230 235 240
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
 245 250 255
 Thr Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile
 260 265 270
 Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
 275 280 285
 Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Leu Leu
 290 295 300
 Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val
 305 310 315 320
 Lys Ala Ala Val Arg Asn Leu Ala Ser His Arg Cys Leu Thr Phe Xaa
 325 330 335
 Trp Arg Asp Arg Ala His Asp Pro His Val Leu Met Ala Leu Thr Xaa
 340 345 350
 Glu Ser Tyr Cys
 355

<210> 2334
 <211> 331

<212> PRT

<213> Mus musculus (M42 7363372-319-4901-8603 988-1980)

<400> 2334

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Cys Pro Leu Leu Ser Gln Asp Gly Lys Arg Thr Cys Glu Met Glu Gly
1      5      10      15
Ala Asn Gln Ser Thr Val Ala Glu Phe Val Leu Leu Gly Leu Ser Asp
20      25      30
His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile Leu Leu Met Tyr
35      40      45
Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu Val Ser Ile Leu
50      55      60
Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser
65      70      75      80
Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Leu Val Leu Asp
85      90      95
Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Gly Cys Ala Val
100     105     110
Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu Leu
115     120     125
Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
130     135     140
Tyr Pro Val Val Met Asn Lys Ser Ala Tyr Val Pro Met Ala Val Ser
145     150     155     160
Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln Ile Ser Leu Ala
165     170     175
Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr Cys
180     185     190
Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Ser Ile Asn
195     200     205
Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu Gly Val Pro Val
210     215     220
Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Arg
225     230     235     240
Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala
245     250     255
His Leu Thr Val Val Leu Val Phe Tyr Gly Thr Ile Leu Phe Met Tyr
260     265     270
Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Val
275     280     285
Ser Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Leu Thr Pro Met Leu
290     295     300
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Val
305     310     315     320
Arg Asn Leu Val Gly Gln Lys Cys Leu Ile Gln
325     330

```

<210> 2335

<211> 324

<212> PRT

<213> Mus musculus (M43 7363372-320-18353-20567 840-1811)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 2335

```

Asn Met Glu Arg Ser Asn Lys Thr Thr Pro Val Ser Ser Phe Ile Leu
1      5      10      15
Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu

```

	20		25		30										
Ile	Leu	Leu	Met	Tyr	Leu	Val	Ile	Leu	Leu	Gly	Asn	Val	Val	Leu	Ile
	35						40					45			
Leu	Val	Ser	Ile	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe
	50					55					60				
Leu	Gly	Asn	Leu	Ser	Phe	Leu	Asp	Ile	Cys	Tyr	Thr	Thr	Ser	Ser	Val
65					70					75					80
Pro	Leu	Ile	Leu	Asp	Ser	Phe	Leu	Thr	Pro	Arg	Lys	Thr	Ile	Ser	Phe
				85					90					95	
Ser	Gly	Cys	Ala	Val	Gln	Met	Phe	Leu	Ser	Phe	Ala	Met	Gly	Ala	Thr
			100					105					110		
Glu	Cys	Val	Leu	Leu	Gly	Met	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
	115						120					125			
Cys	Asn	Pro	Leu	Arg	Tyr	Pro	Val	Val	Met	Ser	Lys	Ala	Ala	Tyr	Val
	130					135					140				
Pro	Met	Ala	Ala	Gly	Ser	Trp	Val	Ser	Gly	Ser	Ile	Thr	Ala	Thr	Val
145					150					155					160
Gln	Ile	Ser	Leu	Ala	Met	Thr	Leu	Pro	Phe	Cys	Gly	Asp	Asn	Val	Ile
			165					170						175	
Asn	His	Phe	Thr	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Ala	Cys	Ala
	180						185						190		
Asp	Ile	Ser	Ile	Asn	Val	Ile	Ser	Met	Ala	Val	Ala	Asn	Ala	Met	Phe
	195						200					205			
Leu	Gly	Val	Pro	Val	Leu	Phe	Ile	Phe	Val	Ser	Tyr	Ile	Phe	Ile	Leu
	210					215					220				
Ser	Thr	Ile	Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Ala	Phe
225					230					235					240
Ser	Thr	Cys	Ser	Ala	His	Leu	Thr	Val	Val	Leu	Val	Phe	Tyr	Gly	Thr
			245					250						255	
Ile	Leu	Phe	Met	Tyr	Gly	Lys	Pro	Lys	Ser	Lys	Asp	Pro	Leu	Gly	Ala
	260						265						270		
Asp	Lys	Gln	Asp	Leu	Ala	Asp	Lys	Leu	Ile	Ser	Leu	Phe	Tyr	Gly	Val
	275						280					285			
Val	Thr	Pro	Met	Leu	Asn	Pro	Ile	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp
	290					295					300				
Val	Lys	Ala	Ala	Val	Thr	Asn	Leu	Val	Gly	Gln	Lys	His	Phe	Lys	Trp
305					310					315					320
Xaa	Trp	Cys	Met												

<210> 2336

<211> 257

<212> PRT

<213> Mus musculus (M44 7363372-320-22007-23346 51-820)

<220>

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2336

Leu	Leu	Phe	Val	Val	Lys	Met	Lys	Arg	Leu	Gln	Thr	Cys	Xaa	Phe	Xaa
1				5					10					15	
Gln	Pro	Ala	Leu	Leu	Arg	Gly	Leu	Ser	Ser	Leu	Lys	Gly	Gln	Arg	Asp
		20					25						30		
Pro	Arg	Leu	Asn	Glu	Cys	Cys	Met	Pro	Leu	Leu	Xaa	Gln	Asp	Pro	Arg
	35					40					45				
Gly	Lys	Ala	Ser	Phe	Leu	Val	Cys	Leu	Val	Leu	Val	Thr	Leu	Ser	Cys
	50				55					60					
Met	Trp	Gln	Glu	Gln	Cys	Pro	Pro	Met	His	Val	Thr	Phe	Val	His	Ser
65					70					75					80

Leu Ala Val Arg Gln Leu Lys Val Ile Asn Ser Arg Ala Ala Cys Val
 85 90 95
 Leu Arg Ser Ala Glu Leu Xaa Ala Thr Gly Ala Thr Tyr Pro Leu Ser
 100 105 110
 Thr Asn Tyr Cys Ile Cys Lys Thr Arg Thr Ser Ala Arg Ala Asp Ile
 115 120 125
 Ser Ile Asn Val Ile Ser Ile Gly Val Glu Leu Gly Val Pro Val Leu
 130 135 140
 Phe Ile Phe Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Gly Ile
 145 150 155 160
 Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala His
 165 170 175
 Leu Thr Met Val Ile Ile Phe Tyr Gly Thr Ile Leu Phe Met Tyr Gly
 180 185 190
 Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Leu Ala
 195 200 205
 Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr Pro Met Leu Asn
 210 215 220
 Leu Arg Thr Thr Val Arg Ala Phe Ile Phe Arg Lys Tyr Phe Ser Gln
 225 230 235 240
 Xaa Trp Trp Gln Gly Met Leu Trp Thr Val Thr His Arg Thr Glu Lys
 245 250 255
 Ile

<210> 2337

<211> 321

<212> PRT

<213> Mus musculus (M45 7363372-320-7359-9353 512-1474)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2337

Asp Ser Met Glu Ile Asn Asn Gln Thr Ser Phe Pro Val Ser Ser Phe
 1 5 10 15
 Ile Leu Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe
 20 25 30
 Met Leu Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Ile
 35 40 45
 Leu Ile Leu Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser
 65 70 75 80
 Ser Val Pro Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile
 85 90 95
 Ser Phe Ser Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly
 100 105 110
 Ala Thr Glu Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala
 130 135 140
 Tyr Val Pro Met Ala Val Ser Ser Trp Ser Gly Gly Ile Ala Val Ser
 145 150 155 160
 Val Val Gln Thr Ser Leu Ala Met Lys Leu Thr Phe Cys Gly Asp Asn
 165 170 175
 Val Ile Asn His Phe Thr Cys Glu Il Leu Ala Val Leu Lys Leu Ala
 180 185 190
 Cys Ala Asp Ile Ser Ile Asn Val Ile Ser Met Gly Val Thr Asn Ile

195	200	205
Ile Phe Leu Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe		
213	215	220
Ile Leu Val Thr Ile Leu Arg Ile Pr Ser Ala Glu Gly Arg Lys Lys		
225	230	235
Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr		
245	250	255
Gly Thr Ile Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu		
260	265	270
Gly Ala Asp Lys Gln Asp Leu Ala Asp Xaa Leu Ile Ser Leu Phe Tyr		
275	280	285
Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn		
290	295	300
Lys Asp Val Arg Ala Ala Val Thr Asn Leu Val Val Leu Lys Lys Ser		
305	310	315
Phe		320

<210> 2338

<211> 300

<212> PRT

<213> Mus musculus (M50 8075174-14-7636-10544 2097-1198)

<220>

<221> VARIANT

<222> (1)...(300)

<223> Xaa = Any Amino Acid

<400> 2338

Gln Asp Leu Val Ala Thr Gly Val Ile Gly Ala Val Leu Ser Thr Met		
1	5	10
Gly Val Val Gly Val Val Gly Asn Val Tyr Thr Leu Val Val Met Cys		
20	25	30
Arg Phe Leu Arg Ala Ser Ala Ser Met Tyr Val Tyr Val Val Asn Leu		
35	40	45
Ala Leu Ala Asp Leu Leu Tyr Leu Leu Ser Ile Pro Phe Ile Val Ala		
50	55	60
Thr Tyr Val Thr Lys Asp Trp His Phe Gly Asp Val Gly Cys Arg Val		
65	70	75
Leu Phe Ser Leu Asp Phe Leu Thr Met His Ala Ser Ile Phe Thr Leu		
85	90	95
Thr Ile Met Ser Ser Glu Arg Tyr Ala Ala Val Leu Arg Pro Leu Asp		
100	105	110
Thr Val Gln Arg Ser Lys Gly Tyr Arg Lys Leu Leu Ala Leu Gly Thr		
115	120	125
Cys Cys Trp His Cys Cys Xaa Pro Tyr Pro Xaa Cys Tyr Ala Ile Arg		
130	135	140
Leu Val Arg Arg Gly Ser Lys Ser Leu Cys Leu Pro Ala Trp Gly Pro		
145	150	155
Arg Ala His Arg Thr Tyr Leu Thr Leu Leu Phe Gly Thr Ser Ile Val		
165	170	175
Gly Pro Gly Leu Val Ile Gly Leu Leu Tyr Ile Arg Leu Ala Arg Ala		
180	185	190
Tyr Trp Leu Ser Gln Gln Ala Ser Phe Lys Gln Thr Arg Arg Leu Pro		
195	200	205
Asn Pro Arg Val Leu Tyr Leu Ile Leu Gly Ile Val Leu Leu Phe Trp		
210	215	220
Ala Cys Phe Leu Pro Phe Val Ala Met Ala Ala Ala Gly Pro Val Pro		
225	230	235
Pro Gly His Ala Thr Asp Thr Arg Ala Ala Arg Ile Ile Asn Tyr Leu		
245	250	255

Thr Ala Cys Leu Thr Tyr Gly Asn Ser Cys Ile Asn Pro Phe Leu Tyr
 260 265 270
 Thr Leu Leu Thr Lys Asn Tyr Arg Glu Tyr Leu Arg Gly Arg Gln Arg
 275 280 285
 Ser Leu Gly S r Ser Cys Arg Gly Pro Gly Ser Ala
 290 295 300

<210> 2339

<211> 340

<212> PRT

<213> Mus musculus (M51 8076974-22-383-3835 1573-554)

<220>

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400> 2339

Cys Leu Phe Phe Pro Gln Arg Asn Leu Asp Ala Met Asn Arg Ser Ala
 1 5 10 15
 Ala His Val Thr Glu Phe Val Leu Leu Gly Phe Pro Gly Ser Trp Lys
 20 25 30
 Ile Gln Ile Phe Leu Phe Val Leu Phe Leu Val Phe Tyr Val Leu Thr
 35 40 45
 Leu Leu Gly Asn Gly Ala Ile Ile Cys Ala Val Arg Cys Asp Ser Arg
 50 55 60
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu
 65 70 75 80
 Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Ile Leu Ala Asn Ile Leu
 85 90 95
 Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr
 100 105 110
 Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met
 115 120 125
 Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr
 130 135 140
 Ile Met Thr Arg Arg Leu Cys Cys Ile Leu Val Ser Ser Cys Trp Leu
 145 150 155 160
 Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Ser Ile Ser Gln Leu
 165 170 175
 Pro Phe Cys Gly Ser Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp
 180 185 190
 Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Phe Ile
 195 200 205
 Phe Tyr Ala Gln Ser Ser Phe Val Leu Phe Phe Thr Ile Ala Tyr Ile
 210 215 220
 Leu Arg Ser Tyr Ile Leu Leu Leu Arg Ala Val Phe Gln Val Pro Ser
 225 230 235 240
 Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val
 245 250 255
 Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro
 260 265 270
 Thr Tyr Gly Ile Pro Ile Leu Met Gln Lys Ile Leu Thr Leu Val Tyr
 275 280 285
 Ser Val Met Thr Pro Leu Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 290 295 300
 Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Leu Gly Met Arg Ile
 305 310 315 320
 Val Lys Asn Met Xaa Val Lys Ala Val Ser Tyr Ser His Val Leu Ile
 325 330 335
 Lys Asn Lys Leu

340

<210> 2340

<211> 325

<212> PRT

<213> Mus musculus (M57 8218295-1-14626-16881 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2340

Cys	Pro	Phe	Leu	Xaa	Val	Met	Ser	Asn	Gln	Thr	Ser	Val	Thr	Glu	Phe
1				5					10					15	
Leu	Leu	Leu	Gly	Val	Thr	Asp	Ile	Gln	Glu	Leu	Asn	Pro	Ile	Leu	Phe
			20					25					30		
Val	Ile	Phe	Phe	Thr	Ile	Tyr	Phe	Val	Asn	Ile	Thr	Gly	Asn	Gly	Ala
		35					40					45			
Ile	Leu	Met	Ile	Val	Ile	Leu	Asp	Pro	Arg	Leu	His	Ser	Pro	Met	Tyr
	50					55					60				
Phe	Phe	Leu	Gly	Asn	Leu	Ala	Cys	Leu	Asp	Ile	Cys	Phe	Ser	Thr	Val
65					70				75					80	
Thr	Leu	Pro	Lys	Met	Leu	Gln	Asn	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Ile
			85					90						95	
Ser	Phe	Leu	Gly	Cys	Ile	Thr	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly
			100					105					110		
Ser	Thr	Glu	Ala	Met	Leu	Leu	Pro	Val	Met	Ala	Phe	Asp	Arg	Phe	Val
		115					120					125			
Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Ser	Val	Ile	Met	Asn	His	Gln	Leu
		130				135					140				
Cys	Ile	His	Met	Thr	Val	Thr	Ile	Trp	Thr	Leu	Gly	Phe	Phe	His	Ala
145					150					155				160	
Leu	Leu	His	Ser	Val	Met	Thr	Ser	Arg	Leu	Ser	Phe	Cys	Gly	Pro	Asn
			165					170						175	
His	Val	His	His	Phe	Phe	Cys	Asp	Ile	Lys	Pro	Leu	Leu	Asp	Leu	Ala
			180					185					190		
Cys	Gly	Asn	Thr	Glu	Leu	Asn	Leu	Trp	Leu	Leu	Asn	Thr	Val	Thr	Gly
		195					200					205			
Thr	Ile	Ala	Leu	Thr	Pro	Phe	Phe	Leu	Thr	Phe	Leu	Ser	Tyr	Phe	Tyr
	210					215					220				
Ile	Ile	Thr	Tyr	Leu	Phe	Leu	Lys	Thr	Arg	Ser	Cys	Ser	Met	Leu	His
225					230					235				240	
Lys	Ala	Leu	Ser	Thr	Cys	Ala	Ser	His	Phe	Met	Val	Val	Ile	Leu	Leu
			245						250					255	
Tyr	Val	Pro	Val	Leu	Phe	Thr	Tyr	Ile	Arg	Pro	Ala	Ser	Gly	Ser	Ser
		260						265					270		
Leu	Asp	Gln	Asp	Arg	Ile	Ile	Ala	Ile	Met	Tyr	Ser	Val	Val	Thr	Pro
	275						280					285			
Ala	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Arg	Ser
	290					295					300				
Ala	Leu	Asn	Arg	Lys	Val	Arg	Arg	Trp	Leu	Xaa	Phe	Glu	Glu	Ile	Xaa
305					310					315				320	
Ile	Thr	Leu	Leu	Trp											
				325											

<210> 2341

<211> 177

<212> PRT

<213> Mus musculus (M63 8218295-1-78460-79066 2-526)

<220>

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 2341

Val	Ser	Ala	His	Val	Cys	Met	Gly	Cys	Xaa	Leu	Ser	Trp	Pro	Val	Arg
1				5					10					15	
Cys	Glu	Ile	Ile	Phe	Gly	Val	Met	His	Thr	Thr	Val	Asn	Phe	Ser	Ile
		20					25					30			
Val	Leu	Cys	Gly	Thr	Ser	Val	Ile	His	Xaa	Phe	Cys	Asp	Val	Leu	Leu
	35					40					45				
Val	Leu	Lys	Leu	Ser	Cys	Leu	Tyr	Asp	His	Val	Ser	Glu	Ile	Ala	Ile
	50					55					60				
Ser	Asp	Phe	Ser	Ile	Ser	Leu	Ala	Phe	Phe	Cys	Phe	Ile	Ser	Pro	Asn
65				70					75					80	
Phe	Thr	Tyr	Val	His	Ile	Phe	Ser	Thr	Glu	Leu	Arg	Met	Pro	Phe	Val
			85					90					95		
Glu	Gly	Lys	Thr	Ser	Val	Phe	Ser	Thr	Cys	Leu	Cys	His	Met	Thr	Ser
		100					105					110			
Ile	Leu	Phe	Ile	Pro	Thr	Gly	Ile	Phe	Glu	Phe	Leu	Arg	Ser	His	Thr
	115					120					125				
Glu	Ser	Ser	Thr	Ser	Leu	Asp	Phe	Ile	Leu	Asn	Phe	Ser	Tyr	Phe	Ser
	130					135				140					
Leu	Ser	Thr	Leu	Asn	Pro	Gly	Ile	Tyr	Ser	Leu	Arg	Asn	Glu	Ala	Val
145				150					155					160	
Asp	Thr	Val	Gln	Arg	Lys	Ile	Phe	Phe	Phe	Lys	Glu	Lys	Tyr	Leu	Phe
			165					170						175	

Leu

<210> 2342

<211> 314

<212> PRT

<213> Mus musculus (M65 8218295-1-89089-90071 35-969)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2342

Ser	Leu	Phe	Tyr	Ser	Gln	Arg	Ser	Arg	Met	Asn	Val	Ala	Asn	Phe	Thr
1				5					10					15	
Ala	Met	Thr	Ile	Phe	Leu	Leu	Leu	Met	Gly	Phe	Ser	Arg	Asn	Ser	Gln
		20					25					30			
Val	Glu	Ile	Ile	Phe	Ser	Thr	Leu	Ala	Leu	Val	Val	Leu	Ile	Gly	Thr
	35					40					45				
Ile	Ser	Ile	Val	Ala	Val	Thr	Ser	Leu	Ser	Ile	Arg	Leu	Cys	Ser	Leu
	50				55						60				
Met	Pro	Phe	Leu	Leu	Ile	His	Leu	Phe	Cys	Phe	Asp	Val	Cys	Tyr	Ile
65				70					75					80	
Ser	Val	Met	Met	Pro	Lys	Ser	Val	Cys	Ser	Ser	Phe	Met	Tyr	Ser	Ala
			85					90					95		
Tyr	Ile	Ser	Leu	Ile	Glu	Cys	Thr	Leu	Gln	Val	Phe	Tyr	Ser	Gln	Ser
	100					105					110				
Ser	Tyr	Thr	Ala	Met	Ala	Ile	Leu	Thr	Val	Met	Ser	Tyr	Asp	Cys	Tyr
	115					120					125				
Met	Ala	Val	Trp	His	Lys	Val	Ile	Thr	Asn	Val	Ser	Thr	Cys	Ile	His
	130				135				140						
Gly	Val	Leu	Ala	Val	Leu	Val	Asn	Gly	Cys	Glu	Ile	Ile	Phe	Gly	Val

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145          150          155          160
Met His Thr Thr Leu Thr Phe Ser Ile Tyr Ile Cys Gly Thr Ser Thr
          165          170          175
Ile Arg Xaa Phe Cys Asp Val Leu Leu Val Leu Lys Leu Ser Phe Thr
          180          185          190
Asn Asp His Val Asn Glu Leu Glu Ser Leu Ala Phe Ser Ser Val Glu
          195          200          205
Gly Arg Thr Lys Ser Phe Ser Thr Cys Leu Gly His Val Ser Val Gly
          210          215          220
Ser Leu Phe Asn Pro Pro Gly Val Phe Glu Phe Leu Asn Pro Tyr Ser
225          230          235          240
Glu Ser Pro Thr Ser Leu Asp Ile Ile Val Thr Val Phe Ile Leu Pro
          245          250          255
Gln Thr Leu Ser Val Glu Ile Tyr Ser Leu Ser Asn Glu Ala Ile Asp
          260          265          270
Thr Ala Xaa Arg Lys Phe Phe Phe Gln Arg Lys Thr Ser Leu Ser Ile
          275          280          285
Leu His Tyr Phe Leu Leu Gly Ser His Ile Xaa Xaa Val Leu Arg Lys
          290          295          300
Thr Thr Val Ser Met Asn Gln Leu Lys Leu
305          310

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<210> 2343

<211> 335

<212> PRT

<213> Mus musculus (M70 8439670-95-9581-11872 695-1697)

<220>

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 2343

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His Asp His Pro Ser Ala Glu Val Gly Gly Ala Met Ala Asn Ser Thr
1          5          10          15
Thr Val Thr Glu Phe Ile Leu Leu Gly Leu Ser Asp Ala Cys Glu Leu
          20          25          30
Gln Val Leu Ile Phe Leu Gly Phe Leu Leu Thr Tyr Phe Leu Ile Leu
          35          40          45
Leu Gly Asn Phe Leu Ile Ile Phe Ile Thr Leu Val Asp Arg Arg Leu
          50          55          60
Tyr Thr Pro Met Tyr Tyr Phe Leu Arg Asn Phe Ala Met Leu Glu Ile
65          70          75          80
Trp Phe Thr Ser Val Ile Phe Pro Lys Met Leu Thr Asn Ile Ile Thr
          85          90          95
Gly His Lys Thr Ile Ser Leu Leu Gly Cys Phe Leu Gln Ala Phe Leu
          100          105          110
Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu Leu Ala Val Met Ser
          115          120          125
Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Ala Thr Ile
          130          135          140
Met Ser Lys Arg Val Cys Val Gln Leu Val Phe Cys Ser Trp Met Ser
145          150          155          160
Gly Leu Leu Leu Ile Ile Val Pro Ser Ser Ile Val Phe Gln Gln Pro
          165          170          175
Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Asn Phe Pro
          180          185          190
Leu Met Glu Leu Ile Cys Ala Asp Thr Ser Leu Val Glu Phe Leu Gly
          195          200          205
Phe Val Ile Ala Asn Phe Ser Leu Leu Gly Thr Leu Ala Val Thr Ala
210          215          220

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Thr Cys Tyr Gly His Ile Leu Tyr Thr Ile Leu His Ile Pro Ser Ala
 225 230 235 240
 Lys Glu Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met Tyr Val Arg Ser Gly
 260 265 270
 Lys Asn Gly Gln Gly Glu Asp His Asn Lys Val Val Ala Leu Leu Asn
 275 280 285
 Thr Val Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn
 290 295 300
 Lys Gln Val Lys Gln Val Phe Arg Glu His Val Ser Lys Phe Gln Lys
 305 310 315 320
 Phe Ser Gln Thr Xaa Arg Lys Ala Pro Leu Gln Thr Cys Leu Thr
 325 330 335

<210> 2344

<211> 139

<212> PRT

<213> Mus musculus (M71 8439670-97-10488-11856 213-627)

<220>

<221> VARIANT

<222> (1)...(139)

<223> Xaa = Any Amino Acid

<400> 2344

Ser Ile Val Cys Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu
 1 5 10 15
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu
 20 25 30
 Ser Leu Ser Leu Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu
 35 40 45
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Leu Pro Thr Phe Pro Pro
 50 55 60
 Ser Leu Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu
 65 70 75 80
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu
 85 90 95
 Ser Phe Phe Leu Ser Ser Leu Ser Phe Leu Ser Phe Tyr Ile Tyr Xaa
 100 105 110
 Trp Leu Val Cys Gly Pro Leu Pro Ser Xaa Gly Thr Val Gly Lys Gln
 115 120 125
 Ser Cys Val Met Met Leu Ile Cys Ser Trp Leu
 130 135

<210> 2345

<211> 331

<212> PRT

<213> Mus musculus (M72 8439916-11-1-1677 434-1425)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 2345

Phe Leu Leu Ala Trp Val His Arg Phe Leu Xaa Arg Arg Met Gly Phe
 1 5 10 15
 Glu Asn Gly Ser Ser Val Thr Glu Phe Ile Leu Val Gly L u Thr Lys
 20 25 30
 Glu Ser Asp Leu Gln Cys Pro Leu Phe Ile Leu Phe Leu Met Met Tyr

```

      35      40      45
Val Val Thr Val Leu Gly Asn Gln Gly Leu Ile Ser Leu Ile Gly Leu
  50      55      60
Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser
  65      70      75      80
Phe Val Asp Leu Trp Tyr Ser Ser Val Phe Thr Pro Lys Met Leu Glu
      85      90      95
Ser Phe Ile Ser Glu Lys Asn Thr Ile Ser Tyr Arg Gly Cys Met Ala
      100      105      110
Gln Leu Phe Phe Phe Cys Phe Phe Ser Ile Ser Glu Cys Tyr Ile Leu
      115      120      125
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu
      130      135      140
Tyr Asn Ile Val Met Ser Pro Lys Gln Cys Leu Ile Leu Met Phe Ser
      145      150      155      160
Ser Tyr Met Met Ala Phe Ser Gly Ala Met Ala His Thr Gly Cys Met
      165      170      175
Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asn His Tyr Phe Cys
      180      185      190
Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn
      195      200      205
Glu Leu Glu Val Phe Val Val Val Gly Ile Asn Ile Ile Val Pro Thr
      210      215      220
Ile Thr Ile Phe Ile Ser Tyr Gly Phe Ile Ile Ala Ser Ile Phe Arg
      225      230      235      240
Ile Ser Ser Lys Glu Asp Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
      245      250      255
His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr
      260      265      270
Leu Lys Pro Ser Ser Ala Glu Ser Met Asn Glu Gly Lys Ile Ser Ser
      275      280      285
Ile Phe Tyr Thr Asn Thr Val Pro Leu Leu Asn Pro Leu Ile Tyr Ser
      290      295      300
Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Ile Lys Thr Leu Ser Lys
      305      310      315      320
Arg Lys Arg Xaa Asn Glu Pro Ser Val Leu Pro
      325      330

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<210> 2346

<211> 333

<212> PRT

<213> Mus musculus (M73 8439916-12-562-4356 2317-1320)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2346

```

Ile Ser Leu Ile Ser Phe Ile Ser Thr Asp Ser Thr Xaa Arg Arg Met
  1      5      10      15
Val Val Thr Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
      20      25      30
Thr Asp Asn Pro Asp Leu Gln Ile Pro Leu Phe Leu Val Phe Leu Val
      35      40      45
Met Tyr Met Ile Thr Ala Phe Gly Asn Leu Thr Leu Ile Leu Leu Thr
      50      55      60
Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
      65      70      75      80
Leu Ser Phe Ile Asp L u Cys Tyr Ser Ser Val Val Thr Pro Lys Leu
      85      90      95

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Leu Met Asn Phe Val Leu Lys Lys Asn Ile Ile Gly Phe Ala Gly Cys
 100 105 110
 Met Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr
 115 120 125
 Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pr
 130 135 140
 Leu Met Tyr Asn Val Thr Met Ser Pro Lys Val Cys Ser Tyr Leu Met
 145 150 155 160
 Leu Gly Ser Tyr Leu Met Gly Phe Ser Asp Ala Met Ile His Thr Gly
 165 170 175
 Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr
 180 185 190
 Phe Cys Asp Leu Leu Pro Leu Met Gln Leu Ser Cys Thr Ser Thr Tyr
 195 200 205
 Ile Asn Glu Val Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Thr Val
 210 215 220
 Pro Ser Ile Val Ile Ile Ile Ser Tyr Gly Phe Ile Leu Ser Asn Ile
 225 230 235 240
 Leu Gln Ile Lys Ser Thr Gly Gly Arg Ser Lys Ala Phe Asn Thr Cys
 245 250 255
 Ser Ser His Ile Ala Val Ser Leu Phe Phe Gly Ser Cys Ala Phe
 260 265 270
 Met Tyr Leu Lys Pro Pro Ser Ala Gly Ser Leu Asn Glu Gly Lys Val
 275 280 285
 Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile
 290 295 300
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Arg Lys Thr Leu
 305 310 315 320
 Ser Arg Arg Lys Phe Xaa Xaa Xaa Ile Tyr Tyr Leu Cys
 325 330

<210> 2347

<211> 343

<212> PRT

<213> Mus musculus (M74 8439916-15-1-3070 860-1887)

<220>

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 2347

Phe Ser Phe Ile Phe Phe Val Ser Thr Asp Ser Leu Arg Glu Asp Met
 1 5 10 15
 Thr Phe Glu Asn Ala Ser Met Val Ile Glu Phe Ile Leu Leu Gly Ile
 20 25 30
 Thr Asp Gln Pro Asp Leu Lys Ile Pro Phe Phe Leu Leu Phe Phe Val
 35 40 45
 Gly Tyr Met Ile Thr Val Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile
 50 55 60
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn
 65 70 75 80
 Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met
 85 90 95
 Leu Met Ser Phe Ile Gln Lys Lys Asn Ile Ile Ser Tyr Thr Gly Cys
 100 105 110
 Met Ile Gln Leu Tyr Phe Phe Cys Phe Phe Val Il Ser Glu Cys Tyr
 115 120 125
 Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 130 135 140
 Leu Leu Tyr Asn Val Thr Leu Ser Ser Lys Val Cys Cys Tyr Leu Met

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145          150          155          160
Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr Gly
          165          170          175
Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr
          180          185          190
Phe Cys Asp Leu Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr
          195          200          205
Ile Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val
          210          215          220
Pro Thr Ile Ile Ile Phe Ile Ser Tyr Gly Phe Ile Leu Phe Ser Val
225          230          235          240
Leu Lys Ile Lys Ser Thr Glu Ser Arg Ser Lys Ala Phe Ser Thr Cys
          245          250          255
Ser Ser His Met Leu Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
          260          265          270
Met Tyr Leu Lys Pro Thr Ser Ala Leu Ser Ile Asn Lys Gly Lys Phe
          275          280          285
Ser Ser Leu Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile
          290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Thr Leu
305          310          315          320
Asn Arg Arg Ile Phe Ser Ser Xaa Thr Gly Tyr Leu Xaa Ala Tyr Thr
          325          330          335
Xaa Thr Ile Glu Arg Leu Cys
          340

```

<210> 2348

<211> 321

<212> PRT

<213> Mus musculus (M75 8439916-16-717-3690 2556-1594)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2348

```

Lys Lys Met Ala Ser Ala Asn Val Ser Leu Val Thr Glu Phe Ile Leu
1          5          10          15
Val Gly Leu Thr Asn Gln Pro Asp Leu Gln Ile Pro Leu Phe Phe Val
          20          25          30
Phe Leu Ile Met Tyr Ile Val Thr Ala Leu Gly Asn Leu Cys Leu Ile
          35          40          45
Ile Leu Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Thr Val Phe Thr
65          70          75          80
Pro Lys Met Leu Met Asn Phe Ile Leu Ser Lys Asn Ala Ile Ser Tyr
          85          90          95
Met Gly Cys Leu Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser
          100          105          110
Glu Cys Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro Lys Leu Cys Leu
          130          135          140
Asn Leu Met Leu Gly Thr Tyr Ala Met Ala Phe Ser Gly Ala Met Ala
145          150          155          160
His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile
          165          170          175
Asn His Tyr Phe Cys Asp Ile Leu Pro Val Met Gln Leu Ser Cys Thr
          180          185          190

```

Ser Thr Tyr Val Asn Glu Leu Val Val Phe Ile Val Val Gly Il Asn
 195 200 205
 Ile Ile Val Pro Ser Ile Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu
 210 215 220
 Ser Ser Ile Phe His Ile Lys Ser Asn Glu Gly Arg Ser Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Ser Ser His Ile Ile Ala Val Cys Leu Phe Phe Gly Ser
 245 250 255
 Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Ser Ser Ser Met Asp Gln
 260 265 270
 Gly Lys Thr Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Arg
 290 295 300
 Lys Thr Leu Ser Arg Trp Lys Phe Xaa Lys Glu Thr Thr Cys Thr Cys
 305 310 315 320
 Leu

<210> 2349

<211> 217

<212> PRT

<213> Mus musculus (M76 8439916-16-8665-10443 1774-1125)

<220>

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 2349

Phe Leu Thr Phe Leu Pro Leu Leu Pro Phe Leu Ser Phe Phe Leu Ser
 1 5 10 15
 Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Glu Cys
 20 25 30
 Cys Val Leu Thr Ser Met Ala Tyr Asp Ser Ile Cys Asn Pro Leu Leu
 35 40 45
 Tyr Asn Leu Phe Met Ser Pro Lys Xaa Cys Leu Asn Leu Ile Leu Gly
 50 55 60
 Ser Phe Phe Ile Ser Phe Ser Asp Ala Val Ala His Ser Thr Cys Arg
 65 70 75 80
 Leu Lys Leu Thr Phe Cys Asp Cys Asp Ile Pro Pro Leu Leu Gln Leu
 85 90 95
 Cys Cys Thr Ser Thr Tyr Val Asn Glu Leu Val Ile Phe Phe Val Val
 100 105 110
 Gly Cys Ile Asn Ile Ile Val Pro Ser Ser Thr Ile Leu Ile Ser Tyr
 115 120 125
 Asp Phe Ile Leu Ser Ser Met Phe Cys Ile Lys Ser Ser Glu Gly Arg
 130 135 140
 Ser Lys Ala Phe Ser Thr Tyr Ser Ser His Val Ile Ser Leu Ser Leu
 145 150 155 160
 Phe Phe Asp Ser Ser Ala Phe Val Tyr Phe Lys Ser Ser Ser Ala Gly
 165 170 175
 Ser Leu Gly Glu Glu Asn Ile Ser Ser Val Phe Tyr Ser Asn Val Val
 180 185 190
 Leu Ile Val Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ser Leu
 195 200 205
 Arg Lys Thr Leu Thr Arg Lys Asn Phe
 210 215

<210> 2350

<211> 333

<212> PRT

<213> Mus musculus (M77 8439916-17-1-2001 619-1618)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2350

```

Ile Ile Leu Xaa Tyr Asn Ser Phe Phe Leu Ser Leu Xaa Ile Pro Leu
 1           5           10           15
Lys Arg Met Asp Ser Val Asn Val Ser Leu Val Thr Glu Phe Leu Leu
          20           25           30
Val Gly Leu Thr His Gln Pro Asp Arg Gln Ile Pro Leu Phe Leu Leu
          35           40           45
Phe Leu Ala Met Tyr Leu Val Thr Ala Leu Gly Asn Leu Gly Leu Ile
          50           55           60
Ile Leu Val Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Phe Thr
          85           90           95
Pro Lys Met Leu Met Asn Phe Ile Leu Arg Gln Asn Ala Ile Ser Tyr
          100          105          110
Met Gln Cys Met Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Val Ser
          115          120          125
Glu Cys Phe Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          130          135          140
Cys Asn Pro Leu Leu Tyr Asn Val Met Ile Ser Pro Gln Val Cys Leu
145          150          155          160
Asn Leu Met Ile Gly Ser Tyr Leu Met Ala Phe Ser Glu Ala Val Ala
          165          170          175
Leu Thr Val Cys Met Leu Thr Leu Thr Phe Cys Asp Gly Asn Ile Asn
          180          185          190
His Tyr Phe Cys Asp Ile Leu Ala Leu Phe Gln Leu Ser Cys Ser Ser
          195          200          205
Thr Tyr Val Asn Lys Leu Val Ala Tyr Val Ile Val Val Ile Asn Ile
          210          215          220
Leu Phe Ser Thr Pro Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
225          230          235          240
Ser Ile Phe Arg Ile Ser Ser Ser Lys Gly Arg Ser Lys Ala Phe Ser
          245          250          255
Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
          260          265          270
Ala Phe Val Tyr Phe Lys Pro Ser Ser Pro Gly Ser Met Glu Trp Ala
          275          280          285
Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn Pro
          290          295          300
Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val Lys Ile Ala Leu Arg Lys
305          310          315          320
Ser Leu Ala Arg Xaa Arg Phe Asp Trp Ile His Met Tyr
          325          330

```

<210> 2351

<211> 299

<212> PRT

<213> Mus musculus (M78 8439916-17-6970-9135 1261-2156)

<220>

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400> 2351

```

Thr Asp Ser Pro Xaa Arg Arg Met Asp Xaa Val Asn Ile Ser Leu Val
 1          5          10          15
Thr Glu Phe Ile Val Val Gly Xaa Ala Glu Gln Pro Asp Leu Gln Ile
          20          25          30
Pro Met Phe Phe Gly Phe Leu Ala Met Tyr Thr Val Thr Ala Leu Glu
          35          40          45
Asn Leu Phe Leu Ile Ile Leu Thr Val Leu Asn Ser His Val His Thr
          50          55          60
Thr Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Val Val Leu Cys Tyr
65          70          75          80
Ser Ser Val Phe Thr Pro Gln Met Leu Met Asn Phe Ile Ile Arg Lys
          85          90          95
Asn Thr Ile Ser Tyr Met Glu Cys Ile Thr Xaa Leu Phe Phe Leu Ser
          100          105          110
Phe Phe Leu Ile Phe Leu Cys Phe Phe Leu Ser Ser Phe Phe Leu Ser
          115          120          125
Phe Phe Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe
          130          135          140
Phe Leu Ser Ser Phe Leu Pro Ser Leu Leu Pro Ser Phe Leu Ser Phe
145          150          155          160
Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu Ser Phe
          165          170          175
Leu Ser Ala Ala Tyr Xaa Leu Gln Cys Ala Met Ile Ser Ile Cys Asn
          180          185          190
Ser Leu Val Tyr Asn Leu Phe Met Arg Pro Xaa Val Leu Ser Glu Pro
          195          200          205
Tyr Ser Trp Val Ile Leu Xaa Phe Ile Tyr Xaa Cys Val Asn Thr Leu
          210          215          220
Ser Ser Gly Ile Glu Thr Asp Thr Val Arg Arg Glu Thr Ser Cys Leu
225          230          235          240
Arg Val Arg Pro Ala Ala Pro Gly His Met Ser Val Ser Leu Glu Phe
          245          250          255
Phe Phe Cys Ser Gly Arg Val Tyr Leu Trp Gly Leu Pro Gln Thr Glu
          260          265          270
Leu Ile Pro Tyr Ala Xaa Leu Pro Val Gln Arg Pro Pro Val Leu Glu
          275          280          285
Glu Ser Leu Glu Gly Arg Arg Ala Arg Asn Val
          290          295

```

<210> 2352

<211> 339

<212> PRT

<213> Mus musculus (M80 8439916-20-13750-16634 2033-1016)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 2352

```

Cys His Ser Phe Phe Leu Leu Leu Ile His Arg Leu Phe Xaa Arg Arg
 1          5          10          15
Met Gly Val Glu Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Gln Gly
          20          25          30
Leu Thr Ser Asp Pro Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
          35          40          45
Leu Ile Tyr Thr Thr Thr Ala Leu Gly Asn Leu Ser Leu Ile Thr Leu
          50          55          60
Ile Ala Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu

```

```

65          70          75          80
Asn Leu Ser Ph  Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pr  Lys
      85          90          95
Met Leu Met Asn Phe Leu Val Ser Lys Asn Phe Ile Ser Tyr Val Gly
      100          105          110
Cys Met Thr Gln Leu Tyr Leu Phe Val Phe Phe Ala Val Ser Glu Cys
      115          120          125
Cys Val Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      130          135          140
Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro Gln Val Cys Ser Tyr Leu
      145          150          155
Met Leu Gly Ser Tyr Ile Met Gly Phe Ser Gly Ala Met Ile His Thr
      165          170          175
Gly Trp Met Leu Arg Leu Thr Phe Cys Asp Arg Ser Ile Ile Asn His
      180          185          190
Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Asn Thr
      195          200          205
Tyr Ala Asn Glu Ile Glu Ile Ile Val Gly Gly Ile Asp Ile Ile
      210          215          220
Val Pro Ser Ile Ile Ile Phe Thr Ser Tyr Gly Phe Val Leu Ser Asn
      225          230          235
Ile Phe Gln Met Arg Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
      245          250          255
Cys Ser Ser His Ile Val Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
      260          265          270
Phe Met Tyr Leu Gln Pro Ser Ser Pro Glu Ser Met Asp Gln Gly Lys
      275          280          285
Arg Ser Ser Val Phe Tyr Thr Ile Leu Val Pro Met Met Asn Pro Leu
      290          295          300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Lys Lys Thr
      305          310          315
Phe Ser Thr Gln Ser Val Xaa Xaa Glu Ile Asn Val Tyr His Tyr Thr
      325          330          335
Tyr Ala Asn

```

<210> 2353

<211> 336

<212> PRT

<213> Mus musculus (M82 8439916-21-1-3132 1296-290)

<220>

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 2353

```

Asn Phe Ile Phe Phe Leu Pro Ile Asp Ser Leu Arg Glu Asp Met Ala
 1          5          10          15
Leu Glu Asn Ala Ser Leu Val Thr Glu Phe Ile Leu Met Gly Leu Thr
      20          25          30
Asn Arg Pro Asp Leu Gln Ile Pro Leu Phe Leu Leu Phe Leu Val Met
      35          40          45
Tyr Val Ile Ala Thr Leu Gly Asn Leu Ala Leu Ile Met Leu Ile Ile
      50          55          60
Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn Leu
      65          70          75          80
Ser Cys Ile Asp Leu Phe Tyr Cys Ser Val Ile Thr Pro Lys Met Leu
      85          90          95
Met Asn Phe Val Leu Lys Lys Asn Val Ile Ser Tyr Glu Gly Cys Met
      100          105          110

```


Ala Gln Phe Tyr Phe Phe Ala Phe Phe Ala Ile Ser Glu Cys Tyr Val
 115 120 125
 Leu Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 130 135 140
 Leu Tyr Asn Ile Val Met Ser Pro Lys Leu Cys Ser Tyr Leu Met Met
 145 150 155 160
 Gly Thr Tyr Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys
 165 170 175
 Ile Leu Arg Leu Thr Phe Cys Asp Lys Asn Thr Ile Asn His Tyr Phe
 180 185 190
 Cys Asp Ile Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr Val
 195 200 205
 Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val Pro
 210 215 220
 Thr Val Ile Ile Phe Thr Ser Tyr Gly Phe Ile Leu Ser Ser Ile Leu
 225 230 235 240
 Lys Ile Ser Ser Thr Ala Gly Met Ser Lys Ala Phe Ser Thr Cys Ser
 245 250 255
 Ser His Ile Ile Ala Leu Cys Leu Phe Phe Gly Ser Cys Thr Phe Met
 260 265 270
 Tyr Leu Lys Pro Ser Ser Val Glu Ser Met Asp Gln Gly Lys Ile Ser
 275 280 285
 Ser Val Phe Tyr Asn Ile Val Val Pro Leu Met Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Ile Lys Lys Thr Ile Thr
 305 310 315 320
 Lys Gly Lys Phe Xaa Ser Glu Phe Val Ile Leu Phe Thr Phe Ser Tyr
 325 330 335

<210> 2354

<211> 316

<212> PRT

<213> Mus musculus (M84 8439916-22-16651-22211 2487-1540)

<400> 2354

Met Ala Leu Ala Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Gln Pro Asp Leu Gln Met Pro Leu Phe Leu Ile Phe Leu
 20 25 30
 Ile Ile Tyr Leu Ile Thr Ala Phe Gly Asn Leu Thr Leu Ile Ile Leu
 35 40 45
 Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Leu Ile Thr Pro Lys
 65 70 75 80
 Met Leu Met Asn Phe Val Leu Glu Lys Asn Ile Ile Ser Tyr Met Gly
 85 90 95
 Cys Met Thr Gln Phe Tyr Phe Phe Gly Phe Phe Ala Ile Ser Glu Cys
 100 105 110
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Val Ala Met Ser Pro Lys Met Cys Ser Tyr Phe
 130 135 140
 Ile Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr
 145 150 155 160
 Gly Cys Val Met Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Ile Glu Leu Phe Ile Val Thr Gly Lys Asp Ile Ile
 195 200 205

Val Pro Thr Val Ile Il Phe Ala Ser Tyr Gly Phe Ile Leu Ser Asn
 210 215 220
 Ile Leu Lys Ile Arg Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Ile Ala Val Ser Met Phe Phe Gly Ser Ser Ala
 245 250 255
 Phe Met Tyr Leu Lys Pro Ser Ser Ala Val Ser Met Asn Glu Ala Lys
 260 265 270
 Phe Ser Ser Ile Phe Tyr Ser Ile Val Val Pro Met Met Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Gly Leu Lys Lys Thr
 290 295 300
 Leu Ser Arg Met Phe Ser His Asn Leu Ile Ser Leu
 305 310 315

<210> 2355

<211> 239

<212> PRT

<213> Mus musculus (M90 8567804-15-6071-7402 605-1319)

<220>

<221> VARIANT

<222> (1)...(239)

<223> Xaa = Any Amino Acid

<400> 2355

Asn Thr Glu Gly His Ser Leu Ile Leu Thr Tyr Asn Val Ser Asn Thr
 1 5 10 15
 Gln Ile Asn Cys Phe Cys Leu Ile Tyr Thr Xaa Tyr Asn Leu Leu Xaa
 20 25 30
 Phe Leu Glu Ile Tyr Phe Cys Pro Leu Leu Ile Pro Cys Val Ala Glu
 35 40 45
 Trp Ser Arg Gly Asp Cys Ile Glu Ile Leu Glu Tyr Asn Ile Cys Ile
 50 55 60
 Phe Ile Lys Leu Met Val Pro Thr Met Ser Ser Leu His Tyr Leu Met
 65 70 75 80
 Asn Ser Ser Val Xaa Tyr Leu Lys Ile Phe His Val Ser Lys Glu Leu
 85 90 95
 Tyr Gly Ser Phe Leu Gly Gly Ile Phe Phe Leu Ala Asn His Cys Arg
 100 105 110
 Glu Ile Glu Ile Ser Asn Arg Thr Thr Glu Met Arg Ile Lys Ala Leu
 115 120 125
 Gln Lys Gly Leu Arg Asp Ile Ser Phe Ile Thr Asn Ser Val Gly Ile
 130 135 140
 Val Ile Leu Ile Ile Ile Tyr Ala Arg Leu Gln Lys Ser Thr Glu Gly
 145 150 155 160
 Thr Val Lys Thr Ser Ser Asn Cys Gly Tyr His Ile Ile Ser Ile Tyr
 165 170 175
 Leu Phe Phe Leu Lys Phe Ala Phe Leu Tyr Ile Phe Lys Tyr Val Ser
 180 185 190
 Arg Met His Gln Gly Ser Val Ser Ser Val Phe Tyr Thr Asn Val Val
 195 200 205
 Pro Ile Cys Asn Thr Leu Ile Tyr Ser Leu Xaa Asn Asp Val Thr Ile
 210 215 220
 Ala Trp Met Asn Val Leu Met Lys Phe Gln Arg His Leu Phe Tyr
 225 230 235

<210> 2356

<211> 202

<212> PRT

<213> Mus musculus (M96 8567804-8-3023-3783 759-153)

<220>

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 2356

```

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe
 1           5           10           15
Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly
      20           25           30
Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr
      35           40           45
Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala
 50           55           60
Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala
65           70           75           80
His Ala Glu Cys Leu Thr Gln Leu Phe Phe Cys Phe Phe Val Leu
      85           90           95
Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala
      100           105           110
Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys
      115           120           125
Leu Glu Ile Thr Lys Gly Trp Ile Ile Leu Tyr Ser Glu Met Glu Lys
      130           135           140
Ser Lys Lys Ser Phe Xaa Met Tyr Ile Ser Ile Leu Leu Phe Phe Ser
145           150           155           160
Leu Phe Gly Asp Ile Ile Ser Leu Lys Ser Phe Met Leu Ser Lys Cys
      165           170           175
Leu Thr Thr Asp Leu His Leu Lys Ser Arg His Ile Cys Lys Phe Cys
      180           185           190
Val Ala Val Ser Asp Asn Val Leu Leu Leu
      195           200

```

<210> 2357

<211> 123

<212> PRT

<213> Mus musculus (M98 8570471-14-891-2711 1429-1795)

<220>

<221> VARIANT

<222> (1)...(123)

<223> Xaa = Any Amino Acid

<400> 2357

```

Leu Cys Gly Ser Gly Thr Leu Ile Phe Ser Ser Glu Met Leu Phe Ile
 1           5           10           15
Phe Leu Gly Lys Xaa Phe Phe Gly Xaa Xaa Asp Leu Ile Val Ala Ile
      20           25           30
Phe Cys Ile Phe Asn Phe Leu Lys Leu Ser Leu Leu Thr Lys Val Pro
      35           40           45
Glu Cys Asp Phe Xaa Asn Lys Leu Ser Xaa Xaa Asn Glu Tyr Ile Xaa
 50           55           60
Asn Ile Val Pro Asp Ser Tyr Xaa Tyr Arg Asn Leu Tyr Trp Gly Asn
65           70           75           80
Gly Asn Met Ser Ser Thr Gly Cys Met Leu Arg Leu Thr Ser Trp Asp
      85           90           95
Gly Asn Thr Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Phe Leu Gln
      100           105           110
Leu Ser Cys Thr Ser Thr Tyr Val His Tyr Thr
      115           120

```

<210> 2358
 <211> 179
 <212> PRT
 <213> Mus musculus (M99 8570471-17-1-2939 17-553)

<220>
 <221> VARIANT
 <222> (1)...(179)
 <223> Xaa = Any Amino Acid

<400> 2358
 Ile Cys Leu Asn Leu Met Leu Val Ser Tyr Phe Ile Ala Phe Ser Glu
 1 5 10 15
 Ser Val Ala His Thr Ala Cys Met Leu Arg Leu Thr Phe Cys Asp Ala
 20 25 30
 Asn Thr Ile Asn Tyr Tyr Phe Cys Asp Ile Pro Pro Leu Leu Gln Leu
 35 40 45
 Ser Cys Thr Thr Thr Arg Val Asn Glu Val Val Ile Phe Val Val Gly
 50 55 60
 Ser Ile Asn Ile Ile Ile Pro Thr Ser Thr Ile Phe Val Ser Tyr Gly
 65 70 75 80
 Phe Ile Leu Ser Ser Ile Phe Leu Ile Thr Ala Ser Glu Gly Arg Ser
 85 90 95
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Ala Phe Leu Phe
 100 105 110
 Phe Gly Ser Gly Ala Ile Arg Tyr Phe Lys Pro Ser Ser Asp Gly Ser
 115 120 125
 Met Asp Glu Gly Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Ile Pro
 130 135 140
 Met Ile Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ile Lys Val
 145 150 155 160
 Ala Leu Arg Arg Thr Leu Arg Lys Arg Asn Phe Xaa Leu Ser Ser Val
 165 170 175
 Val Cys Val

<210> 2359
 <211> 324
 <212> PRT
 <213> Mus musculus (M100 8570471-17-6599-8104 424-1396)

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 2359
 Ile Phe Cys Val Tyr Arg Phe Ser Gln Arg Arg Met Asp Ser Val Asn
 1 5 10 15
 Ile Ser Leu Val Thr Glu Phe Ile Leu Val Gly Leu Thr Asp Lys Pro
 20 25 30
 Tyr Leu Gln Ile Pro Leu Phe Phe Ile Phe Leu Ala Met Tyr Leu Val
 35 40 45
 Thr Ala Leu Gly Asn Leu Ser Leu Ile Ile Leu Thr Val Leu Asn Ser
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val
 65 70 75 80
 Asp Phe Cys Tyr Ser Ser Val Phe Thr Pro Gln M t Leu Met Asn Phe
 85 90 95
 Ile Thr Arg Lys Asn Thr Ile Ser Tyr Met Glu Cys Met Ser Gln Leu

```

      100      105      110
Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr Val Leu Thr Ser
      115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Asn
      130      135      140
Leu Val Met Ser Ser Lys Leu Cys Leu Asn Leu Met Leu Val Ser Tyr
145      150      155      160
Phe Ile Ala Phe Ser Glu Ser Val Ala His Thr Val Cys Ile Met Arg
      165      170      175
Leu Asn Phe Cys Asp Ala Ser Lys Ile Asn His Tyr Phe Cys Asp Ile
      180      185      190
Pro Pro Leu Gln Leu Ser Cys Thr Thr Thr Tyr Ile Asn Lys Leu
      195      200      205
Val Val Phe Val Ala Ser Ser Ile Asn Ile Ile Val Pro Ile Ser Thr
210      215      220
Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe His Ile His
225      230      235      240
Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile
      245      250      255
Ile Ala Ala Phe Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Phe Gln
      260      265      270
Pro Ser Ser Ala Glu Ser Met Asp Glu Gly Lys Ile Ser Ser Val Phe
275      280      285
Tyr Thr Asn Val Ile Pro Met Met Asn Pro Leu Leu Tyr Ser Leu Arg
290      295      300
Asn Lys Asp Ile Lys Val Ala Leu Arg Lys Thr Leu Ser Lys Arg Asn
305      310      315      320
Ile Xaa Leu Tyr

```

<210> 2360

<211> 327

<212> PRT

<213> Mus musculus (M101 8570471-19-17517-20152 1114-134)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2360

```

Leu Phe Ile Phe His Lys Ile Ser Tyr Arg Ser Met Ala Leu Ile Asn
 1      5      10      15
Gly Ser Val Val Thr Glu Phe Ile Leu Leu Gly Leu Thr Asp Gln Pro
      20      25      30
Asp Leu Gln Val Pro Leu Phe Leu Val Phe Leu Leu Met Tyr Met Ile
35      40      45
Thr Ala Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile Val Leu Asn Ser
50      55      60
His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val
65      70      75      80
Asp Phe Cys Tyr Ser Ser Val Ile Ile Pro Lys Met Leu Met Asn Phe
      85      90      95
Ile Leu Lys Lys Asn Phe Ile Ser Tyr Val Gly Cys Met Thr Gln Phe
100      105      110
Tyr Leu Phe Gly Phe Cys Val Ile Leu Glu Cys Tyr Ile Leu Thr Ser
115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Asn
130      135      140
Ile Val Met Ser Pro Lys Met Cys Ser Tyr Leu Met Leu Gly Ser Tyr
145      150      155      160

```

Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys Val Leu Arg
 165 170 175
 Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Phe Cys Asp Leu
 180 185 190
 Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Ile
 195 200 205
 Glu Val Leu Ile Val Ala Gly Lys Asp Ile Ile Val Pro Thr Val Ile
 210 215 220
 Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe Gln Met Lys
 225 230 235 240
 Ser Thr Lys Gly Met Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile
 245 250 255
 Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys
 260 265 270
 Pro Asn Ser Thr Gly Thr Met Asn Asn Gly Lys Ile Pro Ser Ile Ile
 275 280 285
 Tyr Thr Ile Leu Ile Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg
 290 295 300
 Asn Lys Asp Val Lys Val Ala Leu Arg Lys Thr Leu Arg Lys Lys Ile
 305 310 315 320
 Leu Xaa Ser Glu Thr Val Ile
 325

<210> 2361

<211> 341

<212> PRT

<213> Mus musculus (M104 8570471-3-1-2271 2172-1151)

<220>

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400> 2361

Asn Phe Ala Ile Phe Phe Ser Val His Arg Phe Ser Xaa Arg Arg Met
 1 5 10 15
 Ala Leu Val Asn Gly Ser Thr Val Thr Glu Phe Ile Leu Leu Gly Leu
 20 25 30
 Thr Asp Gln Pro Gly Leu Gln Met Pro Leu Phe Leu Leu Phe Leu Leu
 35 40 45
 Met Tyr Met Ile Thr Val Phe Gly Asn Leu Thr Leu Ile Phe Leu Ile
 50 55 60
 Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn
 65 70 75 80
 Leu Ser Phe Val Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met
 85 90 95
 Leu Met Asn Phe Ile Leu Lys Lys Asn Leu Ile Ser Tyr Met Gly Cys
 100 105 110
 Met Ser Gln Leu Tyr Phe Phe Cys Phe Phe Ile Ile Ser Glu Cys Tyr
 115 120 125
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 130 135 140
 Leu Leu Tyr Asn Thr Ala Met Ser Pro Arg Val Cys Ser Tyr Leu Met
 145 150 155 160
 Leu Gly Thr Tyr Leu Met Gly Phe Phe Asp Ala Met Ile His Thr Gly
 165 170 175
 Cys Met Leu Arg Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr
 180 185 190
 Phe Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr
 195 200 205
 Val Asn Glu Thr Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Ile Leu

210	215	220
Pro Ser Ala Ile Ile Ph	Phe Ser Tyr Gly Phe	Ile Leu Ser Asn Ile
225	230	235
Phe Gln Ile Arg Ser Thr	Leu Gly Arg Ser Lys	Ala Phe Ser Thr Cys
245	250	255
Ser Ser His Ile Ile Ala	Val Ser Leu Phe Phe	Gly Ser Cys Gly Phe
260	265	270
Met Tyr Leu Lys Pro Ser	Ser Ala Val Ser Ile	Asp Gln Gly Lys Ile
275	280	285
Ser Ser Ile Phe Tyr Thr	Ile Val Val Pro Met	Met Asn Pro Leu Ile
290	295	300
Tyr Ser Leu Arg Asn Lys	Asp Val Lys Val Ala	Leu Arg Lys Thr Leu
305	310	315
Ser Arg Arg Lys Phe	Leu Lys Val Xaa	Leu Gln Ser Arg His
325	330	335
Cys Xaa Cys Thr Tyr		
340		

<210> 2362

<211> 337

<212> PRT

<213> Mus musculus (M106 8570471-9-3672-5945 1670-660)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 2362

Ile Asn Ile Phe Phe Leu Leu Pro Thr Xaa Asn Met Gln Val Gln Met	
1 5 10 15	
Ala Asp Thr Asn His Ser Thr Val Thr Glu Phe Ile Leu Ala Gly Leu	
20 25 30	
Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu Gly	
35 40 45	
Ile Tyr Leu Leu Thr Val Leu Gly Asn Leu Gly Met Ile Ile Leu Ile	
50 55 60	
Leu Leu Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Ser	
65 70 75 80	
Leu Ser Phe Ile Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro Lys Met	
85 90 95	
Leu Val Asn Phe Val Ala Lys Lys Asn Val Ile Ser Tyr Glu Glu Cys	
100 105 110	
Met Thr Gln Leu Tyr Phe Phe Leu Ala Phe Val Ile Ser Glu Cys His	
115 120 125	
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro	
130 135 140	
Leu Leu Tyr Asn Val Thr Met Ser Tyr Gln Ile Cys Ser Trp Met Val	
145 150 155 160	
Gly Gly Val Tyr Gly Met Gly Leu Ile Gly Ala Ala Val His Thr Leu	
165 170 175	
Cys Met Leu Arg Val Val Phe Cys Lys Ala Asn Ile Ile Asn His Tyr	
180 185 190	
Phe Cys Asp Leu Phe Pro Leu Met Glu Leu Ala Cys Ser Ser Thr Tyr	
195 200 205	
Val Asn Glu Val Val Leu Leu Cys Leu Ser Ala Phe Asn Ile Phe Ile	
210 215 220	
Pro Thr Leu Thr Ile Leu Gly Ser Tyr Ile Phe Ile Ile Ile Ser Ile	
225 230 235 240	
Leu Arg Ile Lys Ser Thr Glu Gly Arg Phe Lys Ala Phe Ser Thr Cys	
245 250 255	

Ser Ser His Phe Ser Ala Val Ser Val Ph Phe Gly Ser Leu Ala Phe
 260 265 270
 Met Tyr Leu Gln Pro Phe Ser Val Ser Ser Lys Asp Lys Gly Lys Val
 275 280 285
 Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met Leu Asn Pro Met Ile
 290 295 300
 Tyr Ser Leu Arg Asn Arg Asp Val Lys Leu Ala Leu Asn Lys Leu Phe
 305 310 315 320
 Gln Lys Lys Phe His Val Xaa Arg Ser Ile Tyr Leu Arg Lys Thr Ile
 325 330 335
 Gln

<210> 2363

<211> 256

<212> PRT

<213> Mus musculus (M107 8571727-11-1262-2044 781-16)

<220>

<221> VARIANT

<222> (1)...(256)

<223> Xaa = Any Amino Acid

<400> 2363

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe
 1 5 10 15
 Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly
 20 25 30
 Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr
 35 40 45
 Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala
 50 55 60
 Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala
 65 70 75 80
 His Ala Glu Cys Leu Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Leu
 85 90 95
 Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala
 100 105 110
 Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys
 115 120 125
 Leu Gly Asn His Lys Arg Leu Asp Tyr Ile Ile Phe Arg Asn Gly Lys
 130 135 140
 Ile Lys Lys Ile Phe Leu Asn Val His Ile Tyr Phe Ile Ile Phe Xaa
 145 150 155 160
 Phe Val Cys Gly Thr Ser Tyr Pro Xaa Ser Leu Ser Cys Xaa Ala Ser
 165 170 175
 Val Xaa Pro Leu Thr Tyr Ile Leu Arg Val Gly Thr Phe Val Ser Phe
 180 185 190
 Val Trp Leu Ser Gln Thr Met Ser Tyr Tyr Phe Ile Ile Ala Asn Leu
 195 200 205
 Trp Asp Asn Leu Xaa Glu Ser Ser Phe Xaa Arg Leu Ile Cys Cys Ser
 210 215 220
 Lys Gly Xaa Ser Lys Glu Gly Lys Xaa Lys Leu Ser Phe Trp Ser
 225 230 235 240
 Phe Phe Ile Val Leu Lys Gln Phe Arg Lys Glu Gly Leu Thr Ser Tyr
 245 250 255

<210> 2364

<211> 333

<212> PRT

<213> Mus musculus (M111 8571727-21-4956-7261 1151-153)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2364

```

Ile Leu Met Leu Xaa Leu Leu Leu Phe Leu Gln Glu Arg Met Val Leu
 1          5          10          15
Glu Asn Ser Ser Ser Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln
          20          25          30
Gln Pro Glu Leu Gln Met Pro Leu Phe Phe Leu Phe Leu Gly Ile Tyr
          35          40          45
Ile Val Ser Met Val Gly Asn Leu Gly Leu Thr Val Leu Ile Val Leu
          50          55          60
Asn Pro His Leu His Asn Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser
          65          70          75          80
Phe Thr Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro Arg Met Leu Val
          85          90          95
Gly Phe Val Lys Gln Asn Thr Ile Ser His Ala Glu Cys Met Thr Gln
          100          105          110
His Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr Ile Leu Thr
          115          120          125
Ala Val Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Lys Pro Leu Leu Tyr
          130          135          140
Gln Val Thr Met Ser His Gln Val Cys Leu Leu Met Thr Val Gly Val
          145          150          155          160
Tyr Val Met Gly Phe Leu Glu Ala Ile Ala His Thr Gly Ser Met Val
          165          170          175
Ser Leu Thr Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Ala Cys Asp
          180          185          190
Ile Leu Pro Leu Leu Lys Leu Ser Cys Thr Ser Thr Thr Ile Asn Glu
          195          200          205
Leu Val Val Phe Ile Val Val Gly Val Asn Val Ile Val Pro Thr Leu
          210          215          220
Thr Ile Phe Ile Ser Tyr Thr Leu Ile Leu Ser Asn Ile Leu Ser Ile
          225          230          235          240
His Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Gly Ser His
          245          250          255
Val Ile Ala Val Ser Leu Phe Phe Gly Ala Ala Ala Phe Met Tyr Leu
          260          265          270
Lys Pro Ser Ser Ala Ser Glu Asp Asp Asp Lys Val Ser Thr Ile Phe
          275          280          285
Tyr Thr Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Tyr Leu Ala Leu Arg Lys Thr Leu Met Lys Arg Ser
          305          310          315          320
Phe Thr Xaa Val Glu Ser Ile Phe Val Met Glu Leu Lys
          325          330

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<210> 2365

<211> 344

<212> PRT

<213> Mus musculus (M112 8571727-22-3043-8090 3092-2061)

<220>

<221> VARIANT

<222> (1)...(344)

<223> Xaa = Any Amino Acid

<400> 2365

Ile Val Cys Phe Ile Ser Leu Phe Xaa Val Met Ser Gln Lys Arg Met
 1 5 10 15
 Ala Pr Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly Phe
 20 25 30
 Ser Asn Gln Pro Ala Leu Gln Leu Pro Leu Phe Phe Val Phe Leu Gly
 35 40 45
 Ile Tyr Val Leu Thr Val Ile Gly Asn Leu Gly Leu Ile Thr Leu Ile
 50 55 60
 Gly Leu Asn Ser Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
 65 70 75 80
 Leu Ser Phe Ile Asp Phe Cys Tyr Ser Cys Val Phe Thr Pro Lys Met
 85 90 95
 Leu Ser Asp Phe Val Ser Glu Asn Ile Ile Ser Tyr Met Gly Cys Met
 100 105 110
 Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr Val
 115 120 125
 Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 130 135 140
 Leu Tyr Thr Val Thr Met Ser Pro Gln Val Cys Thr Leu Leu Met Phe
 145 150 155 160
 Cys Ser Tyr Val Ile Gly Phe Ala Gly Ala Met Ala His Thr Gly Ser
 165 170 175
 Met Leu Thr Leu Thr Phe Cys Asp Ser Asn Met Ile His His Tyr Leu
 180 185 190
 Cys Glu Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Ala
 195 200 205
 Asn Glu Leu Val Phe Phe Ile Val Val Gly Val Val Ile Thr Ala Ser
 210 215 220
 Ser Ile Ser Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile Leu
 225 230 235 240
 Lys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Gly Thr Trp Gly
 245 250 255
 Ser His Val Val Ala Val Ala Leu Phe Phe Gly Ser Gly Ala Phe Thr
 260 265 270
 Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Glu Glu Gly Arg Phe Ala
 275 280 285
 Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Asn Lys Thr Leu Lys
 305 310 315 320
 Arg Val Leu Phe Xaa Xaa Val Trp Cys Tyr His Trp Asn Xaa Ile Leu
 325 330 335
 Gly Lys His Thr Gln Ile His Phe
 340

<210> 2366

<211> 157

<212> PRT

<213> Mus musculus (M113 8571727-23-1650-2708 1059-589)

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400>2366

Ile Arg Phe Ala Gly Ser Ser Val His Thr Gly Cys Val Phe Leu Xaa
 1 5 10 15
 Gly His Ala Ile Asn His Xaa Leu Phe Asn Ile Leu Thr Leu Leu Gln
 20 25 30
 Leu Ser Xaa Ala Thr Thr Tyr Val Asn Val Val Ile Leu Ile Gly Val

35	40	45
Tyr Ile Thr Val Pro Ser Phe Thr Ile Leu Ile Ser Tyr Val Phe Il		
50	55	60
Phe Ile Asn Ile Leu Asn Ile Lys Ser Met Gln Arg Ile Ser Lys Asp		
65	70	75
Phe Ser Ile Cys Arg Phe His Ile Ala Ser Ile Tyr Val Phe Ile Glu		
	85	90
Phe Thr Ala Phe Lys Cys Phe Lys Tyr Ser Tyr Gly Ser Ile Asp Gln		
	100	105
Gly Phe Tyr Ser Ser Val Phe Tyr Thr Asp Val Ile Leu Ile Leu Asn		
	115	120
Ile Ile Ile Tyr Ser Met Cys Ile Met Asp Val Glu Met Ala Leu Met		
	130	135
Asp Ala Leu Met Lys Phe Gln Arg Asn Val Phe His Leu		
145	150	155

<210> 2367

<211> 127

<212> PRT

<213> Mus musculus (M114 8571727-23-3031-3453 387-9)

<220>

<221> VARIANT

<222> (1)...(127)

<223> Xaa = Any Amino Acid

<400>2367

His Ser Ile Gln Tyr Leu Asn Leu Ile Asn Leu Ser Tyr Ile Asp Leu		
1	5	10
Cys Tyr Ser Ser Val Pro Arg Ser Lys Met Leu Met Asn Phe Val Phe		
	20	25
Glu Lys Asn Ala Ile Ser Phe Val Gly Cys Asp Ser Ile Gln Phe Ser		
	35	40
Leu Val Pro Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe		
	50	55
Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Val Ile Phe		
	65	70
Xaa Tyr Tyr Thr Leu Thr Ser Met Ala Tyr Asp Phe Tyr Val Ala Ile		
	85	90
Cys Ser Ser Leu Val His Xaa Val Thr Pro Leu Leu Gln Val Cys Phe		
	100	105
Phe Ser Phe Leu Leu Leu Phe Phe Cys Pro Leu Phe Pro Met		
	115	120
		125

<210> 2368

<211> 133

<212> PRT

<213> Mus musculus (M115 8571727-24-1-1404 400-2)

<400>2368

Cys Asn Val Ile Thr Phe Thr Val Leu Thr Asp Met Asn Trp Gly Arg		
1	5	10
Met Ala Leu Gly Asn Asp Ser Ser Val Lys Glu Phe Ile Leu Leu Gly		
	20	25
Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe Phe Phe Phe Leu		
	35	40
Gly Val Tyr Ile Phe Ser Val Val Gly Asn Leu Gly Leu Ile Val Leu		
	50	55
Ile Val Leu Asn Pro His Leu Gln Thr Pro Met Tyr Tyr Phe Leu Phe		
	65	70
Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys		
		75
		80

	85		90		95
Met	Leu	Val	Ser	Phe	Val
				Lys	Gln
				Asn	Ile
				Ile	Ser
				His	Ala
				Glu	Cys
	100			105	110
Met	Thr	Gln	Leu	Phe	Phe
				Phe	Cys
				Phe	Val
				Ile	Asp
				Glu	Cys
				Tyr	
	115			120	125
Ile	Leu	Thr	Ala	Met	
	130				

<210> 2369

<211> 262

<212> PRT

<213> Mus musculus (M117 8571727-26-4808-6724 1497-715)

<220>

<221> VARIANT

<222> (1)...(262)

<223> Xaa = Any Amino Acid

<400>2369

Ser	Ser	Leu	His	Ala	Ser	His	Ser	His	Glu	Leu	Xaa	Lys	Gly	Ile	Val
1				5					10					15	
Gly	Leu	Phe	Xaa	Ala	Ala	Ser	Tyr	Ser	Thr	Val	Lys	Leu	Pro	Lys	Met
			20					25					30		
Leu	Val	Ser	Phe	Val	Lys	Gln	Asn	Thr	Ile	Ser	Tyr	Ala	Glu	Cys	Met
			35				40						45		
Thr	Gln	Leu	Phe	Phe	Phe	Cys	Phe	Phe	Val	Ile	Asp	Glu	Cys	Tyr	Ile
			50			55					60				
Leu	Thr	Ala	Met	Ala	Tyr	Asp	Met	Phe	Ala	Ala	Ile	Ser	Lys	Pro	Leu
65					70				75					80	
Leu	Tyr	Gln	Val	Thr	Met	Ser	His	Trp	Val	Cys	Leu	Leu	Met	Ile	Val
			85						90					95	
Gly	Val	Tyr	Val	Ile	Gly	Phe	Ser	Gly	Ser	His	Tyr	Thr	Ser	Met	Pro
			100					105						110	
Asp	Leu	Xaa	Trp	Gln	Arg	His	Tyr	Met	Cys	Asp	Ile	Leu	Leu	Leu	Leu
			115				120					125			
Gln	Leu	Ser	Cys	Glu	Ser	Thr	Ser	Ile	Asn	Glu	Leu	Val	Ile	Tyr	Arg
			130			135					140				
Val	Gly	Phe	Asn	Val	Thr	Val	Pro	Ser	Leu	Thr	Ile	Phe	Ile	Ser	Tyr
145				150					155					160	
Thr	Leu	Ile	Leu	Ser	Asn	Ile	Pro	Ser	Ile	His	Ser	Thr	Glu	Gly	Arg
			165					170						175	
Asn	Cys	Gly	Ser	His	Val	Ile	Ala	Leu	Ser	Leu	Leu	Tyr	Gly	Ile	Val
			180				185						190		
Ala	Phe	Thr	Tyr	Leu	Lys	Pro	Ser	Ser	Val	Ser	Val	Asp	Asp	Ala	Asn
			195			200						205			
Val	Ser	Thr	Ile	Phe	Phe	Tyr	Thr	Val	Val	Gly	Pro	Met	Leu	Asn	Pro
			210			215					220				
Phe	Leu	His	Ser	Ile	Arg	Asn	Lys	Asp	Val	His	Thr	Ala	Leu	Arg	Lys
225				230					235					240	
Thr	Leu	Asn	Lys	Ser	Ser	Phe	Thr	Xaa	Val	Xaa	Val	Cys	Ile	Cys	Tyr
			245					250						255	
Glu	Ser	Lys	Ile	Leu	Gly										
			260												

<210> 2370

<211> 329

<212> PRT

<213> Mus musculus (M119 8573058-17-2172-5249 1514-528)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2370

```

Val Met Leu Leu Ala Phe Leu Leu Pro Thr Asp Asp Thr Il Met His
1      5      10      15
Met Ala Met Glu Asn Asp Ser Ser Val Thr Glu Phe Val Phe Met Gly
20      25      30
Leu Thr Glu Gln Pro Glu Leu Arg Leu Pro Leu Phe Phe Val Phe Leu
35      40      45
Leu Asn Tyr Thr Ala Thr Val Met Gly Asn Leu Ser Leu Met Val Leu
50      55      60
Ile Cys Leu Asn Ser His Leu His Asn Pro Met Tyr Phe Phe Leu Phe
65      70      75      80
Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Phe Val Cys Thr Pro Lys
85      90      95
Met Leu Met Gly Phe Val Ser Glu Lys Ser Ile Ile Ser Tyr Thr Gly
100     105     110
Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys
115     120     125
Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
130     135     140
Pro Leu Val Tyr Ala Ile Leu Met Ser Pro Arg Met Cys Ser Leu Leu
145     150     155     160
Met Ile Gly Ser Tyr Leu Met Gly Phe Ala Ser Ala Met Ala His Thr
165     170     175
Gly Cys Met Ile Arg Leu Lys Phe Cys Asp Ser Asn Ile Ile Asn His
180     185     190
Tyr Met Cys Glu Ile Phe Pro Leu Gln Leu Ser Cys Ser Ser Thr
195     200     205
Tyr Ala Asn Glu Leu Val Ser Ser Leu Ile Ala Cys Ile Val Val Ile
210     215     220
Val Ser Gly Leu Val Ile Leu Met Ser Tyr Ala Ser Ile Leu Leu Asn
225     230     235     240
Val Val Gln Met Ser Ser Ala Thr Gly Trp Ser Lys Ala Met Gly Thr
245     250     255
Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly Leu
260     265     270
Leu Thr Tyr Val Lys Pro Ala Ser Ala Glu Ser Val Asp Gln Gly Lys
275     280     285
Phe Phe Ser Val Phe Tyr Thr Leu Met Val Pro Met Leu Asn Pro Leu
290     295     300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Ala Lys Arg Thr
305     310     315     320
Met Asn Arg Ile Thr Ile Xaa Gly Lys
325

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<210> 2371

<211> 335

<212> PRT

<213> Mus musculus (M122 8573058-3-1-3007 1710-2714)

<220>

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400>2371

```

Val Leu Ile Leu Pro Leu His Leu Phe Leu Gln Met Ser Leu Asn Ala
1      5      10      15
Gln Lys Thr Met Glu Asn Asp Ser Ser Val Ser Glu Phe Ile Leu Met

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	20		25		30										
Gly	Leu	Thr	Asp	Gln	Pro	Glu	Leu	Gln	Leu	Pro	Leu	Phe	Val	Leu	Phe
	35						40					45			
Leu	Val	Asn	Tyr	Thr	Val	Thr	Val	Met	Gly	Asn	Leu	Ser	Leu	Met	Asn
	50					55				60					
Leu	Ile	Cys	Leu	Asn	Ser	Asn	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Ile
65				70					75					80	
Phe	Asn	Leu	Ser	Phe	Ile	Asp	Phe	Cys	Tyr	Ser	Met	Val	Phe	Thr	Pro
			85					90					95		
Lys	Met	Leu	Met	Gly	Phe	Val	Val	Glu	Lys	Asn	Ile	Ile	Ser	Phe	Arg
		100						105					110		
Gly	Cys	Met	Thr	Gln	Leu	Phe	Phe	Phe	Leu	Phe	Phe	Val	Asn	Ser	Glu
	115					120						125			
Ser	Tyr	Val	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
	130					135					140				
Gln	Pro	Leu	Leu	Tyr	Lys	Ala	Val	Met	Ser	Pro	Gly	Ile	Cys	Phe	Leu
145				150						155				160	
Leu	Ile	Phe	Cys	Thr	Tyr	Leu	Met	Gly	Leu	Val	Ser	Ala	Leu	Phe	His
			165					170					175		
Thr	Gly	Phe	Met	Ile	Arg	Leu	Asn	Phe	Cys	Asp	Ser	Asn	Val	Ile	Asn
		180						185					190		
His	Tyr	Met	Cys	Asp	Ile	Phe	Pro	Leu	Phe	Arg	Leu	Ser	Cys	Ser	Ser
	195						200					205			
Thr	Tyr	Leu	Thr	Glu	Leu	Val	Ser	Ser	Ala	Val	Val	Gly	Thr	Ala	Ile
	210					215					220				
Ile	Leu	Cys	Cys	Leu	Ile	Ile	Leu	Ile	Ser	Tyr	Gly	Met	Ile	Leu	Tyr
225				230						235				240	
Asn	Ile	Ile	His	Met	Ser	Ser	Gly	Lys	Gly	Trp	Ser	Lys	Ala	Leu	Gly
			245					250						255	
Thr	Cys	Gly	Ser	His	Ile	Ile	Thr	Val	Ser	Leu	Phe	Tyr	Val	Thr	Gly
		260						265					270		
Met	Leu	Ala	Tyr	Val	Lys	Pro	Ser	Ser	Ala	Glu	Thr	Val	Gly	Gln	Gly
	275						280						285		
Lys	Ile	Phe	Ser	Val	Phe	Tyr	Thr	Phe	Leu	Val	Pro	Met	Leu	Asn	Pro
	290					295					300				
Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Val	Lys	Lys
305				310						315				320	
Thr	Trp	Lys	Arg	Leu	Thr	Cys	Xaa	Ile	Thr	His	Ser	Asn	Val	Pro	
			325						330					335	

<210> 2372

<211> 131

<212> PRT

<213> Mus musculus (M123 8573058-5-4486-4920 411-18)

<220>

<221> VARIANT

<222> (1)...(131)

<223> Xaa = Any Amino Acid

<400>2372

Leu	Gly	Gly	Glu	Asp	Arg	Phe	Ser	Leu	Asn	Asn	Glu	Ser	Leu	Ile	Asn
1			5						10					15	
Asn	Ser	Gly	Leu	Val	Pro	Cys	Thr	Phe	His	Ile	Leu	Thr	Ser	Phe	Cys
		20						25					30		
Lys	Ser	Arg	Ser	Xaa	Thr	Phe	Arg	Thr	Cys	Gly	Ser	His	Phe	Ile	Ala
	35					40						45			
Val	Ser	Leu	Phe	Tyr	Gly	Ala	Ser	Ala	Phe	Met	Tyr	Leu	Lys	Pro	Ser
	50					55				60					
Ser	Ala	Ser	Val	Asp	Asp	Lys	Ile	Ser	Thr	Ile	Phe	Tyr	Thr	Ile	
65				70					75					80	

Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp
 85 90 95
 Val His Ile Ala Leu Arg Lys Tyr Phe Glu Glu Lys Ser Phe Ile Xaa
 100 105 110
 Glu Glu Leu Xaa Leu Ile Xaa Met Glu Asn Leu Met Val Cys Gln Ile
 115 120 125
 Tyr Asn Phe
 130

<210> 2373

<211> 167

<212> PRT

<213> Mus musculus (M124 8573058-8-1-894 16-516)

<400>2373

Leu Thr His Gly Ser Thr Pro Thr Gly Pro Ile Thr Ala Pro Ala Leu
 1 5 10 15
 Thr Val Cys Met Val Trp Leu Gln Phe Leu Asp Ser Pro Leu Thr Thr
 20 25 30
 Pro Tyr Met Cys His Ile Phe Pro Leu Leu Gln Val Ser Cys Ser Ser
 35 40 45
 Pro Tyr Val Asn Gln Leu Met Ser Tyr Ile Ala Val Gly Thr Ala Ile
 50 55 60
 Ile Leu Cys Ser Leu Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Phe
 65 70 75 80
 Asn Ile Ile His Ile Ser Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly
 85 90 95
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly
 100 105 110
 Leu Leu Ala Tyr Val Asn Pro Ser Ala Glu Thr Val Gly Gln Ala
 115 120 125
 Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu Val Pro Met Leu Asn Pro
 130 135 140
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Met Lys Lys
 145 150 155 160
 Ser Trp Lys Arg Ile Thr Ser
 165

<210> 2374

<211> 337

<212> PRT

<213> Mus musculus (M126 8574266-10-448-5833 4192-5202)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400>2374

Leu Phe Ser Ser Cys Tyr His Lys Phe Ile Cys Lys Met Thr Ala Arg
 1 5 10 15
 Asn Met Thr Thr Met Ser Gly Phe Leu Leu Met Gly Phe Ser Asp Asn
 20 25 30
 His Glu Leu Gln Ile Leu Gln Ala Leu Leu Phe Leu Leu Thr Tyr Leu
 35 40 45
 Leu Gly Ser Ala Gly Asn Phe Ile Ile Ile Thr Ile Thr Thr Leu Asp
 50 55 60
 Pro Gln Leu Gln Ser Pro Met Tyr Tyr Phe Leu Lys Gln Leu Ser Thr
 65 70 75 80
 Leu Asp Leu Ser Ser Leu Ser Val Thr Val Pro Gln Tyr Val Ala Ser
 85 90 95

Ser Leu Ala Arg Ser Gly Tyr Ile Ser Tyr Gly Gln Cys Met Leu Gln
 100 105 110
 Ile Phe Phe Phe Thr Gly Leu Ala Trp Ser Glu Met Ala Thr Leu Thr
 115 120 125
 Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr
 130 135 140
 Glu Val Ile Met Ser Pro Arg Lys Cys Thr Trp Ala Val Ala Ala Val
 145 150 155 160
 Trp Leu Ser Gly Gly Ile Ser Gly Thr Leu Phe Thr Ala Ser Thr Leu
 165 170 175
 Ser Ile Arg Phe Cys Gly Asp Lys Ile Ile His Gln Phe Phe Cys Asp
 180 185 190
 Ile Pro Gln Leu Leu Lys Leu Ser Cys Ser Asn Asp Tyr Phe Gly Val
 195 200 205
 Leu Glu Val Ser Thr Phe Met Ser Val Met Ala Phe Ala Cys Phe Val
 210 215 220
 Gly Ile Ala Phe Ser Tyr Gly Gln Ile Phe Ser Thr Val Leu Arg Met
 225 230 235 240
 Pro Ser Ala Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Leu Pro His
 245 250 255
 Leu Phe Val Val Ser Phe Phe Leu Ser Thr Gly Ile Cys Ala Tyr Leu
 260 265 270
 Lys Pro Thr Ser Asp Ser Pro Thr Ala Leu Asp Leu Met Leu Ser Ile
 275 280 285
 Phe Tyr Thr Leu Leu Pro Pro Thr Leu Asn Pro Val Ile Tyr Ser Leu
 290 295 300
 Arg Asn Glu Ser Leu Lys Arg Ala Leu Lys Lys Leu Leu Leu Ser Glu
 305 310 315 320
 Glu Phe Ile Arg Lys Lys Cys Leu Phe Tyr Phe Xaa Cys Leu Leu Thr
 325 330 335
 Leu

<210> 2375

<211> 333

<212> PRT

<213> Mus musculus (M127 8574266-13-1078-2817 1563-564)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400>2375

Leu Ser Phe Leu Ser Gly Asp Glu Tyr Gln Leu Leu Ser Val Gln Glu
 1 5 10 15
 Asn Ser Leu Ser Val Lys Arg Phe Ala Phe Ser Lys Phe Ser Glu Val
 20 25 30
 Pro Gly Glu Cys Phe Leu Leu Phe Thr Leu Ile Leu Leu Met Phe Leu
 35 40 45
 Val Ser Leu Thr Gly Asn Glu Leu Ile Val Ile Ala Ile Cys Thr Ser
 50 55 60
 Pro Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Leu
 65 70 75 80
 Leu Glu Ile Gly Tyr Thr Cys Ser Val Ile Pro Lys Met Leu Gln Ser
 85 90 95
 Leu Val Ser Glu Ala Arg Glu Ile Ser Arg Glu Gly Cys Ala Thr Gln
 100 105 110
 Met Phe Phe Ph Thr Phe Phe Gly Ile Thr Glu Cys Cys Leu Leu Ala
 115 120 125
 Ala Met Ala Tyr Asp Arg Cys Met Ala Ile Cys Ser Pro Leu His Tyr

130	135	140
Ala Thr Arg Met Ser His Gly Val Cys Ala His Leu Ala Ile Val Ser		
145	150	155
Trp Gly Met Gly Cys Ile Val Gly Leu Gly Gln Thr Asn Phe Ile Phe		160
	165	170
Ser Leu Asn Phe Cys Gly Pro Cys Glu Ile Asp His Phe Phe Cys Asp		175
	180	185
Leu Pro Pro Val Leu Ala Leu Ala Cys Gly Asp Thr Ser Gln Asn Glu		190
	195	200
Ala Ala Ile Phe Val Ala Ala Ile Leu Cys Ile Ser Ser Pro Phe Leu		205
	210	215
Leu Ile Ile Tyr Ser Tyr Val Arg Ile Leu Val Ala Val Leu Val Met		220
225	230	235
Pro Ser Pro Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His		240
	245	250
Leu Leu Val Val Thr Leu Phe Phe Gly Ser Gly Ser Ile Thr Tyr Leu		255
	260	265
Arg Pro Lys Ser Ser His Leu Pro Gly Met Asp Lys Leu Leu Ala Leu		270
	275	280
Phe Tyr Thr Ala Val Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser Leu		285
	290	295
Arg Asn Lys Glu Val Lys Thr Ala Leu Arg Lys Thr Leu Ser Leu Lys		300
305	310	315
Thr Ser Arg Ala Ile Asn Arg Xaa Gln Asn Leu Ala Glu		320
	325	330

<210> 2376

<211> 356

<212> PRT

<213> Mus musculus (M129 8574266-7-9797-11994 2006-942)

<220>

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400>2376

Asn Phe Phe Leu Gln Ile Xaa Ser Gln Asn Tyr Gln Xaa Gly Xaa Leu	
1 5 10 15	
Lys Glu Ile Met Thr Lys Ser Asn Phe Ser Ser Pro Ile Cys Phe Arg	
20 25 30	
Leu Pro Gly Phe Ser Asp His Leu Xaa Leu Asp Xaa Thr Leu Phe Leu	
35 40 45	
Ala Thr Ser Val Ile Asp Ile Val Met Leu Thr Gln Asn Thr Met Ile	
50 55 60	
Ile Leu Val Ser Phe Leu Asn Ser Arg Leu Gln Thr Pro Met Tyr Phe	
65 70 75 80	
Phe Leu Ser Asn Phe Phe Phe Leu Asp Leu Cys Phe Met Thr Asn Val	
85 90 95	
Leu Xaa Ile Val Xaa Thr Ser Lys Gly Pro Glu Lys Ile Ile Ser Cys	
100 105 110	
Cys Ala Ile His Val Tyr Ile Val Leu Xaa Leu Asp Phe Thr Lys Cys	
115 120 125	
Val Leu Leu Thr Met Met Ala Tyr Asn Pro Val Thr Pro Ile Cys Trp	
130 135 140	
Pro Leu Xaa Tyr Pro Thr Thr His Pro Lys Phe Val Asp Ile His Pro	
145 150 155 160	
Lys Phe Pro Xaa Lys Pro Ala Ala Leu Ala Trp Ile Cys Ser Phe Met	
165 170 175	
Val Phe Thr Ile Gln Thr Thr Leu Val Phe Gln Leu Ser Leu Cys Ser	
180 185 190	

His His Arg Met Asn Asp Phe Leu Cys Val Arg Asn Pro Pro Leu Val
 195 200 205
 Lys Ile Thr Phe Met Asp Thr Thr Ser Leu Glu Lys His Ile Ser Val
 210 215 220
 Phe Thr Phe Leu Xaa Ala Val Ile Pro Cys Gly Glu Tyr Ser Ile Ile
 225 230 235 240
 Tyr Leu Leu Val Leu Leu Lys Val Trp Leu Lys Ile Lys Phe Thr Gly
 245 250 255
 Arg Met Lys Thr Phe Gly Ser Cys Gly Phe His Leu Met Ala Ile Val
 260 265 270
 Leu Phe Phe Gly Asn Glu Ser Ser Val Tyr Met Val Tyr Met Tyr Pro
 275 280 285
 Arg Ala Asn Ala Cys Gln Tyr Arg Lys Phe Ser Val Phe Tyr Met Ile
 290 295 300
 Val Thr Pro Ser Ile Asn Pro Leu Ile Tyr Leu Arg Asn Lys Glu Phe
 305 310 315 320
 Arg Trp Ala Val Gln Arg Leu Val Thr Arg Asp Pro Ser Xaa Gly Lys
 325 330 335
 Ile Arg Gln Ser Leu Thr Ile Phe Gln Ala Phe Gly Ile Gly Arg His
 340 345 350
 Tyr Ile Tyr Cys
 355

<210> 2377

<211> 323

<212> PRT

<213> Mus musculus (M130 8574266-9-11171-19240 5578-6546)

<400>2377

Val Arg Ile Leu Thr Val Asn Thr Asn Met Trp Ile Asn Asn Gln Ser
 1 5 10 15
 Ser Val Asp Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu
 20 25 30
 Glu Thr Pro Leu Phe Val Ile Phe Leu Val Ala Tyr Ile Phe Ala Leu
 35 40 45
 Phe Gly Asn Ile Ser Ile Ile Leu Val Ser Arg Leu Asp Pro Gln Leu
 50 55 60
 Asp Ser Pro Met Tyr Phe Phe Val Ser Asn Leu Ser Leu Leu Asp Leu
 65 70 75 80
 Cys Tyr Thr Thr Ser Thr Val Pro Gln Met Leu Val Asn Leu Arg Gly
 85 90 95
 Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys Val Ala Gln Leu Tyr Ile
 100 105 110
 Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile Leu Leu Ala Ile Met Ala
 115 120 125
 Phe Asp Arg Phe Ala Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile
 130 135 140
 Met Asn Gln Lys Arg Cys Ile His Met Ala Thr Gly Thr Trp Ile Ser
 145 150 155 160
 Gly Phe Ala Asn Ser Leu Val Gln Ser Thr Leu Thr Val Val Ala Pro
 165 170 175
 Arg Cys Gly Gln Arg Val Ile Asp His Phe Phe Cys Glu Val Pro Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Thr Asp Thr Ser Val Asn Glu Ala Glu Leu
 195 200 205
 Asn Val Leu Gly Ala Leu Leu Leu Val Pro Leu Ser Leu Ile Leu
 210 215 220
 Gly Thr Tyr Val Phe Ile Ala Gln Ala Val Leu Lys Leu Arg Ser Ala
 225 230 235 240
 Glu Ser Arg Arg Lys Ala Phe Asn Thr Cys Ala Ser His Leu L u Val
 245 250 255

Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser Met Tyr Val Gln Pro Pro
 260 265 270
 Ser Ser Tyr Ser His Glu Arg Gly Lys Ile Met Ala Leu Phe Tyr Gly
 275 280 285
 Ile Val Thr Pr Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys
 290 295 300
 Asp Val Lys Ala Ala Leu Arg Arg Ala Leu Thr Lys Glu Phe Trp Val
 305 310 315 320
 Lys Ala Arg

<210> 2378

<211> 329

<212> PRT

<213> Mus musculus (M131 8574266-9-30686-36974 2322-3308)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2378

Leu Leu Ser Val Val Phe Phe Xaa Leu Phe Leu Asn Arg Val Ser Arg
 1 5 10 15
 Val Ile Ile Met Asn Val Ser Phe Lys Thr Gly Phe Leu Leu Met Gly
 20 25 30
 Phe Ser Asp Glu Arg Asn Leu Gln Ile Leu His Ala Val Leu Phe Leu
 35 40 45
 Ile Thr Tyr Leu Leu Ala Ile Met Gly Asn Leu Leu Ile Ile Thr Ile
 50 55 60
 Ile Thr Leu Asp Gln Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys
 65 70 75 80
 His Leu Ser Phe Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln
 85 90 95
 Ser Ile Ala Asn Ser Leu Met Asn Asn Gly Phe Ile Ser Leu Gly Gln
 100 105 110
 Cys Met Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val
 115 120 125
 Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 130 135 140
 Pro Leu Gln Tyr Glu Thr Ile Met Asp Pro His Ala Cys Lys Cys Ala
 145 150 155 160
 Val Ile Ala Val Trp Met Ala Gly Gly Leu Ser Gly Leu Leu His Thr
 165 170 175
 Gly Val Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Ile Ile His Gln
 180 185 190
 Phe Phe Cys Asp Ile Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu
 195 200 205
 Phe Ile Asn Glu Ile Ala Val Ala Ala Phe Thr Thr Ser Thr Ala Phe
 210 215 220
 Val Cys Leu Ile Ala Ile Val Phe Ser Tyr Thr Gln Ile Phe Ser Thr
 225 230 235 240
 Val Met Arg Ile Pro Ser Ala Asp Ser Arg Thr Lys Val Phe Ser Thr
 245 250 255
 Cys Leu Pro His Leu Phe Val Val Met Phe Phe Leu Ser Ala Ala Gly
 260 265 270
 Phe Glu Phe Leu Arg Pro Pro Ser Asp Ser Leu Ser Ala Met Asp Leu
 275 280 285
 Val Phe Ser Ile Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Leu
 290 295 300
 Ile Tyr Ser Leu Arg Asn Glu Ala Met Lys Ala Ala Leu Arg Lys Val

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<210> 2379
<211> 324
<212> PRT
<213> Mus musculus (M132 8574266-9-4118-8767 2921-3891)
```

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<220>  
<221> VARIANT  
<222> (1)...(324)  
<223> Xaa = Any Amino Acid
```

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<210> 2380
<211> 341
<212> PRT
```

<213> Mus musculus (M133 8574277-10-1-1870 1597-577)

<220>

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400>2380

```

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val
 1              5              10              15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Met Val Leu Ala
      20              25              30
Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val
      35              40              45
Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn
 50              55              60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
65              70              75              80
Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
      85              90              95
Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu
      100              105              110
Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
      115              120              125
Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala
      130              135              140
Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
      145              150              155              160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe
      165              170              175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
      180              185              190
Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly
      195              200              205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
      210              215              220
Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
      225              230              235              240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
      245              250              255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
      260              265              270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
      275              280              285
Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys
      290              295              300
Leu Arg Ile Leu Ile Xaa Leu Gly Arg Asn Leu Val Ser Tyr Phe Val
      305              310              315              320
Ile Ser Gln His Lys Gln Leu Leu Xaa Lys Ser Met Cys Glu Ile Ser
      325              330              335
Xaa Phe Xaa Ile Cys
      340

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<210> 2381

<211> 284

<212> PRT

<213> Mus musculus (M136 8574277-13-1-992 974-124)

<220>

<221> VARIANT

<222> (1)...(284)

<223> Xaa = Any Amino Acid

<400>2381

```

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
1       5       10      15
Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val
20      25      30
Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val
35      40      45
Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly
50      55      60
Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp
65      70      75      80
Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr
85      90      95
Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly
100     105     110
Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val
115     120     125
Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His
130     135     140
Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr
145     150     155     160
Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr
165     170     175
Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr
180     185     190
Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr
195     200     205
Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met
210     215     220
Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys
225     230     235     240
Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly
245     250     255
Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His
260     265     270
Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg
275     280

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<210> 2382

<211> 314

<212> PRT

<213> Mus musculus (M143 8574277-22-875-4053 855-1796)

<400>2382

```

Tyr Pro Met Gly Ile Leu Ser Thr Gly Asn Gln Thr Val Thr Glu Phe
1       5       10      15
Val Leu Leu Gly Phe His Glu Val Pro Gly Leu His Leu Leu Phe Phe
20      25      30
Ser Val Phe Thr Ile Leu Tyr Ala Ser Ile Ile Thr Gly Asn Met Leu
35      40      45
Ile Ala Val Val Val Val Ser Ser Gln Arg Leu His Thr Pro Met Tyr
50      55      60
Phe Phe Leu Val Asn Leu Ser Phe Ile Glu Ile Val Tyr Thr Ser Thr
65      70      75      80
Val Val Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser
85      90      95
Val Ala Gly Cys Leu Leu Gln Phe Phe Val Phe Gly Ser Leu Ala Thr
100     105     110
Asp Glu Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala

```

115	120	125
Ile Cys His Pro Leu Arg Tyr	Pro His Leu Met Gly	Pro Gln Trp Cys
130	135	140
Leu Gly Leu Val Leu Thr Val	Trp Leu Ser Gly Phe	Met Val Asp Gly
145	150	155
Leu Val Val Ala Leu Met Ala	Gln Leu Arg Phe Cys	Gly Pro Asn Leu
165	170	175
Val Asp His Phe Tyr Cys Asp	Phe Ser Pro Leu Met Val	Leu Ala Cys
180	185	190
Ser Asp Thr Gln Val Ala Gln	Val Thr Thr Phe Val Leu	Ser Val Val
195	200	205
Phe Leu Thr Val Pro Phe Gly	Leu Val Leu Ile Ser Tyr	Ala Gln Ile
210	215	220
Val Val Thr Val Leu Arg Val	Pro Ser Gly Thr Arg	Thr Lys Ala
225	230	235
Phe Ser Thr Cys Ser Ser His	Leu Ala Val Val Ser Thr	Phe Tyr Gly
245	250	255
Thr Leu Met Val Leu Tyr Ile	Val Pro Ser Ala Val His	Ser Gln Leu
260	265	270
Leu Ser Lys Val Ile Ala Leu	Leu Tyr Thr Val Val Thr	Pro Ile Phe
275	280	285
Asn Pro Val Ile Tyr Thr Leu	Arg Asn Gln Glu Val Gln	Gln Ala Leu
290	295	300
Arg Arg Leu Leu Tyr Cys Lys	Pro Thr Glu	
305	310	

<210> 2383

<211> 107

<212> PRT

<213> Mus musculus (M144 8574277-30-676-1123 424-104)

<220>

<221> VARIANT

<222> (1)...(107)

<223> Xaa = Any Amino Acid

<400>2383

Ser Gly Val Leu Gly Asn Lys Leu Ser Leu Cys Leu Xaa Val Xaa Arg
1 5 10 15
Val Phe Phe Ser Cys Gly Xaa Val Pro Ser Ala Gln Gly Lys Arg Lys
20 25 30
Ser Leu Ala Thr Cys Ser Ser His Leu Ser Val Val Leu Leu Phe Tyr
35 40 45
Ser Thr Val Phe Ala Thr Tyr Leu Lys Pro Pro Ser Thr Ser His Ser
50 55 60
Ser Ala Glu Val Val Ala Ala Val Met Tyr Thr Leu Val Thr Pro Thr
65 70 75 80
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Ser
85 90 95
Leu Arg Lys Ile Leu Asn Met Asp Lys Phe Gln
100 105

<210> 2384

<211> 232

<212> PRT

<213> Mus musculus (M148 8574277-5-2944-4486 2-698)

<220>

<221> VARIANT

<222> (1)...(232)

<223> Xaa = Any Amino Acid

<400>2384

Lys Ser Leu Ala Thr Leu Ala Gly Cys Leu Leu Gln Phe Leu Thr Phe
 1 5 10 15
 Thr Ser Leu Asp Ala Asp Glu Tyr Phe Leu Leu Thr Leu Met Ala His
 20 25 30
 Asp His Cys Leu Ala Ile Phe Tyr Ser Leu Xaa Tyr Pro Arg Leu Met
 35 40 45
 Arg Pro Gln Trp Cys Leu Gly Leu Val Ile Ile Val Trp Leu Ser Gly
 50 55 60
 Phe Met Glu Ala Gly Leu Val Val Ala Leu Thr Ala Gln Leu Arg Phe
 65 70 75 80
 Cys Gly Pro Asn Leu Ile Asp His Phe Tyr Cys Asp Phe Ser Pro Leu
 85 90 95
 Met Ile Leu Ala Cys Ser Asp Thr Xaa Val Ala Gln Met Thr Thr Phe
 100 105 110
 Val Leu Phe Val Val Phe Leu Pro Val Leu Ser Gly Leu Ile Leu Met
 115 120 125
 Ser Tyr Ala Gln Phe Val Val Ile Val Leu Arg Ile Pro Ser Gly Ala
 130 135 140
 Arg Arg Thr Lys Ala Phe Phe Thr Cys Ser Ser His Leu Ala Met Met
 145 150 155 160
 Phe Thr Phe Tyr Gly Ser Leu Met Val Trp Tyr Thr Ala Pro Ser Ala
 165 170 175
 Val Leu Ser Leu Gln Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Thr
 180 185 190
 Val Phe Ala Pro Ile Phe Asn Ser Val Ile Tyr Thr Leu Arg Asn Leu
 195 200 205
 Asp Met Gln Lys Ala Leu Arg Arg Leu Leu Tyr Cys Lys Ser Thr Glu
 210 215 220
 Met Xaa Pro Lys Lys Glu Gly Ser
 225 230

<210> 2385

<211> 326

<212> PRT

<213> Mus musculus (M149 8574277-6-4252-5644 1059-82)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2385

Tyr Ile Val Phe Thr Pro Ile Ser Ser Xaa Asn Thr Arg Pro Thr Met
 1 5 10 15
 Asn Cys Ser Gln Ala Pro Thr Phe Ile Leu Leu Gly Leu Ser Ser Asp
 20 25 30
 Ala Glu Lys Trp Gln Pro Leu Phe Ser Ile Phe Leu Val Leu Tyr Leu
 35 40 45
 Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu Ala Ile Gly Thr Asp
 50 55 60
 Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu
 65 70 75 80
 Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala
 85 90 95
 Leu Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln
 100 105 110
 Leu Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Leu Ala
 115 120 125
 Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu Tyr

130	135	140
Pro Leu Leu Met Thr	Pr Cys Arg Cys Arg	Val Leu Val Ser Gly S r
145	150	155
Trp Gly Val Ala His	Cys Val Ser Leu Thr	His Thr Leu Leu Phe Ser
165	170	175
Lys Leu Tyr Phe His	Asp Asn Gln Glu Ile	Pro His Phe Phe Cys Asp
180	185	190
Phe Gly Pro Leu Leu	Leu Ser Cys Ser Asp	Thr Tyr Leu Asn Glu
195	200	205
Ser Leu Met Met Ala	Leu Ser Gly Leu Leu	Ala Ile Ser Ala Phe Leu
210	215	220
Cys Ile Val Ser Ser	Tyr Gly Cys Ile Phe	Tyr Ala Val Ala Lys Val
225	230	235
Pro Ser Ala Gln Gly	Lys Arg Lys Ala Leu	Ala Thr Cys Ser Ser His
245	250	255
Leu Ser Val Val Leu	Leu Phe Tyr Ser Thr	Val Phe Ala Thr Tyr Leu
260	265	270
Lys Pro Pro Ser Ser	Ser His Ser Ser Gln	Glu Val Val Ala Ala Val
275	280	285
Met Tyr Thr Leu Val	Thr Pro Thr Leu Asn	Pro Phe Ile Tyr Ser Leu
290	295	300
Arg Asn Lys Asp Val	Lys Ser Ser Leu Arg	Arg Ile Leu Asn Met Val
305	310	315
Lys Ser Gln Asp Xaa	Gly	
325		

<210> 2386

<211> 321

<212> PRT

<213> Mus musculus (M152 8574277-7-18987-20418 1032-73)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400>2386

Cys Gly Leu Ser Cys	Ser Gln Arg Ser	Arg Arg Asn Val	Leu Ile Ser
1	5	10	15
Leu Xaa Xaa Leu Asn	Phe Phe Leu Met	Gly Phe Ser Arg	Lys Leu Glu
20	25	30	
Val Glu His Asn Phe	Ile Leu Ala Leu	Gly Leu Val Ile	Leu Ile Ala
35	40	45	
Asn Val Phe Ile Ile	Ala Ala Ile Ser	Leu Glu Tyr His	Leu Cys Ser
50	55	60	
Leu Arg His Phe Leu	Leu Glu Gln Leu	Phe Cys Leu Asp	Leu Cys Tyr
65	70	75	80
Ile Ser Met Ile Val	Leu Ser Thr Ile	Lys Ser Ile Cys	Arg Ser Phe
85	90	95	
Met Tyr Ser Ala Tyr	Ile Ser Leu Ile	Glu Cys Thr Leu	Gln Gly Phe
100	105	110	
Ala Phe Thr Leu Cys	Ser Tyr Thr Ser	Met Ala Ile Leu	Thr Val Met
115	120	125	
Ser Cys His Cys Tyr	Val Ile Met Cys	Tyr Lys Val Ile	Ile Ser Val
130	135	140	
Ser Leu Cys Met His	Lys Val Leu Ala	Val Trp Ala Ser	Gly Cys Gly
145	150	155	160
Ile Asn Phe Gly Val	Met His Thr Ala	Val Asn Phe Ser	Ile Ser Leu
165	170	175	
Cys Gly Ala Ser Val	Ile His Xaa Phe	Cys Asn Val Leu	Leu Val Leu
180	185	190	

Lys Leu Ser Cys Ser Asn Asp Cys Val Ser Glu Leu Ser Ile Ile Gly
 195 200 205
 Phe Pro Thr Cys Arg His Phe Ile Ser Ile Ser Phe Ala Tyr Glu His
 210 215 220
 Ile Leu Ser Pro Glu Leu Arg Met Pro Ser Val Lys Gly Arg Thr Arg
 225 230 235 240
 Val Phe Ser Thr Cys Leu Cys His Ile Ser Val Val Ile Leu Phe Ile
 245 250 255
 Pro Thr Gly Val Phe Glu Phe Leu Asn Pro His Ser Lys Ser Pro Thr
 260 265 270
 Xaa Ile Leu His Xaa Thr Leu Phe Leu Val Phe His Thr Phe Leu Ser
 275 280 285
 Ser Thr Leu Asn Pro Glu Ile Asn Ser Leu Arg Asn Glu Ala Thr Glu
 290 295 300
 His His Ser Lys Glu Asn Val Ser Leu Phe Ile Ser Thr Ile Ser Ser
 305 310 315 320
 Leu

<210> 2387

<211> 327

<212> PRT

<213> Mus musculus (M154 8575572-1-103679-105172 492-1471)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2387

His Xaa Met Gly Ala Leu Asn Gln Thr Arg Val Thr Glu Phe Ile Phe
 1 5 10 15
 Leu Gly Leu Thr Asp Asn Trp Val Leu Glu Ile Leu Phe Phe Val Pro
 20 25 30
 Phe Thr Val Thr Tyr Met Leu Thr Leu Leu Gly Asn Phe Leu Ile Val
 35 40 45
 Val Thr Ile Val Phe Thr Pro Arg Leu His Asn Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe
 85 90 95
 Asp Asn Cys Ile Ala Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ser
 100 105 110
 Glu Ile Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Ile Pro Leu His Tyr Ser Asn Val Met Asn Met Lys Val Cys Val
 130 135 140
 Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Ile His Ser Leu Val
 145 150 155 160
 Gln Thr Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile
 165 170 175
 Asp Ser Tyr Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Thr
 180 185 190
 Asp Thr Tyr Leu Thr Gly Ile Leu Ile Val Ser Asn Ser Gly Thr Ile
 195 200 205
 Ser Leu Val Cys Phe Leu Ala Leu Val Thr Ser Tyr Thr Val Ile Leu
 210 215 220
 Phe Ser Leu Arg Lys Lys Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser
 225 230 235 240
 Thr Cys Ser Ala His Phe Met Val Val Thr Leu Phe Phe Gly Pro Cys

				245					250					255	
Ile	Phe	Leu	Tyr	Thr	Arg	Pro	Asp	Ser	Ser	Phe	Ser	Ile	Asp	Lys	Val
			260					265					270		
Val	Ser	Val	Phe	Tyr	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu	Ile
		275						280					285		
Tyr	Thr	Leu	Arg	Asn	Glu	Glu	Val	Lys	Thr	Ala	Met	Lys	His	Leu	Arg
	290				295						300				
Gln	Arg	Arg	Ile	Cys	Ser	Xaa	Asn	His	Val	Cys	Val	Trp	Leu	Val	Xaa
305					310					315					320
Cys	Cys	Asp	Asn	Ser	His	Gly									
				325											

<210> 2388

<211> 330

<212> PRT

<213> Mus musculus (M157 8575572-1-144835-147600 2426-1439)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400>2388

Met	Glu	Lys	Ala	Val	Leu	Ile	Asn	Gln	Thr	Ser	Val	Met	Ser	Phe	Arg
1				5				10						15	
Leu	Thr	Gly	Leu	Ser	Thr	Asn	Pro	Lys	Val	Gln	Met	Ala	Ile	Phe	Phe
		20						25					30		
Ile	Phe	Leu	Ile	Phe	Tyr	Val	Leu	Thr	Leu	Val	Gly	Asn	Ile	Leu	Ile
	35					40					45				
Val	Val	Thr	Ile	Ile	His	Asp	His	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe
	50				55					60					
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Val	Cys	His	Ser	Thr	Val	Thr
65				70					75					80	
Val	Pro	Lys	Met	Leu	Ser	Asp	Thr	Phe	Ser	Glu	Glu	Lys	Leu	Ile	Ser
		85						90					95		
Phe	Asp	Asp	Cys	Val	Val	Gln	Ile	Phe	Phe	Leu	His	Leu	Phe	Ala	Cys
		100					105						110		
Thr	Glu	Ile	Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala
	115					120						125			
Ile	Cys	Lys	Pro	Leu	Arg	Tyr	Met	Thr	Ile	Met	Asn	Trp	Lys	Val	Cys
	130				135					140					
Met	Val	Leu	Gly	Gly	Ala	Met	Trp	Thr	Ala	Gly	Thr	Ile	His	Ser	Ile
145				150						155				160	
Ser	Phe	Thr	Ser	Leu	Thr	Ile	Lys	Leu	Pro	Tyr	Cys	Gly	Pro	Asn	Glu
		165						170					175		
Leu	Asp	Ser	Phe	Phe	Cys	Asp	Val	Pro	Gln	Val	Ile	Glu	Leu	Ala	Cys
	180						185					190			
Thr	Asp	Thr	Arg	Ile	Thr	Glu	Ile	Leu	Val	Val	Ser	Asn	Ser	Gly	Met
	195				200						205				
Ile	Ser	Met	Val	Cys	Phe	Val	Ile	Ile	Val	Val	Ser	Tyr	Ala	Val	Ile
	210				215						220				
Leu	Val	Ser	Leu	Arg	Gln	Gln	Ile	Ser	Asp	Gly	Lys	Arg	Lys	Ala	Leu
225				230					235					240	
Ser	Thr	Cys	Ala	Ala	His	Leu	Thr	Val	Val	Thr	Leu	Phe	Leu	Gly	His
			245					250					255		
Cys	Ile	Phe	Ile	Tyr	Ser	Arg	Pro	Ala	Ile	Ser	Leu	Pro	Glu	Asp	Lys
	260						265					270			
Ile	Val	Ser	Ala	Phe	Phe	Thr	Ala	Ile	Thr	Pro	Leu	Leu	Asn	Pro	Ile
	275					280						285			
Ile	Tyr	Thr	Phe	Arg	Asn	Glu	Asp	Met	Lys	Ser	Ala	Leu	Lys	Lys	Leu
	290				295						300				

Ile Arg Arg Lys Glu Gly Lys Glu Lys Xaa Lys Cys Ile Ser Ser Leu
 305 310 315 320
 Gly Phe Leu Val Ile Xaa Ile Lys Glu Ala
 325 330

<210> 2389

<211> 331

<212> PRT

<213> Mus musculus (M158 8575572-1-18114-22131 1498-507)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400>2389

Cys Leu Ser Ala Ser Leu Asp Ile Ser Lys Met Glu Arg Ile Asn Tyr
 1 5 10 15
 Thr Val Leu Thr Glu Phe Ile Leu Thr Gly Val Pro His Pro Pro Arg
 20 25 30
 Leu Arg Thr Phe Leu Phe Val Phe Phe Leu Leu Ile Tyr Ile Leu Thr
 35 40 45
 Gln Leu Gly Asn Ala Leu Ile Leu Ile Thr Val Cys Ala Asp Thr Gln
 50 55 60
 Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Ala Leu Ser Val Ile
 65 70 75 80
 Asp Met Gly Ile Ser Thr Ile Ile Val Pro Arg Leu Met Met Asn Phe
 85 90 95
 Thr Pro Gly Ile Lys Pro Ile Pro Phe Gly Gly Cys Val Ala Gln Leu
 100 105 110
 Tyr Phe Tyr His Phe Leu Gly Ser Ser Gln Cys Phe Leu Tyr Thr Thr
 115 120 125
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro
 130 135 140
 Val Leu Met Ser Ala Lys Leu Ser Ile Leu Leu Val Ala Gly Ala Trp
 145 150 155 160
 Val Ala Gly Ser Ile His Gly Ala Ile Gln Ala Ile Leu Thr Phe Arg
 165 170 175
 Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile
 180 185 190
 Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu
 195 200 205
 Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser Cys Phe Ser Leu
 210 215 220
 Ile Leu Leu Ser Tyr Ile Tyr Ile Ile Arg Ala Ile Leu Arg Ile Arg
 225 230 235 240
 Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys Gly Ala His Val
 245 250 255
 Thr Ile Val Thr Val Tyr Tyr Val Pro Cys Ala Phe Ile Tyr Leu Arg
 260 265 270
 Pro Asp Ser His Ser Ile Leu Asp Gly Ala Ala Ala Leu Phe Pro Thr
 275 280 285
 Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln
 290 295 300
 Glu Val Lys Leu Ala Leu Arg Arg Met Val Gly Ser Gln Ser Thr Lys
 305 310 315 320
 Ser Glu Val Xaa Ala Pro Leu Leu Phe Xaa Gly
 325 330

<210> 2390

<211> 324

<212> PRT

<213> Mus musculus (M160 8575572-1-54180-57203 1450-479)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400>2390

```

Ile Leu Thr Asp Xaa Asp Met Arg Arg Thr Arg Asn Thr Ser Leu Asp
 1           5           10           15
Ala Val Val Thr Asp Phe Leu Leu Leu Gly Leu Ala His Pro Pro Asn
 20           25           30
Leu Arg Ala Phe Leu Phe Leu Val Phe Phe Leu Ile Tyr Ile Leu Thr
 35           40           45
Gln Leu Gly Asn Leu Leu Ile Leu Leu Thr Val Trp Ala Asp Pro Lys
 50           55           60
Leu His Ala Arg Pro Met Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu
 65           70           75           80
Asp Met Trp Leu Ser Ser Val Ile Val Pro Arg Leu Ile Leu Asn Phe
 85           90           95
Thr Pro Ala Ser Lys Ala Ile Pro Phe Gly Gly Cys Val Ala Gln Leu
100           105           110
Tyr Phe Phe His Phe Leu Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu
115           120           125
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro
130           135           140
Val Leu Met Asn Gly Lys Leu Cys Thr Ile Leu Val Ser Gly Ala Trp
145           150           155           160
Val Ala Gly Ser Ile His Gly Ser Ile Gln Thr Thr Leu Thr Phe Arg
165           170           175
Leu Pro Tyr Cys Gly Pro Asn Gln Ile Asp Tyr Phe Ile Cys Asp Ile
180           185           190
Pro Ala Val Leu Arg Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu
195           200           205
Val Thr Phe Val Asp Ile Gly Val Val Ala Ala Ser Cys Phe Met Leu
210           215           220
Ile Leu Leu Ser Tyr Ala Asn Ile Val His Ala Ile Leu Lys Ile Arg
225           230           235           240
Thr Ala Asp Gly Arg Lys Arg Ala Phe Ser Thr Cys Gly Ser His Leu
245           250           255
Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg
260           265           270
Ala Gly Ser Lys Ser Pro Phe Asp Gly Ala Val Ala Val Phe Tyr Thr
275           280           285
Val Val Thr Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln
290           295           300
Glu Val Lys Ser Ala Leu Lys Arg Leu Thr Ala Gly Arg Arg Asp Val
305           310           315           320
Gly Gly Glu Lys

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<210> 2391

<211> 329

<212> PRT

<213> Mus musculus (M162 8576192-11-46369-50310 3151-2165)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2391

Phe Ser Xaa Ser His Tyr Arg Gln Asn Met Thr Gly Asn Asn Gln Thr
 1 5 10 15
 Leu Ile Ser Lys Phe Leu Leu Leu Gly Leu Pro Ile Leu Ser Glu Tyr
 20 25 30
 His Phe Leu Phe Tyr Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile
 35 40 45
 Leu Gly Asn Leu Leu Ile Ile Ala Leu Val Arg Leu Asp Ser His Leu
 50 55 60
 His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu
 65 70 75 80
 Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln Asn Met Gln Ser
 85 90 95
 Gln Val Pro Ser Ile Ser Tyr Val Gly Cys Leu Thr Gln Leu Tyr Phe
 100 105 110
 Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu Val Val Met Ala
 115 120 125
 Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile
 130 135 140
 Met Ser Thr Lys Phe Cys Thr Ser Leu Val Leu Leu Leu Trp Met Leu
 145 150 155 160
 Thr Thr Ser Asn Ala Leu Met His Thr Leu Leu Met Ala Arg Leu Ser
 165 170 175
 Phe Cys Glu Lys Asn Val Ile Leu Arg Phe Phe Cys Asp Ile Ser Ala
 180 185 190
 Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Val Asn Glu Leu Met Ile
 195 200 205
 Phe Ile Met Gly Gly Ile Ile Ile Ile Ile Pro Phe Leu Leu Ile Val
 210 215 220
 Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys Val Pro Ser Thr
 225 230 235 240
 Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ser Asn Asn Ser Thr Val Lys Glu Ser Ala Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300
 Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys Ser Lys Lys Ile Ser
 305 310 315 320
 Leu Xaa Trp Lys Tyr Phe Arg Met Ile
 325

<210> 2392

<211> 275

<212> PRT

<213> Mus musculus (M163 8576192-5-7971-9031 1060-236)

<220>

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400>2392

Ile Ile Ile Leu Ile Ile Leu Asp Phe His Leu His Thr Pro Ile Tyr
 1 5 10 15
 Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Ph Ser Ser Val
 20 25 30
 Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Thr Ile

```

      35      40      45
Ser Tyr Val Gly Cys Leu Thr Gln Met Tyr Phe Pro Asn Val Phe Ala
  50      55      60
Asn Leu Glu Asn Phe Leu Met Phe Met Ala Tyr Asp Arg Tyr Val
  65      70      75      80
Ala Ile Cys Tyr Pro Leu Arg Tyr Thr Ser Ile Met Ser Pro Ile Leu
      85      90      95
Cys Val Cys Met Val Phe Met Ser Trp Leu Leu Thr Met Leu Asn Ser
      100      105      110
Thr Leu His Thr Val Leu Ile Val Lys Leu Ser Phe Cys Glu Asp Asn
      115      120      125
Val Ile Pro His Phe Phe Cys Asp Ile Ser Ala Val Leu Lys Leu Ala
      130      135      140
Cys Ser Asp Ile Tyr Ile Asn Glu Leu Thr Ile Phe Ile Thr Gly Ala
      145      150      155      160
Phe Ile Ile Val Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln
      165      170      175
Ile Val Cys Ser Ile Leu Lys Phe Ser Ser Thr Arg Gly Ile Ala Lys
      180      185      190
Ile Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
      195      200      205
Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Thr Asn Asn Ser Thr
      210      215      220
Val Lys Asp Thr Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met
      225      230      235      240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala
      245      250      255
Leu Ile Arg Val Leu Cys Lys Lys Glu Ile Ser Leu Xaa Trp Gln Tyr
      260      265      270
Leu His Leu
      275

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<210> 2393

<211> 327

<212> PRT

<213> Mus musculus (M165 8576192-7-12279-14147 678-1658)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2393

```

Trp Arg Ile Arg Met Ile Ile Asn Asn Gln Thr Ala Ile Pro Gln Phe
  1      5      10      15
Ile Leu Leu Gly Leu Pro Ile Leu Pro Glu Gln Gln Gln Met Phe Tyr
      20      25      30
Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile
      35      40      45
Ile Ile Ile Leu Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr
      50      55      60
Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
      65      70      75      80
Thr Met Pro Lys Leu Leu Gln Asn Ile Gln Ser Gln Asp Pro Ser Ile
      85      90      95
Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Met Val Phe Ala
      100      105      110
Asn Thr Glu Asn Val Leu Leu Val Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Leu
      130      135      140

```

Cys Val Ser Leu Val Val Leu Thr Trp Val Phe Thr Val Leu Tyr Ser
 145 150 155 160
 Met Leu His Thr Leu Leu Ala Arg Leu Ser Phe Cys Glu Asp Asn
 165 170 175
 Val Ile Thr His Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala
 180 185 190
 Cys Ser Asp Thr Tyr Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Thr
 195 200 205
 Leu Asp Thr Val Val Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln
 210 215 220
 Ile Val Cys Ser Ile Leu Lys Phe Ser Thr Lys Gln Gly Ile Ala Lys
 225 230 235 240
 Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Ile Ile Gly Val Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr
 260 265 270
 Val Lys Glu Ile Val Met Ala Leu Met Tyr Thr Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala
 290 295 300
 Leu Ile Arg Val Leu Cys Lys Lys Gln Ile Pro Leu Xaa Cys Leu Tyr
 305 310 315 320
 Trp Asn Phe Xaa Ile Xaa Ile
 325

<210> 2394

<211> 316

<212> PRT

<213> Mus musculus (M166 8576192-8-1-1469 247-1198)

<400>2394

Arg Gly Arg Met Val Met Asn Asn Gln Thr Val Ile Ser Gln Leu Leu
 1 5 10 15
 Leu Val Gly Leu His Ile Pro Pro Asp His Gln Gln Gly Phe Tyr Thr
 20 25 30
 Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile
 35 40 45
 Ile Pro Leu Ile Ile Met Asp Ser Pro Phe Pro Thr His Pro Met Tyr
 50 55 60
 Leu Phe Leu Ile Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
 65 70 75 80
 Thr Val Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Ser Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Met Val Phe Gly
 100 105 110
 Asp Met Glu Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Thr Met Ser Pro Lys Phe
 130 135 140
 Cys Val Cys Val Gly Ala Leu Ser Trp Val Phe Thr Ile Met Tyr Ser
 145 150 155 160
 Met Val His Thr Leu Leu Ser Arg Leu Ser Phe Cys Glu Asp Asn
 165 170 175
 Val Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala
 180 185 190
 Cys Ser Asp Ile Phe Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly
 195 200 205
 Pro Val Val Ala Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg
 210 215 220
 Ile Val Ser Ser Ile Leu Lys Val Ser Ser Ser Gln Gly Ile His Lys
 225 230 235 240

Ile Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pr Ser Ala Asn Asn Ser Thr
 260 265 270
 Val Lys Lys Ile Ala Met Ala M t Met Tyr Thr Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Ser Arg Asp Met Lys Glu Ala
 290 295 300
 Leu Ile Arg Val Leu Cys Lys Lys Lys Ile Ser Leu
 305 310 315

<210> 2395

<211> 244

<212> PRT

<213> Mus musculus (M167 8576192-8-6530-9303 730-2)

<220>

<221> VARIANT

<222> (1)...(244)

<223> Xaa = Any Amino Acid

<400>2395

Tyr Leu Ser Arg Gly Leu Pro Ser Phe Glu Gly Leu Thr Gln Ala Xaa
 1 5 10 15
 Leu Asn Thr Xaa Ser Asn His His Ile Pro Thr Ile Val His Arg Thr
 20 25 30
 Ile Asp Asp Ile Cys Asn Ser Phe Xaa Cys Leu Phe Phe Ala Leu Gly
 35 40 45
 Ser Asn Pro Leu Phe Gln Met Ser Gln Lys Tyr Cys Ile Xaa Xaa Tyr
 50 55 60
 Ile Gly Asn Leu His Ser Lys Gly Ile Tyr Ile Phe Asn Gly Leu Thr
 65 70 75 80
 Ser Ile Arg Leu Leu Gln Ile Ile Leu Thr Phe Leu Ser Met Lys Ala
 85 90 95
 Leu Cys Ser Ser Pro Lys Phe Ser Asn Ile Leu Ser Cys Ser Ser Ala
 100 105 110
 Leu Leu Leu Ile Lys Ser Lys Ser Phe Val Ser Asn Xaa Tyr His Leu
 115 120 125
 Thr His Ile Glu Cys Xaa Leu Tyr Ser Leu Asn Ser Ile Leu His Arg
 130 135 140
 Tyr Tyr Ala Leu Val Met Lys Cys Ser Gln Asn Ser Tyr Ile Glu Ser
 145 150 155 160
 Leu Val Leu Asp Ala Met Phe Arg Gly Gly Ser Gly Arg His Gly Gly
 165 170 175
 Val Phe Lys Thr Leu Thr His Gln Leu Ser Pro Leu Ile Pro Lys Val
 180 185 190
 Xaa Ser Ser Met Gly Ile His Lys Ala Phe Ser Thr Ser Gly Ser Asp
 195 200 205
 Arg Asp Leu Ser Met Val Ser Val Tyr Tyr Gly Lys Val Ile Asp Leu
 210 215 220
 Phe Leu Ser Pro Ser Ser Asn Met Asn Thr Met Lys Glu Thr Ile Ile
 225 230 235 240
 Ser Val Met Tyr

<210> 2396

<211> 338

<212> PRT

<213> Mus musculus (M168 8576195-11-1440-4165 2456-1443)

<220>

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400>2396

Cys Xaa Xaa His Phe Ile Leu Ser Leu Leu Gln Met Lys Val Met Lys
 1 5 10 15
 Gln Met Val Thr Glu Ser Asn Ser Ser Val Thr Glu Phe Ile Leu Met
 20 25 30
 Gly Leu Thr Val Gln Lys Glu Leu Gln Leu Pro Leu Phe Ile Leu Phe
 35 40 45
 Leu Leu Asn Tyr Thr Ala Thr Val Val Gly Asn Leu Ser Leu Met Asn
 50 55 60
 Leu Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile
 65 70 75 80
 Phe Asn Leu Ser Cys Ile Asp Phe Cys Tyr Ser Phe Val Ser Asn Pro
 85 90 95
 Thr Met Leu Arg Ser Phe Val Thr Glu Gln Asn Thr Ile Ser Tyr Glu
 100 105 110
 Gly Cys Met Ser Gln Leu Phe Phe Cys Phe Phe Val Asn Ser Glu
 115 120 125
 Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 130 135 140
 His Pro Leu Lys Tyr Thr Thr Val Met Ser Pro Lys Ile Cys Cys Leu
 145 150 155 160
 Leu Val Phe Gly Ser Tyr Leu Met Gly Phe Ala Gly Ala Leu Thr His
 165 170 175
 Thr Gly Phe Met Ile Arg Leu Ser Phe Cys Asn Ser Asn Ile Ile Asn
 180 185 190
 His Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Thr Ser
 195 200 205
 Thr Tyr Val Asn Glu Leu Val Ser Ser Ala Val Val Gly Thr Ile Ile
 210 215 220
 Ile Leu Ser Ser Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Ser
 225 230 235 240
 Asn Ile Leu His Met Ser Ser Ser Lys Gly Trp Ser Lys Ala Leu Gly
 245 250 255
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly
 260 265 270
 Leu Leu Ala Tyr Ile Lys Pro Thr Ser Ala Glu Thr Val Asp Gln Gly
 275 280 285
 Lys Phe Leu Ser Ile Phe Tyr Thr Leu Val Val Pro Met Leu Asn Pro
 290 295 300
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg
 305 310 315 320
 Thr Met Lys Arg Val Thr Thr Xaa Met Asn Ser Cys Ala Phe Ile Val
 325 330 335
 Leu Pro

<210> 2397

<211> 340

<212> PRT

<213> Mus musculus (M169 8576195-13-2329-4897 1250-2268)

<220>

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400>2397

```

Ile Ser Cys Leu Val Val Ser Pro Ser Ile Leu Gln Thr Ser His Thr
 1          5          10          15
Lys Gln Ile Thr Met Glu Asn Asp Ser Phe Val Ser Glu Phe Ile Leu
 20          25          30
Met Gly Leu Thr Asp His Pro Glu Leu Gln Leu Ser Leu Phe Val Leu
 35          40          45
Phe Leu Met Asn Tyr Thr Ala Ile Val Met Gly Asn Leu Ser Leu Met
 50          55          60
Ile Leu Ile Phe Leu Asn Ser Asn Leu His Thr Pro Met Tyr Phe Phe
 65          70          75          80
Ile Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr
 85          90          95
Pro Lys Met Leu Met Ser Phe Phe Leu Glu Lys Asn Thr Ile Ser Phe
100          105          110
Arg Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser
115          120          125
Glu Ser Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
130          135          140
Cys Lys Pro Leu Leu Tyr Lys Thr Ile Met Val Pro Arg Ile Cys Cys
145          150          155          160
Leu Leu Met Phe Val Ser Tyr Leu Ile Gly Phe Thr Ser Ala Met Ile
165          170          175
Leu Thr Gly Leu Met Phe Arg Leu Asn Phe Cys Asn Asn His Ile Ile
180          185          190
Asn His Tyr Met Cys Asp Ile Phe Pro Val Ile Gln Ile Ser Cys Ser
195          200          205
Asp Thr Tyr Leu Asn Glu Leu Val Ser Thr Ala Val Val Gly Thr Gly
210          215          220
Ile Ile Leu Cys Ser Leu Leu Ile Leu Met Ser Tyr Ala Leu Ile Leu
225          230          235          240
Phe Asn Ile Leu Asn Met Ser Ser Gly Lys Gly Trp Ser Lys Ala Met
245          250          255
Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser
260          265          270
Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala Glu Thr Val Gly Gln
275          280          285
Gly Lys Phe Phe Ser Leu Phe Tyr Thr Phe Leu Val Pro Met Leu Asn
290          295          300
Pro Leu Ile Tyr Ser Leu Gln Asn Lys Asp Val Lys Val Ala Val Lys
305          310          315          320
Lys Thr Leu Lys Arg Ile Ser Asn Xaa Leu Glu Pro Leu Ala Leu His
325          330          335
Arg Thr Leu Ser
340

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<210> 2398

<211> 336

<212> PRT

<213> Mus musculus (M171 8576195-15-1361-3546 1172-2177)

<220>

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400>2398

```

Phe Xaa Leu Met Leu Leu Gln Met Gln His Met Lys Gln Met Ile Met
 1          5          10          15
Glu Asn Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Tyr
 20          25          30
Gln Pro Glu Leu Trp Trp Pro Leu Phe Val Leu Phe Leu Val Asn Tyr

```

35	40	45
Thr Ala Thr Val Met Gly Asn Leu Ser Leu Met Thr Leu Ile Cys Leu		
50	55	60
Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile Leu Asn Leu Ser		
65	70	75
Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met		
85	90	95
Gly Phe Val Ser Glu His Asn Thr Ile Ser Phe Thr Gly Cys Met Thr		
100	105	110
Gln Leu Phe Phe Cys Leu Phe Val Asn Ser Glu Cys Tyr Val Leu		
115	120	125
Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu Leu		
130	135	140
Tyr Thr Val Val Met Ser Pro Arg Ala Cys Ser Leu Leu Met Leu Ala		
145	150	155
Ala His Leu Met Gly Val Ser Ser Ala Val Val His Thr Gly Cys Ile		
165	170	175
Ile Gln Leu Arg Phe Cys Gly Ser Lys Val Ile Asn His Tyr Met Cys		
180	185	190
Asp Thr Phe Pro Leu Leu Glu Leu Ser Cys Gly Ser Ser His Val Asn		
195	200	205
Glu Leu Val Ser Ser Val Ser Val Ala Val Val Val Val Ile Ser Ser		
210	215	220
Leu Ile Ile Val Ser Ser Tyr Ala Leu Ile Leu Val Asn Val Ile His		
225	230	235
Leu Ser Ser Ser Lys Gly Trp Ser Lys Ala Val Ser Thr Cys Ser Ser		
245	250	255
His Ile Ile Thr Val Ala Leu Phe Tyr Gly Phe Gly Leu Leu Ala His		
260	265	270
Ile Lys Pro Ser Ser Ala Glu Ser Val Val Gln Arg Lys Phe Phe Ser		
275	280	285
Val Val Tyr Thr Phe Val Leu Pro Leu Leu Asn Pro Leu Ile Tyr Ser		
290	295	300
Ser Gly Asn Lys Asp Phe Lys Leu Leu Gly Thr Ile Asp Arg Leu Ala		
305	310	315
Gly Ser Asn Leu Ala Ser Phe Phe Phe Leu Ser Pro Leu Leu Ser Lys		
325	330	335

<210> 2399

<211> 326

<212> PRT

<213> Mus musculus (M172 8576195-20-3387-5132 199-1176)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2399

Ile Leu Thr Asp Met Thr Xaa Glu Gly Met Ala Ser Gly Asn Asp Ser		
1	5	10
Thr Thr Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu		
20	25	30
Leu Gln Leu Pro Phe Phe Phe Leu Phe Leu Gly Ile Tyr Val Val Ser		
35	40	45
Ile Val Gly Asn Leu Gly Leu Ile Val Leu Ile Val Leu Asn Pro His		
50	55	60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp		
65	70	75
Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys Met Leu Val Gly Phe Val		
85	90	95

Lys Gln Asn Ile Ile Ser His Ala Glu Cys Met Thr Gln Leu Phe Phe
 100 105 110
 Phe Ala Phe Phe Val Ile Asp Glu Cys Cys Ile Leu Thr Ala Met Ser
 115 120 125
 Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys Val Thr
 130 135 140
 Met Ser Tyr Glu Val Cys Phe Met Met Thr Val Ser Val Tyr Met Met
 145 150 155 160
 Gly Phe Val Gly Ala Ile Ala His Thr Ile Cys Met Leu Arg Leu Thr
 165 170 175
 Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Met Cys Asp Ile Pro Pro
 180 185 190
 Leu Leu Lys Leu Ser Cys Thr Asn Thr Ser Val Asn Glu Leu Val Val
 195 200 205
 Phe Ile Val Val Gly Val Asn Val Ile Gly Pro Thr Leu Ile Ile Phe
 210 215 220
 Thr Ser Tyr Thr Leu Ile Ile Phe Asn Ile Ser His Ile Arg Ser Thr
 225 230 235 240
 Glu Gly Arg Ser Lys Ala Ile Ser Thr Cys Ser Ser His Ile Ile Ala
 245 250 255
 Val Ser Ile Phe Phe Gly Ala Ser Ala Phe Met Tyr Leu Lys Pro Ser
 260 265 270
 Pro Val Gly Ser Val Gly Glu Asp Lys Val Ser Thr Val Phe Tyr Thr
 275 280 285
 Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys
 290 295 300
 Asp Val His Ile Ala Leu His Lys Thr Leu Lys Lys Ser Met Leu Ile
 305 310 315 320
 Xaa Ile Glu Thr Phe Phe
 325

<210> 2400

<211> 337

<212> PRT

<213> Mus musculus (M174 8576195-24-446-3721 1969-959)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400>2400

Leu Leu Phe Leu Gln Arg Pro Ser Met Lys Gln Met Ala Thr Lys Asn
 1 5 10 15
 Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Asp Gln Pro
 20 25 30
 Glu Leu Gln Leu Pro Leu Phe Phe Leu Phe Leu Leu Asn His Thr Val
 35 40 45
 Ile Val Val Gly Asn Leu Ser Leu Met Ser Leu Ile Ile Leu Asn Ser
 50 55 60
 Asn Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile
 65 70 75 80
 Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe
 85 90 95
 Val Ser Glu Lys Asn Ile Ile Pro Phe Thr Gly Cys Met Thr Gln Leu
 100 105 110
 Phe Phe Phe Cys Phe Phe Ala His Ser Glu Ser Trp Val Leu Thr Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys
 130 135 140
 Ala Ile Met Leu Pro Arg Ile Cys Cys Leu Leu Met Phe Val Ser Tyr

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145          150          155          160
Leu Ile Gly Phe Ala Ser Ala Met Val Leu Ala Gly Leu Met Ile Arg
          165          170          175
Leu Asn Phe Cys Asn Asn Asn Ile Ile Asn His Tyr Met Cys Asp Ile
          180          185          190
Phe Pro Val Leu Arg Ile Ser Cys Ser Asn Thr Tyr Leu Asn Glu Leu
          195          200          205
Val Ser Thr Ala Val Val Gly Thr Ala Ile Ile Leu Cys Ser Leu Ile
          210          215          220
Ile Phe Ile Ser Tyr Ala Met Ile Leu Phe Asn Ile Val His Met Ser
225          230          235          240
Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile
          245          250          255
Ile Thr Val Ser Phe Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys
          260          265          270
Pro Ser Ser Ala Glu Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe
          275          280          285
Tyr Thr Phe Leu Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Lys Val Ala Val Lys Lys Thr Ile Lys Arg Ile Thr
305          310          315          320
Ser Xaa Leu Lys Gln Phe Glu Leu Val Cys Phe His Phe Leu Ser Ile
          325          330          335
Ile

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<210> 2401

<211> 325

<212> PRT

<213> Mus musculus (M175 8576195-26-1-5230 3083-4056)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400>2401

```

Leu Phe Ser Ser Arg Phe Ser Met Ile Ser Met Leu Ala Gly Asn Gly
1          5          10          15
Ser Ser Val Thr Glu Phe Val Leu Ala Gly Leu Thr Asp Arg Pro Glu
          20          25          30
Leu Gln Leu Pro Leu Phe Tyr Leu Phe Leu Ile Ile Tyr Ile Ile Thr
          35          40          45
Val Val Gly Asn Leu Gly Leu Ile Ile Leu Ile Gly Leu Asn Pro His
          50          55          60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp
65          70          75          80
Leu Cys Tyr Ser Ser Val Phe Ser Pro Lys Met Leu Ile Asn Phe Val
          85          90          95
Ser Glu Lys Asn Ser Ile Ser Tyr Ala Gly Cys Met Thr Gln Leu Phe
          100          105          110
Leu Phe Leu Phe Phe Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met
          115          120          125
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val
          130          135          140
Thr Met Ser Pro Gln Ile Cys Ser Val Ile Ser Phe Ala Ala Tyr Gly
145          150          155          160
Met Gly Phe Ala Gly Ser Ser Ala His Thr Gly Cys Met Leu Arg Leu
          165          170          175
Thr Phe Cys Asn Val Asn Val Ile Asn His Tyr Leu Cys Asp Ile L u
          180          185          190

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Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val
 195 200 205
 Val Leu Ile Val Val Gly Ile Asn Ile Thr Val Pro Ser Phe Thr Ile
 210 215 220
 Leu Ile Ser Tyr Val Phe Ile Leu Ala Asn Ile Leu Asn Ile Lys Ser
 225 230 235 240
 Thr Gln Gly Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His Ile Met
 245 250 255
 Ala Ile Ser Leu Phe Phe Gly Ser Ala Ala Phe Met Tyr Leu Lys Tyr
 260 265 270
 Ser Ser Gly Ser Met Glu Gln Gly Lys Ile Ser Ser Val Phe Tyr Thr
 275 280 285
 Asn Val Gly Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 290 295 300
 Asp Val Lys Val Ala Leu Arg Lys Ser Leu Ile Lys Ile Gln Arg Lys
 305 310 315 320
 Asp Arg Phe Xaa Leu
 325

<210> 2402

<211> 204

<212> PRT

<213> Unknown (p124-dir-0-7 conceptual translation of range 2-613)

<400>2402

Phe Leu Glu Phe Ala Phe Thr Pro Ala Cys Ile Leu Arg Phe Pro Val
 1 5 10 15
 Thr Ile Val Thr Gly Asp Arg Thr Ile Ser Phe Ser Asn Cys Phe Phe
 20 25 30
 Phe Gln Leu Phe Phe Ile Phe Leu Gly Val Met Glu Phe Phe Leu Leu
 35 40 45
 Ala Pro Thr Ser Tyr Asp Cys Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 His Ser Thr Val Met Thr Arg Gly Val Cys Thr Leu Leu Val Leu Ser
 65 70 75 80
 Ser Phe Leu Ser Thr Tyr Leu Asn Leu Phe Pro Pro Val Val Met Asp
 85 90 95
 Phe Trp Leu Asp Cys Cys Asp Pro Asn Ile Leu Lys His Phe Ile Cys
 100 105 110
 Asp Ser Ser Ser Val Met Glu Leu Leu Cys Thr Asp Thr Arg Phe Leu
 115 120 125
 Glu Leu Met Thr Phe Pro Leu Ser Leu Val Leu Met Thr Ala Ser Tyr
 130 135 140
 Thr Ala Ile Ile Cys Ala Ile Leu Arg Leu Pro Tyr Ala Gln Gln Arg
 145 150 155 160
 Arg Lys Val Phe Ser Ile Cys Ser Ser His Arg Val Gly Phe Ser Ile
 165 170 175
 Thr Tyr Gly Ser Cys Ile Phe Met Tyr Ile Asn Thr Val Ala Asp Lys
 180 185 190
 Asp Arg Val Gly Val Arg Gln Gly Leu Gly Gly Pro
 195 200

<210> 2403

<211> 312

<212> PRT

<213> Unknown (OR2B8)

<400>2403

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Phe Leu

20 25 30
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
 35 40 45
 Ser His Leu Asp Pro His Leu His Asn Pro Met Tyr Phe Phe Phe Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
 65 70 75 80
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
 115 120 125
 Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
 130 135 140
 Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
 145 150 155 160
 Val Leu Ile Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
 165 170 175
 Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
 180 185 190
 Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
 195 200 205
 Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
 210 215 220
 Val Val Arg Ile Lys Ser Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
 245 250 255
 Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
 260 265 270
 Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
 290 295 300
 Leu Trp Lys Asn Tyr Asp Ser Arg
 305 310

<210> 2404

<211> 315

<212> PRT

<213> Unknown (OR12D3)

<400>2404

Met Glu Asn Val Thr Thr Met Asn Glu Phe Leu Leu Leu Gly Leu Thr
 1 5 10 15
 Gly Val Gln Glu Leu Gln Pro Phe Phe Gly Ile Phe Leu Ile Ile
 20 25 30
 Tyr Leu Ile Asn Leu Ile Gly Asn Gly Ser Ile Leu Val Met Val Val
 35 40 45
 Leu Glu Pro Gln Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Cys Leu Asp Ile Ser Tyr Ser Ser Val Thr Leu Pro Lys Leu Leu
 65 70 75 80
 Val Asn Leu Val Cys Ser Arg Arg Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Thr Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Ile Leu
 100 105 110
 Leu Ala Ile Met Ala Phe Asp Arg Phe Val Ala Ile Cys Asn Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Val Cys Ile Leu Leu Ala Ala

130	135	140
Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met		
145	150	155
Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe		160
	165	170
Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu		175
	180	185
Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala		190
	195	200
Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu		205
	210	215
Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys		220
225	230	235
Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe		240
	245	250
Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile		255
	260	265
Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile		270
	275	280
Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe		285
	290	295
Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His		300
305	310	315

<210> 2405

<211> 115

<212> PRT

<213> Unknown (3273654-dir-0-5 conceptual translation of range 1-345)

<400>2405

Leu Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ser Cys Ser Asn Thr
1 5 10 15
Phe Ser Asp Asn Ile Val Lys Tyr Phe Leu Gly Ala Leu Tyr Gly Leu
20 25 30
Phe Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Ile Ser Ser
35 40 45
Ile Leu Arg Ile Pro Ser Leu Gly Gly Lys Tyr Lys Ala Phe Ser Thr
50 55 60
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Leu Val Thr Ala Ser
65 70 75 80
Thr Val Tyr Leu Gly Ser Val Ala Ser His Ser Pro Arg Asn Asp Val
85 90 95
Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
100 105 110
Ile Cys Ser
115

<210> 2406

<211> 139

<212> PRT

<213> Unknown (3810857-dir-0-6 conceptual translation of range 1-417)

<220>

<221> VARIANT

<222> (1)...(139)

<223> Xaa = Any Amino Acid

<400>2406

Met Ala Xaa Asp Arg Phe Val Ala Ile Cys His Pro Leu Asn Tyr Thr
1 5 10 15
Val Ile Met Asn Pro Arg Ile Cys Gly Leu Leu Val Leu Leu Ser Trp

	20		25		30
Ile Ile Met Phe Trp Val Ser Leu Ile His Met Leu Leu Met Lys Gln					
35		40		45	
Leu Asn Phe Ser Thr Ser Thr Glu Ile Pro His Phe Phe Cys Glu Leu					
50		55		60	
Thr Glu Leu Leu Arg Val Gly Arg Ser Asp Thr Phe Thr Gln Asn Ile					
65		70		75	80
Phe Leu Tyr Leu Gly Tyr Cys Arg Ala Gly Met Phe Pro Val Ile Gly					
	85		90		95
Ile Ala Phe Ser Tyr Phe His Ile Val Ser Ala Leu Met Lys Met Ser					
	100		105		110
Ser Ile Lys Asn Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu					
	115		120		125
Cys Val Val Ser Met Phe Tyr Gly Thr Gly Leu					
130		135			

<210> 2407

<211> 211

<212> PRT

<213> Unknown (p106-dir-0-8 conceptual translation of range 2-633)

<220>

<221> VARIANT

<222> (1)...(211)

<223> Xaa = Any Amino Acid

<400>2407

Leu Val Asp Leu Cys Leu Val Thr Thr Leu Val Pro Lys Met Leu Val	
1	5 10 15
Asn Leu Leu Thr His Ser Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr	
	20 25 30
Gln Met Phe Phe Phe Met Val Phe Ala Cys Ser Asn Thr Leu Leu Leu	
	35 40 45
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Pro Leu Ser	
	50 55 60
Tyr Val Thr Ile Met Arg Pro Gln Phe Cys Gly Leu Leu Ala Leu Leu	
	65 70 75 80
Ser Trp Thr Ile Ser Leu Leu Asn Ala Val Leu His Ser Pro Leu Val	
	85 90 95
Met Arg Leu Leu Phe Cys Thr Glu Arg Glu Ile Pro Leu Phe Tyr His	
	100 105 110
Asp Leu Thr Xaa Val Leu Arg Leu Ser Cys Thr Asp Met Leu Ile Asn	
	115 120 125
Asp Ile Leu Val Tyr Leu Leu Thr Ala Leu Leu Ser Ile Phe Pro Phe	
	130 135 140
Thr Gly Ile Leu Phe Ser Tyr Thr Gln Ile Cys Ser Ser Ile Val Lys	
	145 150 155 160
Ile Pro Ser Thr Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser	
	165 170 175
Tyr Leu Cys Val Val Leu Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr	
	180 185 190
Leu Ser Ser Ser Val Thr Lys Ser Ser Trp Lys Ser Ser Val Ala Ser	
	195 200 205
Val Ile Cys	
210	

<210> 2408

<211> 159

<212> PRT

<213> Unknown (4877338-dir-0-6 conceptual translation of range 2-478)

<220>

<221> VARIANT

<222> (1)...(159)

<223> Xaa = Any Amino Acid

<400>2408

```

Ile Cys His Pro Leu Arg Tyr Thr Val Ser Met Asn Pro Arg Leu Cys
 1              5              10              15
Val Gln Leu Ile Leu Leu Ser Leu Phe Ile Ser Ile Ala Asp Ala Leu
              20              25              30
Leu His Ser Leu Met Val Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu
              35              40              45
Ile Ser Leu Phe Cys Glu Val Val Gln Val Ile Lys Arg Ala Cys Ser
 50              55              60
Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Phe Ala Ala Gly Ile Phe
65              70              75              80
Ala Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ile Gln Ile Val
              85              90              95
Ser Ser Ile Leu Xaa Met Pro Ser Ser Gly Arg Lys Xaa Lys Ala Phe
              100             105             110
Ser Thr Cys Glu Ser His Leu Ser Val Val Ser Phe Phe Tyr Gly Thr
              115             120             125
Ala Phe Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser Ser Arg Lys
              130             135             140
Thr Ala Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Val Met
145             150             155

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<210> 2409

<211> 310

<212> PRT

<213> Unknown (p22-dir-0-11 conceptual translation of range 1-930)

<400>2409

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1              5              10              15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
              20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
              35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50              55              60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65              70              75              80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
              85              90              95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
              100             105             110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
              115             120             125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
              130             135             140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
145             150             155             160
Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
              165             170             175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
              180             185             190
His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
              195             200             205
Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
210             215             220

```

Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Ph Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg
 305 310

<210> 2410

<211> 310

<212> PRT

<213> Unknown (p23-dir-0-11 conceptual translation of range 1-930)

<400>2410

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg
 305 310

<210> 2411

<211> 215

<212> PRT

<213> Unknown (p139-dir-0-8 conceptual translation f range 2-646)

<400>2411

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
          35          40          45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
          50          55          60
Cys Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Ser Leu
65          70          75          80
Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Phe Leu Leu
          85          90          95
Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys
          100          105          110
Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr His Ile Ile
          115          120          125
His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
          130          135          140
Gly Phe Met Thr Lys Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
145          150          155          160
Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser
          165          170          175
His Leu Gly Val Val Ser Leu Phe Tyr Gly Met Leu Ala Met Val Tyr
          180          185          190
Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
          195          200          205
Met Tyr Ala Val Val Thr Pro
          210          215

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<210> 2412

<211> 312

<212> PRT

<213> Unknown (p182-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2412

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125

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Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu
 290 295 300
 Arg Arg Leu Phe Gln Arg Pro Lys
 305 310

<210> 2413

<211> 312

<212> PRT

<213> Unknown (p184-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2413

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His His
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu

195	200	205
Thr Pro Leu Gly Phe Met Thr Thr Ser His Val Cys Ile Val Arg Thr		
210	215	220
Ile Leu Gln Ile Pro S r Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala		
245	250	255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val		
260	265	270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
275	280	285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu		
290	295	300
Arg Arg Leu Phe Gln Arg Pro Lys		
305	310	

<210> 2414

<211> 312

<212> PRT

<213> Unknown (p183-dir-0-11 conceptual translation of range 1-936)

<400>2414

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly	
1	5
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu	
20	25
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala	
35	40
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala	
50	55
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys	
65	70
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly	
85	90
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn	
100	105
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys	
115	120
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu	
130	135
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr	
145	150
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr	
165	170
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr	
180	185
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu	
195	200
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr	
210	215
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr	
225	230
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala	
245	250
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val	
260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile	
275	280
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu	
290	295
Arg Arg Leu Phe Gln Arg Pro Lys	

305

310

<210> 2415

<211> 312

<212> PRT

<213> Unknown (p186-dir-0-11 conceptual translation of range 1-936)

<400>2415

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr
145          150          155          160
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
          165          170          175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
          180          185          190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
          210          215          220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
          245          250          255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
          260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
          275          280          285
His Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu
          290          295          300
Arg Arg Leu Phe Gln Arg Pro Lys
305          310

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<210> 2416

<211> 215

<212> PRT

<213> Unknown (p140-dir-0-8 conceptual translation of range 2-646)

<400>2416

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
          35          40          45

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Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu
 65 70 75 80
 Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr Leu Leu
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Phe Phe Cys
 100 105 110
 Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
 130 135 140
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Cys
 180 185 190
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2417

<211> 215

<212> PRT

<213> Unknown (p141-dir-0-8 conceptual translation of range 2-646)

<400>2417

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Asn Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Lys Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu
 65 70 75 80
 Gly Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys
 100 105 110
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
 130 135 140
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
 145 150 155 160
 Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Tyr
 180 185 190
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2418

<211> 312

<212> PRT

<213> Unknown (p187-dir-0-11 conceptual translation of range 1-936)

<400>2418

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Glu
      85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
      130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
      145          150          155          160
Leu Leu Met Asn Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
      165          170          175
Leu Phe Cys Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr
      180          185          190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
      195          200          205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val His Ile Val Arg Thr
      210          215          220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
      225          230          235          240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
      245          250          255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
      260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Val Leu Gly Arg Val Leu
      290          295          300
Gly Arg Pro Phe Gln Arg Pro Lys
      305          310

```

<210> 2419

<211> 211

<212> PRT

<213> Unknown (p167-dir-0-8 conceptual translation of range 2-634)

<400>2419

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1           5           10           15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
      20           25           30
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
      35           40           45
Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr
      50           55           60
Val Thr Ala Met Ser Pro Gly Leu Cys Val L u Leu Leu Cys Leu Cys
      65           70           75           80
Trp Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met Thr Thr Val

```

85								90				95			
Thr	Phe	Cys	Gly	Ser	Arg	Lys	Ile	His	Tyr	Leu	Phe	Cys	Glu	Met	Tyr
100								105				110			
Val	Leu	Leu	Arg	Leu	Ala	Cys	Ser	Asn	Thr	His	Ile	Ile	His	Thr	Val
115								120				125			
Leu	Val	Ala	Thr	Gly	Cys	Phe	Phe	Leu	Thr	Pro	Leu	Gly	Phe	Thr	Thr
130								135				140			
Thr	Ser	Tyr	Val	Arg	Ile	Val	Arg	Thr	Ile	Leu	Gln	Ile	Pro	Ser	Val
145								150				155			
Pro	Lys	Lys	Tyr	Lys	Thr	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Gly	Val
165								170				175			
Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu	Val	Met	Val	Tyr	Leu	Gln	Pro	Leu
180								185				190			
His	Thr	Tyr	Ser	Met	Lys	Asp	Ser	Val	Ala	Thr	Val	Met	Tyr	Ala	Val
195								200				205			
Val	Thr	Pro													
210															

<210> 2420

<211> 210

<212> PRT

<213> Unknown (p168-dir-0-8 conceptual translation of range 2-632)

<400>2420

[illegible]

<210> 2421

<211> 313

<212> PRT

<213> Unknown (p145-dir-0-11 conceptual translation of range 1-937)

<400>2421

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
1 5 10 15

Ile Ser Glu Ser Pro Glu Gln Gln Gln Met Leu Ph Trp Met Phe Leu
 20 25 30
 Val Arg Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Asn Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
 165 170 175
 Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
 180 185 190
 His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
 210 215 220
 Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
 245 250 255
 Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
 290 295 300
 Gln Gly Lys Ala Phe Gln Lys Leu Thr
 305 310

<210> 2422

<211> 214

<212> PRT

<213> Unknown (3831606-dir-0-8 conceptual translation of range 2-642)

<400>2422

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu
 65 70 75 80
 Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
 85 90 95
 Thr Arg Val Thr Ph Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
 100 105 110
 Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
 115 120 125

His Thr Val Leu Val Ala Thr Gly Cys Ph Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 2423

<211> 319

<212> PRT

<213> Unknown (p35-dir-0-11 conceptual translation of range 1-954)

<400>2423

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ser Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
 165 170 175
 Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
 180 185 190
 His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala
 210 215 220
 Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Ser Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Leu Gly
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Asn Leu Gln Pro Leu Gln Thr Tyr
 260 265 270
 Ser Met Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro
 275 280 285
 Met Ile Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met His Gly
 290 295 300
 Ala Leu Gly Arg Leu Arg Gln Gly Lys Ala Phe Gln Lys Leu Thr
 305 310 315

<210> 2424

<211> 313

<212> PRT

<213> Unknown (p34-dir-0-11 conceptual translation of range 1-937)

<400>2424

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20          25          30
Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65          70          75          80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85          90          95
Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100         105         110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115         120         125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
 130         135         140
Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
 145         150         155         160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
 165         170         175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
 180         185         190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195         200         205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala
 210         215         220
Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
 225         230         235         240
Cys Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Val Gly
 245         250         255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
 260         265         270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
 275         280         285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
 290         295         300
Gln Gly Lys Ala Phe Gln Lys Leu Thr
305          310

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<210> 2425

<211> 313

<212> PRT

<213> Unknown (p87-dir-0-11 conceptual translation of range 1-937)

<400>2425

```

Met Asp Gly Asp Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Arg Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Phe Ile Ile Leu Ala
 35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50          55          60
Asn Phe Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys

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65 70 75 80
 Met Pro Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Pro Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Met Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
 165 170 175
 Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
 180 185 190
 His Val Asn His Thr Val Leu Val Ala Met Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
 210 215 220
 Ile Leu Gln Ile Pro Pro Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
 245 250 255
 Ile Val Tyr Leu Gln Pro Pro Gln Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Val Val Val Thr Pro Met Ile Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Asp Leu Gly Arg Leu Arg
 290 295 300
 Gln Gly Lys Ala Phe Gln Lys Leu Thr
 305 310

<210> 2426

<211> 313

<212> PRT

<213> Unknown (p136-dir-0-11 conceptual translation of range 1-939)

<400>2426

Met Asp Gly Gly Asn Gln Ser Lys Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Ala Leu Ile Ile Leu Ala
 35 40 45
 Ile Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Val
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ala Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Phe Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Leu Phe Cys Glu Met Tyr Val Leu Leu Gln Leu Ala Cys Ser Asn Ile

180	185	190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu		
195	200	205
Ile Pro Leu Gly Phe Met Il Thr Ser Tyr Ala Arg Ile Val Arg Ala		
210	215	220
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly		
	245	250
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val		
	260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
	275	280
Tyr Ser Leu Lys Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu		
	290	295
Gln Gly Lys Ala Phe Trp Lys Leu Thr		300
305	310	

<210> 2427

<211> 313

<212> PRT

<213> Unknown (p163-dir-0-11 conceptual translation of range 1-939)

<400>2427

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly		
1	5	10
Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu		
	20	25
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala		
	35	40
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala		
	50	55
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys		
65	70	75
Met Leu Val Asn Leu Gln Ser Gln Asp Lys Ala Ile Ser Tyr Ala Gly		
	85	90
Cys Leu Thr Gln Leu Tyr Phe Leu Leu Ser Leu Val Thr Leu Asp Asn		
	100	105
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys		
	115	120
Pro Leu His Tyr Val Thr Ala Met Ser Pro Arg Leu Cys Ile Leu Leu		
	130	135
Leu Ser Leu Cys Trp Val Phe Ser Val Leu Tyr Gly Leu Ile His Thr		
145	150	155
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr		
	165	170
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile		
	180	185
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu		
	195	200
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala		
	210	215
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly		
	245	250
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Thr Lys Asp Ser Val		
	260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
	275	280
Tyr Ser Leu Arg Asn Lys Asp Ile His Gly Ala Leu Gly Arg Leu Leu		
		285

290 295 300
 Gln Gly Lys Ala Ph Gln Lys Leu Thr
 305 310

<210> 2428

<211> 312

<212> PRT

<213> Unknown (p18-dir-0-11 conceptual translation of range 1-936)

<400>2428

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 2429

<211> 312

<212> PRT

<213> Unknown (p32-dir-0-11 conceptual translation of range 1-936)

<400>2429

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30

Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Ile Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Phe Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Thr His Phe Lys Arg Leu Thr
 305 310

<210> 2430

<211> 312

<212> PRT

<213> Unknown (p130-dir-0-11 conceptual translation of range 1-936)

<400>2430

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140

Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Thr Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Leu Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 2431

<211> 215

<212> PRT

<213> Unknown (p143-dir-0-8 conceptual translation of range 2-646)

<400>2431

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Ser Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Pro Gly Cys Leu Thr
 20 25 30
 Gln Leu Phe Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ile Leu
 65 70 75 80
 Cys Trp Ala Leu Ser Ile Leu Tyr Gly Leu Ile His Thr Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
 100 105 110
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Asn
 115 120 125
 His Met Met Leu Ile Ala Thr Gly Cys Phe Val Phe Leu Val Pro Phe
 130 135 140
 Gly Phe Met Ile Met Ser Tyr Ile Cys Ile Val Arg Ala Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Ser Asn Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ala Leu Phe Tyr Gly Thr Leu Cys Met Val Tyr
 180 185 190
 Leu Lys Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2432

<211> 312

<212> PRT

<213> Unknown (p89-dir-0-11 conceptual translation of range 1-935)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2432

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
          20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
          35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
          85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
          100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
          130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn
          165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
          180          185          190
Arg Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Pro Val
          195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
          210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Cys Phe Val Tyr Gly Thr Val Met Gly
          245          250          255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
          260          265          270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
          290          295          300
Lys Arg Ile Ser Ser Xaa Pro Met
305          310

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<210> 2433

<211> 312

<212> PRT

<213> Unknown (p88-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2433

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly

```

```

1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Ph Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
180          185          190
His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
245          250          255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
260          265          270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
290          295          300
Lys Arg Ile Ser Ser Xaa Pro Met
305          310

```

<210> 2434

<211> 312

<212> PRT

<213> Unknown (p33-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2434

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Ile Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80

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Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
 145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Gly Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Asp Tyr Gly Thr Val Lys Gly
 245 250 255
 Lys Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
 290 295 300
 Lys Arg Ile Ser Ser Xaa Pro Met
 305 310

<210> 2435

<211> 312

<212> PRT

<213> Unknown (p43-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2435

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
 20 25 30
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
 35 40 45
 Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr

145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Il
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
 245 250 255
 Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn
 290 295 300
 Lys Arg Ile Ser Ser Xaa Pro Met
 305 310

<210> 2436

<211> 309

<212> PRT

<213> Unknown (p180-dir-0-11 conceptual translation of range 1-927)

<400>2436

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
 20 25 30
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
 35 40 45
 Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
 145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
 245 250 255
 Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Il Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
 20 25 30
 Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
 65 70 75 80
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
 85 90 95
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
 100 105 110
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
 115 120 125
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
 130 135 140
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
 145 150 155 160
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
 180 185 190
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
 195 200 205
 Tyr Thr Ala Val Thr Pro
 210

<210> 2439

<211> 214

<212> PRT

<213> Unknown (p191-dir-0-8 conceptual translation of range 2-643)

<400>2439

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
 20 25 30
 Gln Met Tyr Phe Met Ile Gly Leu Ala Asn Thr Asp Ser Tyr Ile Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
 65 70 75 80
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
 85 90 95
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
 100 105 110
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
 115 120 125
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
 130 135 140
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
 145 150 155 160
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
 180 185 190
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
 195 200 205

Tyr Thr Ala Val Thr Pro
210

<210> 2440

<211> 222

<212> PRT

<213> Unknown (3983387-dir-0-8 conceptual translation of range 1-666)

<400>2440

Ala	Asn	Leu	Ser	Phe	Val	Asp	Val	Cys	Phe	Thr	Thr	Asn	Leu	Ile	Pro
1				5					10					15	
Arg	Leu	Leu	Ala	Gly	His	Val	Ala	Gly	Thr	Arg	Thr	Ile	Ser	Tyr	Val
			20					25					30		
His	Cys	Leu	Thr	Gln	Thr	Tyr	Phe	Leu	Ile	Ser	Phe	Ala	Asn	Val	Asp
			35				40					45			
Thr	Phe	Leu	Leu	Ala	Ala	Met	Ala	Leu	Asp	Arg	Phe	Val	Ala	Ile	Cys
			50			55					60				
Tyr	Pro	Leu	Gln	Tyr	His	Thr	Ile	Ile	Thr	Pro	Gln	Leu	Cys	Val	Gly
65					70				75					80	
Leu	Ala	Ala	Val	Val	Trp	Met	Cys	Ser	Ala	Leu	Ile	Ser	Leu	Met	His
			85					90					95		
Thr	Leu	Leu	Met	Ser	Arg	Leu	Ser	Phe	Cys	Ser	Ser	Ile	Pro	Glu	Ile
			100					105					110		
Ser	His	Phe	Tyr	Cys	Asp	Ala	Tyr	Leu	Leu	Met	Lys	Leu	Ala	Cys	Ser
			115				120					125			
Asp	Thr	Arg	Val	Asn	Gln	Leu	Val	Phe	Leu	Gly	Ala	Val	Val	Leu	Phe
			130			135					140				
Val	Ala	Pro	Cys	Ile	Leu	Ile	Val	Val	Ser	Tyr	Val	Arg	Ile	Thr	Met
145					150					155				160	
Val	Val	Leu	Gln	Ile	Pro	Ser	Ala	Lys	Gly	Arg	His	Lys	Thr	Phe	Ser
			165					170						175	
Thr	Cys	Ser	Ser	His	Leu	Ser	Val	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Val
			180					185					190		
Leu	Gly	Ile	Tyr	Ile	Arg	Pro	Pro	Asp	Ser	Phe	Ser	Thr	Gln	Asp	Thr
			195			200						205			
Val	Ala	Thr	Ile	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn		
			210			215						220			

<210> 2441

<211> 314

<212> PRT

<213> Unknown (205837-dir-0-11 conceptual translation of range 1-942)

<400>2441

Met	Thr	Arg	Arg	Asn	Gln	Thr	Ala	Ile	Ser	Gln	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Leu	Pro	Phe	Pro	Pro	Glu	Tyr	Gln	His	Leu	Phe	Tyr	Ala	Leu	Phe	Leu
			20					25					30		
Ala	Met	Tyr	Leu	Thr	Thr	Leu	Leu	Gly	Asn	Leu	Ile	Ile	Ile	Ile	Leu
			35				40					45			
Ile	Leu	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser
			50			55					60				
Asn	Leu	Ser	Phe	Ala	Asp	Leu	Cys	Phe	Ser	Ser	Val	Thr	Met	Pro	Lys
65					70					75				80	
Leu	Leu	Gln	Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile	Pro	Tyr	Ala	Gly
			85					90					95		
Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Leu	Gly	Asn
			100					105					110		
Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe
			115				120					125			
Pro	Leu	His	Tyr	Met	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Val	Ser	Leu

130	135	140
Val Val Leu Ser Trp	Val Leu Thr Thr Phe His Ala Met Leu His Thr	
145	150	155
Leu Leu Met Ala Arg	Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His	160
	165	170
Tyr Phe Cys Asp Met	Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr	175
	180	185
His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val		190
	195	200
Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser		205
	210	215
Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr		220
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		240
	245	250
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr		255
	260	265
Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile		285
	290	295
Met Cys Lys Lys Gln Ile Pro Ser Phe Leu		300
305	310	

<210> 2442

<211> 221

<212> PRT

<213> Unknown (3769630-dir-0-8 conceptual translation of range 1-663)

<400>2442

Leu Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro	
1	5
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala	10
	15
	20
Gly Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly	25
	30
	35
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys	40
	45
	50
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser	55
65	60
	65
Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His	70
	75
	80
Thr Leu Leu Met Ala Arg Leu Ser Phe Arg Glu Asp Ser Val Ile Pro	85
	90
	95
His Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Pro Asp	100
	105
	110
Thr His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val	115
	120
	125
Val Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser	130
145	135
	140
Ser Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser	145
	150
	155
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Ile Tyr Gly Thr Val	160
	165
	170
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu	175
	180
	185
Thr Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met	190
	195
	200
	205
	210
	215
	220

<210> 2443

<211> 314

<212> PRT

<213> Unknown (1504111-dir-0-11 conceptual translation of range 1-942)

<400>2443

```

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
          20           25           30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35           40           45
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65           70           75           80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
          85           90           95
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
          130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
          195          200          205
Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
          210          215          220
Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Arg Ile
          290          295          300
Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
305           310

```

<210> 2444

<211> 221

<212> PRT

<213> Unknown (3769633-dir-0-8 conceptual translation of range 1-663)

<400>2444

```

Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
 1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
          20           25           30
Gly Cys Leu Ser Gln Ile Tyr Phe Leu Phe Phe Gly Asp Leu Gly
          35           40           45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50           55           60
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
65           70           75           80

```

```

Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
      85                      90                      95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro
      100                      105                      110
His Phe Phe Cys Asp Thr Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
      115                      120                      125
Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu
      130                      135                      140
Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser
      145                      150                      155                      160
Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Glu Ala Phe Ser
      165                      170                      175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val
      180                      185                      190
Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu
      195                      200                      205
Thr Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met
      210                      215                      220

```

<210> 2445

<211> 221

<212> PRT

<213> Unknown (3769632-dir-0-8 conceptual translation of range 1-663)

<400>2445

```

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
  1                      5                      10                      15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Val
      20                      25                      30
Gly Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly
      35                      40                      45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys
      50                      55                      60
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
      65                      70                      75                      80
Leu Val Val Leu Ser Trp Val Arg Thr Thr Phe His Ala Met Leu His
      85                      90                      95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro
      100                      105                      110
His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
      115                      120                      125
Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu
      130                      135                      140
Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser
      145                      150                      155                      160
Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser
      165                      170                      175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val
      180                      185                      190
Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu
      195                      200                      205
Thr Val Met Ser Leu Met Tyr Thr Ala Val Thr Pro Met
      210                      215                      220

```

<210> 2446

<211> 157

<212> PRT

<213> Unknown (902347-dir-0-6 conceptual translation of range 2-472)

<400>2446

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys

```

1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile His Val Ile Pro Leu Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

```

<210> 2447

<211> 157

<212> PRT

<213> Unknown (902682-dir-0-6 conceptual translation of range 2-472)

<400>2447

```

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys
1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile Leu Val Ile Pro Phe Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

```

<210> 2448

<211> 221

<212> PRT

<213> Unknown (3769627-dir-0-8 conceptual translation of range 1-663)

<400>2448

```

Gly Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu
35           40           45
Ser Phe Leu Leu Glu Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys
50           55           60

```

```

Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
65          70          75          80
Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
          85          90          95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro
          100         105         110
His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp
          115         120         125
Thr His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile
          130         135         140
Val Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala
145         150         155         160
Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser
          165         170         175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
          180         185         190
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu
          195         200         205
Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
          210         215         220

```

<210> 2449

<211> 221

<212> PRT

<213> Unknown (3769629-dir-0-8 conceptual translation of range 1-663)

<220>

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400>2449

```

Ser Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
1          5          10          15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
          20          25          30
Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu
          35          40          45
Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
          50          55          60
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
65          70          75          80
Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
          85          90          95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro
          100         105         110
His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp
          115         120         125
Arg His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile
          130         135         140
Val Ile Pro Phe Val Leu Ile Ile Val Ser Xaa Ala Arg Val Val Ala
145         150         155         160
Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser
          165         170         175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
          180         185         190
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu
          195         200         205
Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
          210         215         220

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<210> 2450

<211> 314

<212> PRT

<213> Unknown (205845-dir-0-11 conceptual translation of range 1-942)

<400>2450

Met	Thr	Glu	Glu	Asn	Gln	Thr	Val	Ile	Ser	Gln	Phe	Leu	Leu	Leu	Phe
1				5					10					15	
Leu	Pro	Ile	Pro	Ser	Glu	His	Gln	His	Val	Phe	Tyr	Ala	Leu	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Thr	Thr	Val	Leu	Gly	Asn	Leu	Ile	Ile	Ile	Ile	Leu
		35					40					45			
Ile	His	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser
	50					55					60				
Asn	Leu	Ser	Phe	Ser	Asp	Leu	Cys	Phe	Ser	Ser	Val	Thr	Met	Pro	Lys
65					70					75					80
Leu	Leu	Gln	Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile	Pro	Phe	Ala	Gly
			85						90					95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Tyr	Leu	Tyr	Phe	Ala	Asp	Leu	Glu	Ser
			100					105					110		
Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe
			115					120					125		
Pro	Leu	His	Tyr	Met	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Val	Ser	Leu
	130					135					140				
Val	Val	Leu	Ser	Trp	Val	Leu	Thr	Thr	Phe	His	Ala	Met	Leu	His	Thr
145					150					155					160
Leu	Leu	Met	Ala	Arg	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Met	Ile	Pro	His
			165						170					175	
Phe	Phe	Cys	Asp	Ile	Ser	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr
			180					185					190		
His	Val	Asn	Glu	Leu	Val	Ile	Phe	Val	Met	Gly	Gly	Leu	Val	Ile	Val
	195					200						205			
Ile	Pro	Phe	Val	Leu	Ile	Ile	Val	Ser	Tyr	Ala	Arg	Val	Val	Ala	Ser
	210				215						220				
Ile	Leu	Lys	Val	Pro	Ser	Val	Arg	Gly	Ile	His	Lys	Ile	Phe	Ser	Thr
225					230					235					240
Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Ile
			245						250					255	
Gly	Leu	Tyr	Leu	Cys	Pro	Ser	Ala	Asn	Asn	Ser	Thr	Val	Lys	Glu	Thr
			260					265					270		
Val	Met	Ala	Met	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe
			275				280						285		
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Met	Lys	Glu	Ala	Leu	Ile	Arg	Val
	290					295						300			
Leu	Cys	Lys	Lys	Lys	Ile	Thr	Phe	Cys	Leu						
305					310										

<210> 2451

<211> 192

<212> PRT

<213> Unknown (2921663-dir-1-7 conceptual translation of range 101-676)

<400>2451

Met	Tyr	Phe	Phe	Leu	Tyr	Phe	Thr	Asp	Leu	Glu	Ser	Phe	Leu	Leu	Val
1				5					10					15	
Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Met	His	Tyr
			20					25					30		
Thr	Ala	Ile	Cys	Phe	Leu	Leu	His	Tyr	Thr	Ala	Ile	Met	Ser	Pro	Met
		35					40					45			
Leu	Cys	Leu	Ser	Val	Val	Ala	Leu	Ser	Trp	Val	Leu	Thr	Thr	Phe	His
	50					55						60			

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 65 70 75 80
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 85 90 95
 Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 100 105 110
 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 115 120 125
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 130 135 140
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 145 150 155 160
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
 165 170 175
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 180 185 190

<210> 2452

<211> 323

<212> PRT

<213> Unknown (p25-dir-0-11 conceptual translation of range 1-969)

<400>2452

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
 130 135 140
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
 145 150 155 160
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
 165 170 175
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
 195 200 205
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
 210 215 220
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
 225 230 235 240
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300

Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
 305 310 315 320
 Phe Leu Leu

<210> 2453

<211> 314

<212> PRT

<213> Unknown (p181-dir-0-11 conceptual translation of range 1-942)

<400>2453

Met Met Glu Gln Asn Gln Thr Ser Thr Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Ile
 305 310

<210> 2454

<211> 149

<212> PRT

<213> Unknown (p166-dir-0-6 conceptual translation of range 2-448)

<400>2454

Ph Ser Asp Leu Cys Phe Ser Ser Val Thr Il Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Val Asp Cys Leu Thr

20 25 30
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pr Leu His
 50 55 60
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
 65 70 75 80
 Ser Trp Val Leu Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Val Pro His Phe Phe Cys
 100 105 110
 Asp Met Pro Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
 115 120 125
 Glu Ser Gly Ile Phe Ile Thr Gly Gly Leu Ile Leu Gly Ile Pro Phe
 130 135 140
 Leu Leu Ile Leu Gly
 145

<210> 2455

<211> 314

<212> PRT

<213> Unknown (p17-dir-0-11 conceptual translation of range 1-942)

<400>2455

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu S r Arg Val

290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2456

<211> 314

<212> PRT

<213> Unknown (p90-dir-0-11 conceptual translation of range 1-942)

<400>2456

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met His Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Phe Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu
 305 310

<210> 2457

<211> 314

<212> PRT

<213> Unknown (p175-dir-0-11 conceptual translation of range 1-942)

<400>2457

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30

Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pr Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Ile Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2458

<211> 314

<212> PRT

<213> Unknown (p170-dir-0-11 conceptual translation of range 1-942)

<400>2458

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu
 130 135 140

Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu
 305 310

<210> 2459

<211> 314

<212> PRT

<213> Unknown (p31-dir-0-11 conceptual translation of range 1-942)

<400>2459

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Ala Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255

Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Asp Met Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2460

<211> 324

<212> PRT

<213> Unknown (890-dir-5-12 conceptual translation of range 642-1613)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400>2460

Arg Gln Ser Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val
 1 5 10 15
 Leu Leu Gly Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala
 20 25 30
 Leu Phe Leu Ala Met Tyr Val Thr Thr Ile Leu Gly Asn Leu Leu Ile
 35 40 45
 Ile Val Leu Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Leu
 50 55 60
 Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr
 65 70 75 80
 Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro
 85 90 95
 Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp
 100 105 110
 Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Phe Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Leu Cys
 130 135 140
 Phe Ser Leu Leu Val Leu Ser Trp Val Leu Thr Met Phe His Ala Val
 145 150 155 160
 Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asn Thr Ile
 165 170 175
 Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser
 180 185 190
 Asp Thr Gln Val Asn Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile
 195 200 205
 Leu Val Ile Pro Phe Leu Leu Ile Ile Thr Ser Tyr Ala Arg Ile Val
 210 215 220
 Ser Ser Ile Leu Lys Val Pro Ser Ala Ile Gly Ile Cys Lys Val Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr
 245 250 255
 Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys
 260 265 270
 Glu Thr Ile Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg
 290 295 300
 Arg Val Ile Cys Arg Lys Lys Ile Thr Phe Ser Val Xaa Trp Xaa His
 305 310 315 320
 Leu Ile Leu Leu

<210> 2461

<211> 162

<212> PRT

<213> Unknown (4877306-dir-0-6 conceptual translation of range 2-487)

<400>2461

Val	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg
1				5					10					15	
Leu	Cys	Leu	Phe	Leu	Val	Leu	Leu	Pro	Trp	Ile	Leu	Thr	Thr	Phe	His
		20						25					30		
Ala	Met	Leu	His	Thr	Leu	Leu	Met	Ala	Arg	Leu	His	Phe	Cys	Glu	Asp
		35					40					45			
Asn	Val	Ile	Pro	His	Phe	Phe	Cys	Asp	Ser	Ser	Ala	Leu	Leu	Lys	Leu
	50					55					60				
Ser	Cys	Ser	Asp	Thr	Arg	Val	Asn	Glu	Leu	Val	Ile	Phe	Phe	Val	Gly
65				70					75					80	
Gly	Leu	Ile	Ile	Ile	Ile	Pro	Phe	Leu	Leu	Ile	Ile	Met	Ser	Tyr	Ala
			85					90					95		
Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys	Val	Pro	Ser	Ala	Lys	Gly	Ile	Cys
		100						105					110		
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Leu	Phe
		115					120					125			
Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr	Leu	Cys	Pro	Ser	Ala	His	Asn	Ser
	130					135					140				
Thr	Val	Lys	Glu	Thr	Val	Met	Ser	Met	Met	Tyr	Thr	Val	Val	Ala	Pro
145					150					155					160
Met	Leu														

<210> 2462

<211> 216

<212> PRT

<213> Unknown (p194-dir-0-8 conceptual translation of range 2-649)

<400>2462

Phe	Thr	Asp	Leu	Cys	Phe	Ser	Thr	Val	Thr	Met	Pro	Asn	Phe	Leu	Gln
1				5					10					15	
Asn	Met	Gln	Ser	Gln	Val	Ser	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ala
		20						25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Val	Glu	Ser	Leu	Leu	Leu
		35					40					45			
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His
	50					55					60				
Tyr	Thr	Arg	Ile	Met	Ser	Pro	Asn	Leu	Cys	Val	Ser	Met	Val	Leu	Leu
65				70					75					80	
Ser	Trp	Ala	Leu	Thr	Leu	Cys	Ala	Met	Leu	His	Thr	Leu	Leu	Leu	
			85					90					95		
Thr	Arg	Leu	Ser	Phe	Cys	Lys	Asn	Asn	Val	Ile	Pro	His	Phe	Phe	Cys
		100						105					110		
Asp	Leu	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ile	His	Ile	Asn
		115					120					125			
Glu	Leu	Met	Ile	Met	Ile	Ile	Gly	Ala	Leu	Val	Val	Ile	Leu	Pro	Phe
	130					135					140				
Leu	Leu	Ile	Ile	Val	Ser	Tyr	Ala	His	Ile	Val	Ser	Ser	Ile	Leu	Lys
145					150					155					160
Val	Pro	Ser	Thr	Arg	Gly	Ile	His	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser
				165				170						175	
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Ser	Val	Ile	Val	Leu	Tyr
			180					185						190	

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2463

<211> 157

<212> PRT

<213> Unknown (902674-dir-0-6 conceptual translation of range 2-472)

<400>2463

Ile Cys Phe Pro Leu His Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys
 1 5 10 15
 Val Ser Met Val Leu Leu Ser Trp Ala Leu Thr Thr Leu Cys Ala Met
 20 25 30
 Leu Arg Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Lys Asn Asn Val
 35 40 45
 Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys
 50 55 60
 Ser Asp Ile His Ile Asn Glu Leu Met Ile Met Ile Ile Gly Ala Leu
 65 70 75 80
 Val Val Ile Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala His Ile
 85 90 95
 Val Ser Ser Ile Leu Lys Val Pro Ser Thr Arg Gly Ile His Lys Val
 100 105 110
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
 115 120 125
 Ser Val Ile Val Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val
 130 135 140
 Lys Asp Thr Val Met Ser Met Met Tyr Thr Val Val Thr
 145 150 155

<210> 2464

<211> 216

<212> PRT

<213> Unknown (p197-dir-0-8 conceptual translation of range 2-649)

<220>

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400>2464

Phe Thr Asp Leu Xaa Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80
 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
 85 90 95
 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
 115 120 125
 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
 130 135 140

Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile S r S r Ile Leu Lys
 145 150 155 160
 Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2465

<211> 216

<212> PRT

<213> Unknown (p195-dir-0-8 conceptual translation of range 2-650)

<400>2465

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Leu
 1 5 10 15
 Asn Met Gln Ser Gln Ile Pro Ser Ile Ser Tyr Ala Ser Cys Leu Ala
 20 25 30
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Ala Leu Glu Asn Phe Leu Leu
 35 40 45
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Met Val Val Met
 65 70 75 80
 Cys Trp Val Leu Thr Thr Phe Asp Ala Met Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
 115 120 125
 Glu Val Val Ile Phe Ile Ile Gly Gly Leu Gly Val Val Leu Pro Phe
 130 135 140
 Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Thr Gln Gly Ile Gln Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Gly Pro Ser Ala Tyr Tyr Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2466

<211> 157

<212> PRT

<213> Unknown (902672-dir-0-6 conceptual translation of range 2-472)

<400>2466

Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys
 1 5 10 15
 Val Ser Met Val Val Met Cys Arg Val Leu Thr Thr Phe Asp Ala Met
 20 25 30
 Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
 35 40 45
 Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
 50 55 60
 Ser Asp Thr His Val Asn Glu Val Val Ile Phe Ile Ile Gly Gly Leu

65		70		75		80									
Gly	Val	Val	Leu	Pro	Phe	Leu	Leu	Ile	Thr	Val	Ser	Tyr	Ala	Arg	Ile
			85					90						95	
Ile	Ser	Ser	Ile	Leu	Lys	Val	Pro	Ser	Thr	Gln	Gly	Ile	Gln	Lys	Val
			100					105						110	
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly
		115					120					125			
Thr	Ile	Ile	Gly	Leu	Tyr	Leu	Gly	Pro	Ser	Ala	Tyr	Tyr	Ser	Thr	Leu
	130					135					140				
Lys	Asp	Thr	Val	Met	Ser	Met	Met	Tyr	Thr	Val	Val	Thr			
145					150					155					

<210> 2467

<211> 216

<212> PRT

<213> Unknown (p196-dir-0-8 conceptual translation of range 2-649)

<400>2467

Phe	Ser	Asp	Phe	Cys	Phe	Ser	Ser	Val	Thr	Ile	Pro	Lys	Leu	Leu	Gln
1			5					10					15		
Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ala
		20					25					30			
Gln	Met	Tyr	Phe	Phe	Leu	Leu	Phe	Ala	Asp	Leu	Glu	Ser	Phe	Leu	Leu
		35				40					45				
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His
	50				55					60					
Tyr	Thr	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Leu	Cys	Leu	Val	Ala	Leu
65				70				75					80		
Ser	Trp	Leu	Leu	Thr	Val	Ile	Ser	Leu	Ser	His	Thr	Leu	Leu	Met	
			85				90					95			
Ala	Arg	Leu	Ser	Phe	Cys	Ala	Asn	Asn	Val	Ile	Pro	His	Phe	Phe	Cys
		100				105						110			
Asp	Met	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ile	Gln	Ile	Asn
		115				120					125				
Lys	Leu	Met	Ile	Phe	Ile	Leu	Gly	Gly	Leu	Val	Ile	Ile	Val	Pro	Phe
	130				135					140					
Leu	Leu	Ile	Phe	Ser	Ser	Tyr	Ala	Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys
145				150				155					160		
Val	Pro	Ser	Ser	Arg	Ser	Ile	Arg	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
			165				170						175		
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr
		180				185						190			
Leu	Cys	Pro	Ser	Ala	Asn	Asn	Ser	Thr	Ile	Lys	Glu	Thr	Val	Met	Ala
		195				200					205				
Val	Met	Tyr	Thr	Val	Val	Thr	Pro								
	210				215										

<210> 2468

<211> 216

<212> PRT

<213> Unknown (p91-dir-0-8 conceptual translation of range 2-649)

<400>2468

Phe	Ser	Asp	Met	Cys	Phe	Ser	Ser	Val	Ser	Ile	Pro	Lys	Leu	Leu	Val
1			5					10					15		
Asn	Met	Gln	Ser	Lys	Lys	Pro	Ala	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ser
		20					25					30			
Gln	Met	Tyr	Phe	Phe	Leu	Phe	Phe	Ala	Asp	Leu	Glu	Ser	Phe	Leu	Leu
		35				40					45				
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	His
	50					55					60				

Tyr Ile Val Ile Met Ser Pro Lys Leu Cys Ser S r Leu Val Val Leu
 65 70 75 80
 Ser Trp Val Leu Thr Ala Phe His Ala Leu Leu His Thr Leu Leu Met
 85 90 95
 Ser Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Gln Pro Asn
 115 120 125
 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Val Pro Phe
 130 135 140
 Leu Leu Ile Ile Thr Ser Tyr Ala His Ile Ile Ser Ser Ile Leu Arg
 145 150 155 160
 Val Pro Ser Val Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Thr Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser
 195 200 205
 Ile Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2469

<211> 314

<212> PRT

<213> Unknown (p29-dir-0-11 conceptual translation of range 1-942)

<400>2469

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
 130 135 140
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
 180 185 190
 Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
 210 215 220
 Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr
 260 265 270

Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Thr Leu Gly Arg Val
 290 295 300
 Phe Ser Thr Lys Lys Ile Phe Leu Ser Leu
 305 310

<210> 2470

<211> 314

<212> PRT

<213> Unknown (p132-dir-0-11 conceptual translation of range 1-942)

<400>2470

Met Thr Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Cys Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu Gln Tyr Thr Thr Ile Met Ser Ser Lys Gly Cys Leu Ala Leu
 130 135 140
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Arg Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Gln Val Asn Gly Trp Val Met Phe Phe Thr Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Leu Ile Met Ser Tyr Ala Arg Ile Leu Ser Thr
 210 215 220
 Ile Leu Arg Val Pro Cys Ala Gly Gly Ile Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Thr Asn His Asn Thr Val Lys Asp Thr
 260 265 270
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser
 290 295 300
 Leu Gln His Lys Glu Asn Phe Phe Val Phe
 305 310

<210> 2471

<211> 310

<212> PRT

<213> Unknown (205831-dir-0-11 conceptual translation of range 1-930)

<400>2471

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro

```

1           5           10           15
Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
20
Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
35
Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
50
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
65
Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
85
Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
100
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
115
His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
130
Leu Leu Trp Met Leu Thr Ser His Ala Met Met His Thr Leu Leu
145
Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
165
Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
180
Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
195
Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
210
Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
225
Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
245
Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
260
Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275
Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
290
Ser Met Lys Ile Thr Leu
305
310

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<210> 2472

<211> 221

<212> PRT

<213> Unknown (3769635-dir-0-8 conceptual translation of range 1-663)

<400>2472

```

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu
1           5           10           15
Lys Leu Leu Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala
20
Gly Cys Leu Thr Gln Ile Phe Phe Phe Leu Leu Phe Gly Tyr Leu Gly
35
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
50
Phe Pro Leu His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys
65
Leu Leu Leu Val Phe Trp Ile Met Thr Ser Ser His Ala Met Val His
85
Thr Leu Leu Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu
100
Asn Phe Phe Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp
105
110

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115	120	125
Thr Tyr Val Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile		
130	135	140
Val Ile Pr Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser		
145	150	155
Ser Ile Leu Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser		160
	165	170
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile		175
	180	185
Ile Gly Leu Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly		190
	195	200
Ser Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		205
210	215	220

<210> 2473

<211> 221

<212> PRT

<213> Unknown (3769637-dir-0-8 conceptual translation of range 1-663)

<400>2473

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro		
1	5	10
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala		15
	20	25
Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Ala Asp Met Glu		30
	35	40
Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys		45
	50	55
Phe Pro Leu His Tyr Thr Thr Ile Met Ser Thr Lys Val Cys Ala Ser		60
65	70	75
Leu Leu Ile Leu Leu Trp Met Leu Thr Thr Ser His Ala Leu Leu His		80
	85	90
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu		95
	100	105
His Phe Phe Cys Asp Ile Thr Ala Leu Leu Lys Leu Ser Cys Ser Asp		110
	115	120
Thr Tyr Val Asn Glu Met Met Met His Ile Leu Gly Gly Leu Ile Ser		125
	130	135
Val Ile Pro Phe Leu Phe Ile Val Met Ser Tyr Val Arg Ile Phe Phe		140
145	150	155
Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile His Lys Val Phe Ser		160
	165	170
Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile		175
	180	185
Phe Gly Leu Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu		190
	195	200
Ile Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		205
210	215	220

<210> 2474

<211> 221

<212> PRT

<213> Unknown (3769639-dir-0-8 conceptual translation of range 1-663)

<220>

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400>2474

Gly Asn Phe Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro

1	5	10	15
Lys	Leu	Leu	Gln
20	Asn	Met	Gln
25	Ser	Gln	Val
30	Pro	Ser	Ile
35	Ser	Tyr	Ala
40	Phe	Met	Val
45	Phe	Ala	Asp
50	Met	Tyr	Val
55	Ala	Arg	Ala
60	Val	Ile	Cys
65	Thr	Thr	Val
70	Thr	Thr	Val
75	Thr	Thr	Val
80	Thr	Thr	Val
85	Thr	Thr	Val
90	Thr	Thr	Val
95	Thr	Thr	Val
100	Thr	Thr	Val
105	Thr	Thr	Val
110	Thr	Thr	Val
115	Thr	Thr	Val
120	Thr	Thr	Val
125	Thr	Thr	Val
130	Thr	Thr	Val
135	Thr	Thr	Val
140	Thr	Thr	Val
145	Thr	Thr	Val
150	Thr	Thr	Val
155	Thr	Thr	Val
160	Thr	Thr	Val
165	Thr	Thr	Val
170	Thr	Thr	Val
175	Thr	Thr	Val
180	Thr	Thr	Val
185	Thr	Thr	Val
190	Thr	Thr	Val
195	Thr	Thr	Val
200	Thr	Thr	Val
205	Thr	Thr	Val
210	Thr	Thr	Val
215	Thr	Thr	Val
220	Thr	Thr	Val

<210> 2475

<211> 312

<212> PRT

<213> Unknown (205843-dir-0-11 conceptual translation of range 1-936)

<400>2475

1	5	10	15
Met	Thr	Gly	Asn
20	Asn	Gln	Thr
25	Leu	Ile	Leu
30	Glu	Phe	Leu
35	Leu	Leu	Leu
40	Gly	Asn	Leu
45	Val	Thr	Met
50	Val	Thr	Met
55	Val	Thr	Met
60	Val	Thr	Met
65	Val	Thr	Met
70	Val	Thr	Met
75	Val	Thr	Met
80	Val	Thr	Met
85	Val	Thr	Met
90	Val	Thr	Met
95	Val	Thr	Met
100	Val	Thr	Met
105	Val	Thr	Met
110	Val	Thr	Met
115	Val	Thr	Met
120	Val	Thr	Met
125	Val	Thr	Met
130	Val	Thr	Met
135	Val	Thr	Met
140	Val	Thr	Met
145	Val	Thr	Met
150	Val	Thr	Met
155	Val	Thr	Met
160	Val	Thr	Met
165	Val	Thr	Met
170	Val	Thr	Met
175	Val	Thr	Met
180	Val	Thr	Met
185	Val	Thr	Met
190	Val	Thr	Met
195	Val	Thr	Met
200	Val	Thr	Met
205	Val	Thr	Met
210	Val	Thr	Met
215	Val	Thr	Met
220	Val	Thr	Met

210	215	220
Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Il Phe		
	245	250
Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile		255
	260	265
Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val		285
	290	295
Ile Cys Thr Lys Lys Ile Ser Leu		300
305	310	

<210> 2476

<211> 216

<212> PRT

<213> Unknown (p198-dir-0-8 conceptual translation of range 2-649)

<400>2476

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln		
1	5	10
Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr		15
	20	25
Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu		30
	35	40
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His		45
	50	55
Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu		60
65	70	75
Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met		80
	85	90
Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys		95
	100	105
Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn		110
	115	120
Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe		125
	130	135
Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys		140
145	150	155
Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser		160
	165	170
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr		175
	180	185
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala		190
	195	200
Met Met Tyr Thr Val Val Thr Pro		205
210	215	

<210> 2477

<211> 236

<212> PRT

<213> Unknown (3810822-dir-0-8 conceptual translation of range 1-708)

<400>2477

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ser Asp Leu Cys Phe		
1	5	10
Ser Ser Val Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp		15
	20	25
Thr Ser Ile Thr Tyr Val Gly Cys Leu Thr Gln Ser Val Leu Phe Leu		30
	35	40
		45

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Ile Phe Phe Gly Gly Leu Glu Ile Phe Leu Leu Val Val Met Ala Tyr
 50          55          60
Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr Ser Ser Ile Met
65          70          75          80
Ser Leu Lys Phe Cys Val Cys Ala Val Leu Ile Ser Trp Ile Asn Ser
      85          90          95
Pro Trp Tyr Ser Lys Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe
      100          105          110
Cys Glu Asp Asn Ile Ile Cys His Phe Phe Cys Asp Met Ser Ala Leu
      115          120          125
Leu Lys Leu Ala Cys Ser Asp Ile Tyr Ile Asn Glu Leu Val Ile Phe
      130          135          140
Ile Leu Gly Gly Pro Leu Val Val Ile Pro Phe Leu Leu Ile Val Val
145          150          155          160
Ser Tyr Val Gln Ile Ile Phe Ser Ile Leu Lys Ala Ser Ser Thr Arg
      165          170          175
Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Thr Tyr Leu Thr Val Val
      180          185          190
Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Glu
      195          200          205
Lys Leu Tyr Ser Lys Glu Ala Ser Ile Thr Met Met Tyr Thr Val Val
      210          215          220
Thr Pro Met His Pro Phe Ile Tyr Thr Leu Arg Asn
225          230          235

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<210> 2478

<211> 216

<212> PRT

<213> Unknown (OST044-dir-0-8 conceptual translation of range 2-649)

<400>2478

```

Leu Ala Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
 1          5          10          15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
      20          25          30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
      35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50          55          60
Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
65          70          75          80
Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu Leu Leu
      85          90          95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
      100          105          110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
      115          120          125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
      130          135          140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
145          150          155          160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
      165          170          175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
      180          185          190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
      195          200          205
Leu Met Tyr Thr Val Val Thr Pro
210          215

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<210> 2479

<211> 216

<212> PRT

<213> Unknown (hg152-dir-0-8 conceptual translation of range 1-648)

<400>2479

```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
1      5      10      15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
20      25      30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
35      40      45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50      55      60
Tyr Thr Val Val Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
65      70      75      80
Ser Trp Ile Leu Ser Cys Asp Ser Ser Leu Ser His Thr Leu Leu Leu
85      90      95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
100     105     110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
115     120     125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
130     135     140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
145     150     155     160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
165     170     175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
180     185     190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
195     200     205
Leu Met Tyr Thr Val Val Thr Pro
210     215

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<210> 2480

<211> 112

<212> PRT

<213> Unknown (1142973-dir-0-5 conceptual translation of range 1-336)

<400>2480

```

His Pro Leu His Tyr Ile Thr Ile Met Ser Gln Ser Arg Cys Ala Met
1      5      10      15
Leu Val Ala Val Ser Trp Val Ile Ala Ser Ala Cys Ala Leu Leu His
20      25      30
Ser Leu Leu Leu Asp Gln Leu Ser Phe Cys Ala Asp His Thr Val Pro
35      40      45
His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp
50      55      60
Thr Ser Leu Asn Gln Leu Val Ile Phe Thr Ala Gly Leu Ala Ala Ile
65      70      75      80
Met Leu Pro Phe Leu Cys Ile Leu Ile Ser Tyr Gly Arg Ile Gly Phe
85      90      95
Thr Ile Leu Gln Val Pro Thr Thr Lys Gly Ile Cys Lys Ala Leu Ser
100     105     110

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<210> 2481

<211> 216

<212> PRT

<213> Unknown (hg32-dir-0-8 conceptual translation of range 1-648)

<400>2481

```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
1      5      10      15
Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly Cys Ile Ser
20     25     30
Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser Phe Leu Ile
35     40     45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50     55     60
Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu Val Ala Gly
65     70     75     80
Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu Asp Thr Leu Leu Leu
85     90     95
Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His Tyr Phe Cys
100    105    110
Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn
115    120    125
Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met Leu Pro Phe
130    135    140
Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr Ile Leu Gln
145    150    155    160
Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser
165    170    175
His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile Gly Leu Tyr
180    185    190
Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile Ile Ala Ser
195    200    205
Val Ile Tyr Thr Ala Val Thr Pro
210    215

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<210> 2482

<211> 223

<212> PRT

<213> Unknown (3983375-dir-0-8 conceptual translation of range 1-669)

<400>2482

```

Ser His Leu Ala Phe Thr Asp Ile Ser Phe Ser Ser Val Thr Ala Pro
1      5      10      15
Lys Met Leu Met Asn Met Leu Thr His Ser Gln Ser Ile Ser His Ala
20     25     30
Gly Cys Val Ser Gln Ile Tyr Phe Phe Leu Leu Phe Gly Cys Ile Asp
35     40     45
Asn Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
50     55     60
His Pro Leu His Tyr Thr Thr Ile Met Ser Gln Ser Leu Cys Val Leu
65     70     75     80
Leu Val Met Val Ser Trp Ala Phe Ser Ser Ser Asn Gly Leu Val His
85     90     95
Thr Leu Leu Phe Ala Arg Leu Ser Leu Phe Arg Asp Asn Thr Val His
100    105    110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ser Ser Ser Asp
115    120    125
Thr Thr Ile Asn Glu Leu Val Ile Leu Thr Leu Ala Val Val Val Ile
130    135    140
Thr Val Pro Phe Ile Cys Ile Leu Val Ser Tyr Gly His Met Gly Ala
145    150    155    160
Thr Ile Leu Arg Thr Pro Ser Ile Lys Gly Ile Cys Lys Ala Leu Ser
165    170    175
Thr Cys Gly Ser His Leu Cys Val Val Ser Leu Tyr Tyr Gly Ala Ile
180    185    190
Ile Gly Leu Tyr Phe Phe Pro Ser Ser Asn Asn Thr Asn Asp Lys Asp
195    200    205

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Val Ile Val Ala Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn
 210 215 220

<210> 2483

<211> 176

<212> PRT

<213> Unknown (3273636-dir-0-7 conceptual translation of range 4-531)

<400>2483

Gln Ala Leu Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro Leu His
 1 5 10 15
 Tyr Arg Thr Ile Met Arg Asp Gly Phe Cys Val Leu Leu Val Val Gly
 20 25 30
 Ser Trp Phe Phe Ser Cys Val His Ala Leu Leu His Thr Leu Leu Leu
 35 40 45
 Ser Arg Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro His Phe Phe Cys
 50 55 60
 Asp Phe Thr Ala Val Leu Lys Met Thr Cys Ser Asp Thr Ser Ile Asn
 65 70 75 80
 Glu Leu Val Ile Phe Ile Glu Gly Gly Leu Leu Thr Ser Leu Pro Leu
 85 90 95
 Ser Ala Ile Leu Gly Ser Tyr Val Arg Ile Gly Ala Ser Ile Leu Arg
 100 105 110
 Val Pro Ser Met Lys Arg Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser
 115 120 125
 His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile Ala Met Thr Tyr
 130 135 140
 Phe Phe Pro Ser Ser Tyr Asn Ser Lys Val Lys Gly Ile Ile Ala Ser
 145 150 155 160
 Val Ile Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Cys Ser
 165 170 175

<210> 2484

<211> 222

<212> PRT

<213> Unknown (4877296-dir-0-8 conceptual translation of range 2-667)

<400>2484

Ser His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Leu Pro
 1 5 10 15
 Lys Met Leu Met Asn Met Gln Thr Arg Cys Gln Ala Ile Thr Tyr Ala
 20 25 30
 Gly Cys Ile Ser Gln Val Tyr Cys Phe Ile Phe Phe Gly Cys Leu Asp
 35 40 45
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
 50 55 60
 His Pro Leu His Tyr Thr Ala Ile Met Arg Asp Glu Leu Cys Val Ile
 65 70 75 80
 Leu Val Ala Gly Arg Trp Leu Ala Ala Cys Ala Gln Ala Leu Leu His
 85 90 95
 Thr Leu Leu Val Asp Gln Leu Thr Leu Cys Ala Gly Thr Val Ile Pro
 100 105 110
 His Phe Phe Cys Asp Leu Ala Val Leu Lys Ser Ser Cys Ser Asp
 115 120 125
 Thr Ser Leu Asn Glu Leu Leu Ile Leu Thr Glu Gly Gly Leu Ile Phe
 130 135 140
 Thr Leu Pro Leu Gly Gly Ile Leu Gly Ser Tyr Ile Arg Met Ala Ala
 145 150 155 160
 Ile Ile Leu Lys Val Pro Ser Phe Thr Arg Ile Phe Lys Ala Leu Ser
 165 170 175
 Thr Cys Gly Ser His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile

	180		185		190
Ala Gly Val Tyr Tyr Phe Pro Ser Ser Gly Asn Ser Lys Val Lys Asp					
195		200		205	
Ile Val Ala Ser Leu Met Tyr Met Val Val Thr Pro Met Leu					
210		215		220	

<210> 2485

<211> 173

<212> PRT

<213> Unknown (3273660-dir-0-7 conceptual translation of range 1-519)

<400>2485

Gln Ala Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Leu Leu His					
1	5		10		15
Tyr Ser Thr Ile Met Arg Gln Glu Leu Cys Val Ser Leu Val Ser Gly					
20		25		30	
Ser Trp Phe Leu Cys Cys Ile Tyr Ala Leu Leu His Thr Leu Leu Leu					
35		40		45	
Val Gln Leu Ser Phe Ser Val Asp Asn Thr Ile Pro His Ser Asn Leu					
50		55		60	
Ile Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn Glu Leu					
65		70		75	80
Val Ile Phe Pro Val Arg Gly Thr Leu Leu Ile Leu Ser Leu Phe Ser					
85		90		95	
Ile Leu Gly Ser Tyr Ile His Ile Gly Pro Thr Leu Leu Ser Val Ser					
100		105		110	
Ser Thr Arg Asp Ser Lys Val Cys Ser Thr Cys Gly Phe His His Phe					
115		120		125	
Ser Val Ser Leu Tyr His Arg Lys Leu Ala Asn Val Ser Phe Phe Ser					
130		135		140	
Leu Ser Trp Asp Ser Asn Gly Lys Asp Val Thr Thr Ser Val Val Tyr					
145		150		155	160
Ala Val Val Thr Pro Met Val Asn Pro Phe Ile Cys Ser					
	165		170		

<210> 2486

<211> 135

<212> PRT

<213> Unknown (3273658-dir-0-6 conceptual translation of range 1-405)

<400>2486

Ile Tyr Ala Leu Leu His Thr Leu Leu Leu Val Gln Leu Ser Phe Ser					
1	5		10		15
Val Asp Asn Thr Ile Pro His Ser Asn Leu Ile Ala Leu Leu Lys Leu					
20		25		30	
Ser Cys Ser Asp Thr Ser Leu Asn Glu Leu Val Ile Phe Pro Val Arg					
35		40		45	
Gly Thr Leu Leu Ile Pro Ser Leu Leu Ser Ile Leu Gly Ser Tyr Ile					
50		55		60	
His Ile Gly Pro Thr Leu Leu Ser Val Ser Ser Thr Arg Asp Ser Lys					
65		70		75	80
Val Cys Ser Thr Cys Gly Phe His His Phe Ser Val Ser Leu Tyr His					
85		90		95	
Arg Lys Arg Ala Asn Val Ser Phe Phe Ser Ser Ser Trp Asp Ser Asn					
100		105		110	
Gly Lys Asp Val Thr Thr Ser Val Val Tyr Ala Val Val Thr Pro Met					
115		120		125	
Leu Asn Pro Phe Ile Cys Ser					
130		135			

<210> 2487

<211> 176

<212> PRT

<213> Unknown (3273646-dir-0-7 conceptual translation of range 1-528)

<400>2487

Gln Ala Leu Ala Tyr Asp Arg Phe Leu Ala Val Cys His Pro Leu His
 1 5 10 15
 Tyr Ala Ile Phe Met Arg Glu Arg Leu Cys Ile Phe Leu Leu Ala Gly
 20 25 30
 Ser Trp Leu Leu Ser Gly Ala Ser Ala Leu Thr His Thr Leu Leu Val
 35 40 45
 Val Gln Leu Ser Phe Cys Ala Asp Asn Ile Ile Leu His Phe Phe Cys
 50 55 60
 Asp Leu Val Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn
 65 70 75 80
 Glu Leu Val Ile Phe Thr Val Gly Ser Val Gly Leu Val Phe Pro Leu
 85 90 95
 Ser Gly Ile Leu Val Ser Tyr Gly Arg Ile Gly Leu Ser Ile Leu Arg
 100 105 110
 Val Pro Ser Thr Lys Gly Val Cys Lys Ala Leu Ser Thr Cys Gly Ser
 115 120 125
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Met Ala Val Tyr
 130 135 140
 Phe Ser Ser Ser Ser Gly Gln Ser His Glu Lys Asp Ile Ile Ala Ser
 145 150 155 160
 Met Met Tyr Thr Val Val Thr Pro Met Val Asn Pro Val Ile Cys Ser
 165 170 175

<210> 2488

<211> 313

<212> PRT

<213> Unknown (205815-dir-0-11 conceptual translation of range 1-939)

<400>2488

Met Ser Ser Thr Asn Gln Ser Ser Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Arg Gln Pro Gln Gln Gln Gln Leu Leu Phe Leu Leu Phe Leu
 20 25 30
 Ile Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Gly Thr Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys
 65 70 75 80
 Val Leu Ala Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Ala Val Phe Gly Asn Met Asp Asn
 100 105 110
 Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu
 130 135 140
 Val Val Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
 165 170 175
 Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180 185 190
 His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val
 195 200 205
 Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala

210	215	220
Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile		240
	245	250
Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met		255
	260	265
Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val		285
	290	295
Leu Ala Met Arg Phe Pro Ser Lys Gln		300
305	310	

<210> 2489

<211> 216

<212> PRT

<213> Unknown (hg91-dir-0-8 conceptual translation of range 1-648)

<400>2489

Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala		
1	5	10
Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr		15
	20	25
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu		30
	35	40
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His		45
	50	55
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly		60
	65	70
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met		75
	85	90
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys		95
	100	105
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn		110
	115	120
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe		125
	130	135
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg		140
	145	150
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser		155
	165	170
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala		190
	195	200
Val Met Tyr Pro Val Val Thr Pro		205
210	215	

<210> 2490

<211> 157

<212> PRT

<213> Unknown (902718-dir-0-6 conceptual translation of range 2-472)

<400>2490

Ile Cys His Pro Leu Gln Tyr Thr Thr Lys Met Thr His Gln Leu Cys		
1	5	10
Ala Leu Leu Val Val Gly Ser Trp Val Val Ala Asn Leu Asn Cys Leu		15
	20	25
Leu His Ile Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ile		30
	35	40
		45


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Ile Pro His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys
 50          55          60
Ser Asp Thr His Leu Asn Glu Leu Met Ile L u Thr Glu Gly Ala Val
65          70          75          80
Il  Ile Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Val
      85          90          95
Thr Cys Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala
      100          105          110
Phe Ser Thr Arg Gly Ser His Pro Ala Val Val Cys Leu Phe Tyr Gly
      115          120          125
Thr Ile Ile Ala Glu Tyr Phe Ser Ser Ser Ser Pro His Ser Ala Gly
      130          135          140
Arg Asp Met Ala Gly Ala Met Met Tyr Thr Val Val Thr
145          150          155

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<210> 2491

<211> 221

<212> PRT

<213> Unknown (3769625-dir-0-8 conceptual translation of range 1-663)

<400>2491

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Ser Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Ala Pro
1          5          10          15
Ser Val Leu Ala Asn His Ile Leu Gly Ser Gln Lys Ile Ser Phe Ser
      20          25          30
Gly Cys Leu Thr Gln Leu Tyr Phe Leu Cys Ile Phe Gly Asp Met Asp
      35          40          45
Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
      50          55          60
His Pro Leu Arg Tyr Thr Lys Met Thr His Gln Val Cys Ala Leu
65          70          75          80
Leu Val Met Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His
      85          90          95
Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Ser Ile Ile Pro
      100          105          110
His Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp
      115          120          125
Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met
      130          135          140
Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Trp
145          150          155          160
Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala Phe Ser
      165          170          175
Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Leu Tyr Gly Thr Val
      180          185          190
Ile Thr Val Tyr Phe Asn Pro Ser Thr Ser Tyr Ser Ala Gly Arg Asp
      195          200          205
Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Met
210          215          220

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<210> 2492

<211> 221

<212> PRT

<213> Unknown (3769644-dir-0-8 conceptual translation of range 1-663)

<400>2492

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Thr Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Ser Thr Val Pro
1          5          10          15
Lys Val Leu Ala Asn His Ile Leu Gly Ser Gln Glu Ile Ser Phe Ser
      20          25          30
Gly Cys Leu Thr Gln Met Tyr Phe Leu Ser Val Phe Ala Asp Met Asp

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35	40	45
Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys		
50	55	60
His Pro Leu His Tyr Thr Glu Lys Met Thr Arg Gln Leu Cys Ala Leu		
65	70	75
Leu Val Val Glu Ser Trp Val Ala Ala Asn Leu Asn Ala Leu Leu His		
85	90	95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Gly Asp Asn Ile Ile Pro		
100	105	110
His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp		
115	120	125
Thr His Leu Asn Glu Leu Met Ile Leu Thr Val Ala Gly Leu Ile Leu		
130	135	140
Leu Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Ile Leu Ile Ala Cys		
145	150	155
Ala Val Val Arg Val Ser Ser Thr Gly Gly Arg Trp Lys Ala Phe Ser		
165	170	175
Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile		
180	185	190
Ile Ala Val Tyr Phe Asn Pro Ala Ser Ser His Ser Ala Gly Arg Asp		
195	200	205
Met Ala Ser Ala Met Met Tyr Thr Val Val Thr Pro Met		
210	215	220

<210> 2493

<211> 327

<212> PRT

<213> Unknown (2808536-dir-0-11 conceptual translation of range 16-996)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2493

Val Cys Phe Xaa Ile His Cys Leu Leu Cys Ser Trp Val Gln Thr Tyr	
1	5
Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu Leu Leu Gly Leu	
20	25
Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu Ser	
35	40
Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile	
50	55
Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn	
65	70
Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu	
85	90
Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu	
100	105
Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu	
115	120
Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu	
130	135
His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala Leu Leu Val Thr	
145	150
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu	
165	170
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe	
180	185
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu	
195	200
	205

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Ser Glu Val Met Ile L u Thr Glu Ala Ala Leu Val Thr Il Thr Pro
210 215 220
Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
225 230 235 240
Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
245 250 255
Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
260 265 270
Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
275 280 285
Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
290 295 300
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
305 310 315 320
Val Lys Phe Phe Ser Val Gln
325

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<210> 2494

<211> 312

<212> PRT

<213> Unknown (2370144-dir-0-11 conceptual translation of range 1-936)

<400>2494

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Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
1 5 10 15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
20 25 30
Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
35 40 45
Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
65 70 75 80
Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
85 90 95
Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
100 105 110
Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
115 120 125
Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
130 135 140
Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
145 150 155 160
Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
165 170 175
Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asn Thr
180 185 190
His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
195 200 205
Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
210 215 220
Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
225 230 235 240
Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
245 250 255
Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
260 265 270
Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
275 280 285
Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val
290 295 300

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Ile Gly Arg Val Val Phe Ser Val
305 310

<210> 2495

<211> 216

<212> PRT

<213> Unknown (2921659-dir-0-8 conceptual translation of range 2-649)

<400>2495

Phe	Val	Asp	Ile	Cys	Phe	Ser	Phe	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1				5					10					15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Asn	Phe	Leu	Leu
		35				40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55					60					
Tyr	Thr	Ala	Lys	Val	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65				70				75						80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
		85					90						95		
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105						110		
Asp	Val	Thr	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
		115				120						125			
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe
	130					135				140					
Leu	Cys	Ile	Leu	Ala	Ser	Tyr	Met	His	Ile	Thr	Cys	Thr	Val	Leu	Lys
145				150				155						160	
Val	Pro	Ser	Thr	Lys	Gly	Arg	Trp	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
			165				170							175	
His	Leu	Ala	Val	Val	Leu	Leu	Phe	Tyr	Ser	Thr	Ile	Ile	Ala	Val	Tyr
		180					185						190		
Phe	Asn	Pro	Leu	Ser	Ser	His	Ser	Ala	Glu	Lys	Asp	Thr	Met	Ala	Thr
	195					200						205			
Val	Leu	Tyr	Thr	Val	Val	Thr	Pro								
	210					215									

<210> 2496

<211> 216

<212> PRT

<213> Unknown (2921657-dir-0-8 conceptual translation of range 2-649)

<400>2496

Phe	Val	Asp	Ile	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1				5					10					15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Tyr	Phe	Leu	Leu
		35				40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55					60					
Tyr	Thr	Ala	Lys	Met	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65				70				75						80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
		85					90						95		
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105						110		
Asp	Val	Thr	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
	115					120						125			
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe

130	135	140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys		
145	150	155
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser		160
	165	170
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr		190
	195	200
Val Leu Tyr Thr Val Val Thr Pro		205
210	215	

<210> 2497

<211> 216

<212> PRT

<213> Unknown (2921653-dir-0-8 conceptual translation of range 2-649)

<400>2497

Phe Val Asp Ile Cys Phe Ser Ser Thr Thr Val Pro Lys Met Leu Ala		
1	5	10
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Leu Cys Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu		30
	35	40
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His		45
	50	55
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly		60
	65	70
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met		75
	85	90
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys		95
	100	105
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn		110
	115	120
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe		125
	130	135
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys		140
	145	150
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser		155
	165	170
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr		175
	180	185
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Pro Thr		190
	195	200
Val Leu Tyr Thr Val Val Thr Pro		205
210	215	

<210> 2498

<211> 216

<212> PRT

<213> Unknown (2921655-dir-0-8 conceptual translation of range 2-649)

<400>2498

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala		
1	5	10
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Val Phe Thr Phe Val Asp Met Asp Asn Phe Leu Leu		30
	35	40
Ala Val Met Ala Tyr Asp His Phe Val Ala Glu Cys His Pro Leu His		45
	50	55
		60

Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
 65 70 75 80
 Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
 100 105 110
 Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
 115 120 125
 Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
 130 135 140
 Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
 145 150 155 160
 Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
 180 185 190
 Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr
 195 200 205
 Val Leu Tyr Thr Val Val Thr Pro
 210 215

<210> 2499

<211> 216

<212> PRT

<213> Unknown (2921651-dir-0-8 conceptual translation of range 2-649)

<400>2499

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asp His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
 50 55 60
 Tyr Thr Ala Arg Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
 65 70 75 80
 Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Pro Leu Ser Phe Tyr Ala Asp Asn Ala Ile Thr His Phe Phe Cys
 100 105 110
 Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
 115 120 125
 Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
 130 135 140
 Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
 145 150 155 160
 Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
 180 185 190
 Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Ile Ala Thr
 195 200 205
 Val Leu Tyr Thr Val Val Thr Pro
 210 215

<210> 2500

<211> 216

<212> PRT

<213> Unknown (2921692-dir-0-8 conceptual translation of range 2-649)

<400>2500

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Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala
 1           5           10           15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
          20           25           30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu
          35           40           45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
          50           55           60
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65           70           75           80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
          85           90           95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
          100          105          110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115          120          125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
          130          135          140
Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys
145          150          155          160
Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
          165          170          175
His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr
          180          185          190
Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr
          195          200          205
Val Leu Tyr Thr Val Val Thr Pro
          210          215

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<210> 2501

<211> 224

<212> PRT

<213> Unknown (4877342-dir-0-8 conceptual translation of range 2-673)

<220>

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400>2501

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Cys Asn Leu Ser Phe Gly Asp Ile Cys Phe Ser Ser Thr Thr Val Pro
 1           5           10           15
Lys Met Leu Ala Asn His Ile Leu Arg Lys Gln Thr Ile Pro Phe Ser
          20           25           30
Arg Cys Leu Ala Gln Met Tyr Phe Val Phe Thr Phe Met Asp Met Asp
          35           40           45
Asn Phe Leu Leu Ala Met Met Ala Tyr Asp His Phe Val Ala Val Cys
          50           55           60
His Pro Leu His Tyr Tyr Ala Lys Met Thr His Gln Leu Cys Ala Leu
65           70           75           80
Leu Val Thr Gly Ser Trp Val Ile Ala Asn Leu Asp Met Leu Leu His
          85           90           95
Thr Leu Leu Met Ala Xaa Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro
          100          105          110
His Phe Phe Cys Asp Val Thr Thr Leu Leu Lys Leu Ser Cys Ser Asp
          115          120          125
Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Arg Pro Val Met
          130          135          140
Ser Thr Pro Phe Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Asn Cys
145          150          155          160

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Ala Val Leu Arg Val Gln Ser Thr Lys Gly Arg Trp Lys Thr Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ala Met Val Phe Leu Phe Tyr Gly Thr Met
 180 185 190
 Ile Phe Leu Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Ile Asp
 195 200 205
 Ile Ala Ala Ala Ala Met Arg Cys Leu Tyr Met Val Thr Pro Met Leu
 210 215 220

<210> 2502

<211> 216

<212> PRT

<213> Unknown (p105-dir-0-8 conceptual translation of range 2-649)

<400>2502

Leu Val Asp Phe Cys Phe Thr Ser Ala Thr Val Pro Lys Met Leu Leu
 1 5 10 15
 Asn Ile His Arg Gln Ile Gln Ser Ile Ser His Glu Gly Cys Leu Thr
 20 25 30
 Gln Ile Tyr Phe Cys Ile Leu Leu Ala Asn Met Asp Asn Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Gln
 50 55 60
 Tyr Thr Thr Ile Met Ser Leu Gln Leu Cys Cys Leu Met Leu Ala Gly
 65 70 75 80
 Ser Trp Leu Ile Ala Asn Phe His Ser Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Asp Phe Cys Ala Lys Asn Val Met Pro Tyr Phe Phe Cys
 100 105 110
 Asp Leu Val Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Asn
 115 120 125
 Gln Leu Met Ile Leu Leu Val Gly Gly Leu Ile Val Leu Ile Pro Phe
 130 135 140
 Leu Cys Ile Leu Ile Ser Tyr Thr His Ile Val Ser Val Val Leu Lys
 145 150 155 160
 Val Pro Ser Ala Leu Gly Lys Gln Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Ile Leu Phe Tyr Gly Thr Ile Thr Gly Val Tyr
 180 185 190
 Leu Asn Pro Ser Ser Ser His Ser Ala Glu Lys Asp Ser Val Ala Ser
 195 200 205
 Val Met Tyr Met Val Val Thr Pro
 210 215

<210> 2503

<211> 216

<212> PRT

<213> Unknown (p110-dir-0-8 conceptual translation of range 2-649)

<400>2503

Phe Val Asp Leu Cys Gln Ala Ser Thr Thr Met Pro Lys Met Leu Ile
 1 5 10 15
 Asn Ile Leu Thr His Ser Lys Ala Ile Pro Tyr Ala Gly Cys Leu Ile
 20 25 30
 Gln Met Tyr Ser Phe His Leu Phe Gly Thr Met Asp Ser Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Ile Leu Leu Val Gly Gly
 65 70 75 80
 Pro Trp Gly Thr Thr Asn Leu Gln Ser Val Val His Thr Ser Leu Met

				85				90				95			
Ala	Lys	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Lys	Ile	Pr	His	Phe	Phe	Cys
100				105				110							
Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Ile	Asn
115				120				125							
Glu	Leu	Val	Val	Leu	Val	Phe	Gly	Ile	Phe	Met	Gly	Ile	Ser	Pro	Leu
130				135				140							
Val	Cys	Ile	Leu	Leu	Ser	Tyr	Ile	Cys	Ile	Phe	Cys	Ala	Val	Leu	Gln
145				150				155				160			
Val	Pro	Ser	Ala	Glu	Gly	Lys	Arg	Lys	Ala	Phe	Ser	Thr	Arg	Gly	Ser
165				170				175							
His	Leu	Thr	Val	Val	Leu	Leu	Phe	Tyr	Gly	Thr	Ile	Phe	Ala	Val	Tyr
180				185				190							
Leu	Gln	Pro	Ser	Gly	Pro	Thr	Ser	Pro	Glu	Lys	Asp	Lys	Ala	Ala	Ala
195				200				205							
Val	Met	Cys	Ala	Val	Val	Ile	Pro								
210				215											

<210> 2504

<211> 216

<212> PRT

<213> Unknown (p94-dir-0-8 conceptual translation of range 2-649)

<400>2504

Phe	Val	Asp	Leu	Cys	Gln	Ala	Ser	Thr	Thr	Met	Pro	Lys	Met	Leu	Ile
1				5					10					15	
Asn	Ile	Leu	Thr	His	Ser	Lys	Ala	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ile
			20					25					30		
Gln	Met	Tyr	Ser	Phe	His	Leu	Phe	Gly	Thr	Met	Asp	Ser	Phe	Leu	Leu
		35					40					45			
Ala	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Phe	His	Pro	Leu	Arg
	50					55					60				
Tyr	Ala	Thr	Ile	Met	Ser	Pro	Arg	Leu	Cys	Ile	Leu	Leu	Val	Gly	Gly
65					70				75					80	
Pro	Trp	Gly	Thr	Thr	Asn	Leu	Gln	Ser	Val	Val	His	Thr	Ser	Leu	Met
				85					90					95	
Ala	Lys	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Lys	Ile	Pro	His	Phe	Phe	Cys
			100					105					110		
Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Ile	Asn
		115					120					125			
Glu	Leu	Val	Val	Leu	Val	Phe	Gly	Ile	Phe	Met	Gly	Ile	Ser	Pro	Leu
	130					135					140				
Val	Cys	Ile	Leu	Leu	Ser	Tyr	Ile	Cys	Ile	Phe	Cys	Ala	Val	Leu	Gln
145					150					155				160	
Val	Pro	Ser	Ala	Glu	Gly	Lys	Arg	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
				165					170					175	
His	Leu	Thr	Val	Val	Leu	Val	Phe	Tyr	Gly	Thr	Ile	Phe	Ala	Val	Tyr
			180					185					190		
Val	Gln	Pro	Ser	Gly	Pro	Thr	Ser	Pro	Glu	Lys	Asp	Lys	Ala	Ala	Ala
		195					200					205			
Val	Met	Cys	Ala	Val	Val	Ile	Pro								
	210					215									

<210> 2505

<211> 169

<212> PRT

<213> Unknown (4877330-dir-0-7 conceptual translation of range 3-509)

<400>2505

Asn Leu Ser Leu Val Asp Val Phe Leu Ser Ser Thr Thr Val Pro Lys
1 5 10 15

Met Leu Val Asn Leu Trp Thr Gln Pro Ser His Pro S r Val Cys Leu
 20 25 30
 Ala Gln Met His Ala Phe His Leu Phe Gly Thr Ile Asp Ser Phe Leu
 35 40 45
 Leu Ala Val Met Ala Ile Asp Arg Phe Met Ala Ile Val His Arg Leu
 50 55 60
 Cys Tyr Leu Ala Ile Met Ser Pro Arg Val Trp Gly Leu Leu Val Gly
 65 70 75 80
 Glu Pro Trp Gln Ile Thr Asn Leu Gln Ser Leu Val His Thr Cys Leu
 85 90 95
 Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Pro His Phe Phe
 100 105 110
 Cys Asp Leu Ile Pro Leu Pro Lys Leu Ser Ser Ser Asp Thr His Thr
 115 120 125
 Asn Glu Pro Val Ile Phe Pro Phe Gly Ile Ile Leu Gly Ile Ser Ser
 130 135 140
 Leu Ala Cys Ile Leu Phe Ser Tyr Thr Ser Ile Phe Gln Ala Val Phe
 145 150 155 160
 Lys Ile Leu Ser Ala Gln Val Lys Trp
 165

<210> 2506

<211> 315

<212> PRT

<213> Unknown (3184261-dir-59-13 conceptual translation of range 6034-6978)

<400>2506

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly
 1 5 10 15
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu
 20 25 30
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala
 35 40 45
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser
 100 105 110
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His
 115 120 125
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu
 130 135 140
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr
 145 150 155 160
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His
 165 170 175
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr
 180 185 190
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr
 195 200 205
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr
 210 215 220
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe
 245 250 255
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys
 260 265 270

Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pr Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro
 305 310 315

<210> 2507

<211> 216

<212> PRT

<213> Unknown (p97-dir-0-8 conceptual translation of range 2-649)

<400>2507

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Val Ser Gly Asn Lys Ala Ile Pro Tyr Ala Gly Cys Arg Thr
 20 25 30
 Gln Val Phe Phe Phe Ile Trp Phe Pro Gly Val Asp Ser Ile Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Tyr Ser Met Ile Met Thr Pro Lys Val Cys Ala Phe Leu Ile Val Val
 65 70 75 80
 Ser Trp Phe Gly Ala Tyr Ala Ile Ala Leu Ile His Thr Val Leu Leu
 85 90 95
 Thr His Leu Ser Phe Cys Gly His Ser Glu Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asn Leu Met Val Asn Thr Val Gly Ala Leu Thr Ile Ile Ile Pro Phe
 130 135 140
 Ile Gly Ile Leu Ile Ser Tyr Thr Gln Ile Phe Met Thr Val Leu Arg
 145 150 155 160
 Ile Pro Ser Thr Val Gly Lys Trp Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr
 180 185 190
 Phe Ser Pro Thr Thr Thr His Thr Ala Gln Gln Asp Thr Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2508

<211> 216

<212> PRT

<213> Unknown (p99-dir-0-8 conceptual translation of range 2-649)

<400>2508

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Val Ser Gly Asn Lys Met Ile Pro Tyr Pro Gly Cys Leu Thr
 20 25 30
 Gln Val Phe Phe Phe Ile Trp Phe Ala Gly Ile Asp Ser Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Tyr Ser Thr Val Met Thr Leu Arg Val Cys Val Leu Leu Leu Met Val
 65 70 75 80
 Ser Trp Phe Ser Ala Phe Ile Asn Ala Leu Thr His Ala Ala Leu Leu
 85 90 95
 Thr Pro Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys

100	105	110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn		
115	120	125
Asp Leu Met Val Tyr Thr Val Gly Ala Leu Pro Ile Ile Thr Pro Phe		
130	135	140
Ile Gly Ile Leu Ile Ser Tyr Thr Arg Ile Phe Met Ala Val Leu Arg		
145	150	155
Val Pro Ser Ala Gly Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser		
165	170	175
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr		
180	185	190
Phe Ser Pro Thr Ser Thr Arg Thr Ala Gln Glu Asp Thr Val Ala Ala		
195	200	205
Val Met Tyr Thr Val Val Thr Pro		
210	215	

<210> 2509

<211> 216

<212> PRT

<213> Unknown (p96-dir-0-8 conceptual translation of range 2-649)

<400>2509

Leu Val Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Asn		
1	5	10
Asn Tyr Ile Ser Gln Asn Arg Thr Ile Ser Tyr Ala Gly Cys Leu Thr		
20	25	30
Gln Val Phe Phe Phe Leu Trp Phe Ala Gly Met Asp Ser Val Leu Leu		
35	40	45
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Ser Leu His		
50	55	60
Tyr Ser Thr Val Met Thr Pro Lys Ile Cys Ala Leu Leu Val Gly Val		
65	70	75
Ser Trp Phe Trp Ala Tyr Asn Asn Ala Leu Ile His Thr Val Leu Leu		
85	90	95
Thr Arg Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys		
100	105	110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn		
115	120	125
Asp Leu Met Ile Tyr Thr Val Gly Ala Leu Thr Ile Ile Leu Pro Phe		
130	135	140
Ile Gly Ile Met Ile Ser Tyr Val His Ile Phe Met Ala Val Leu Lys		
145	150	155
Ile Ser Ser Val Ser Gly Lys Gln Lys Val Phe Ser Thr Cys Gly Ser		
165	170	175
His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr		
180	185	190
Phe Ser Pro Thr Ser Thr His Thr Ala Gln Gln Asp Thr Ala Ala Thr		
195	200	205
Val Met Tyr Thr Val Val Thr Pro		
210	215	

<210> 2510

<211> 216

<212> PRT

<213> Unknown (p92-dir-0-8 conceptual translation of range 2-649)

<400>2510

Leu Phe Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val		
1	5	10
Asn His Ile Ser Lys Asn Lys Val Ile Pro Tyr Ser Met Cys Leu Thr		
20	25	30

Gln Thr Phe Phe Phe Ser Trp Phe Ile Gly Thr Asp Gly Val L u L u
 35 40 45
 Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Cys Thr Met Ile Ile Thr Pro Arg Val Cys Val Phe Leu Val Ala Val
 65 70 75 80
 Ser Trp Ile Trp Thr Cys Val Asn Ser Leu Ile His Thr Thr Ser Leu
 85 90 95
 Asn Arg Leu Ser Phe Cys Gly His Asn Glu Ile His His Phe Phe Cys
 100 105 110
 Asp Leu Ser Ala Leu Ile Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asp Leu Leu Ile Tyr Thr Val Gly Gly Leu Lys Ala Ile Val Pro Phe
 130 135 140
 Ile Gly Ile Leu Leu Ser Tyr Ile His Ile Phe Val Ala Val Leu Arg
 145 150 155 160
 Ile Pro Ser Ala Gly Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
 180 185 190
 Phe Ser Pro Thr Ser Thr His Thr Ala Gln Lys Asp Thr Ala Val Ala
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2511

<211> 216

<212> PRT

<213> Unknown (p95-dir-0-8 conceptual translation of range 2-649)

<220>

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400>2511

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Thr Leu Val
 1 5 10 15
 Asn Tyr Val Ser Gly Asn Lys Ala Ile Leu Tyr Ile Ser Cys Leu Ala
 20 25 30
 Gln Val Phe Phe Phe Ser Trp Phe Ala Gly Leu Asp Ser Ile Leu Leu
 35 40 45
 Ala Ser Met Ala Tyr Asp Arg Xaa Ile Ala Ile Cys Asp Pro Leu His
 50 55 60
 Tyr Thr Thr Val Met Thr Pro Arg Val Cys Val Leu Leu Val Ala Met
 65 70 75 80
 Cys Leu Phe Gly Gly Cys Ala Asn Ser Leu Thr His Asn Ile Leu Leu
 85 90 95
 Thr Gln Leu Ser Phe Cys Gly His Thr Glu Ile Pro Leu Phe Phe Cys
 100 105 110
 Asp Leu Asn Val Val Ile Arg Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asp Trp Met Ile Tyr Thr Met Gly Gly Leu Thr Ala Ile Ile Pro Phe
 130 135 140
 Ser Gly Ile Leu Ile Ser Tyr Ile His Ile Phe Val Ala Met Leu Arg
 145 150 155 160
 Ile Leu Ser Ala Gln Gly Lys Trp Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ile Ala Val Tyr Leu Leu Asn Gly Thr Ile Ile Gly Val Tyr
 180 185 190
 Leu Asn Pro Thr Ser Ser His Thr Ala Gln Gln Asp Thr Ala Ser Ala

195 200 205
Val Met Tyr Thr Met Val Thr Pro
210 215

<210> 2512

<211> 216

<212> PRT

<213> Unknown (p125-dir-0-8 conceptual translation of range 2-649)

<400>2512

Phe Val Asp Leu Cys Phe Thr Thr Thr Thr Val Pro Lys Met Leu Val
1 5 10 15
Asn His Ile Ser Gly Asn Lys Thr Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30
Gln Met Phe Phe Phe Ile Trp Phe Ala Ser Ile Asp Ser Phe Leu Leu
35 40 45
Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
50 55 60
Tyr Ala Ser Leu Met Ile Pro Arg Leu Cys Ala Leu Leu Val Ala Thr
65 70 75 80
Ser Trp Ser Phe Ala Cys Ile Asn Ala Leu Thr His Thr Val Leu Leu
85 90 95
Thr Gln Leu Ser Phe Cys Ser His Asn Glu Ile Pro His Phe Phe Cys
100 105 110
Asp Leu Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ile Asn
115 120 125
Asp Val Leu Val Tyr Thr Val Gly Ala Leu Pro Ile Leu Met Pro Phe
130 135 140
Val Gly Ile Leu Val Ser Tyr Thr Arg Ile Phe Ala Ala Val Leu Arg
145 150 155 160
Ile Pro Ser Ala Arg Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Val Ile Gly Val Tyr
180 185 190
Leu Ser Pro Met Ser Tyr His Thr Val Glu Lys Asp Thr Ala Ala Ala
195 200 205
Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 2513

<211> 216

<212> PRT

<213> Unknown (p123-dir-0-8 conceptual translation of range 2-649)

<400>2513

Phe Val Asp Leu Cys Leu Thr Thr Thr Thr Val Pro Lys Met Leu Leu
1 5 10 15
Asn Ile Gln Thr Gln Lys Lys Thr Ile Ser Tyr Ala Gly Cys Leu Thr
20 25 30
Gln Met Tyr Phe Phe Leu Leu Leu Leu Asp Leu Asp Asn Met Ile Leu
35 40 45
Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys His Pro Leu His
50 55 60
Tyr Thr Ser Val Met Leu Pro Ser Leu Cys Gly Leu Leu Met Ala Val
65 70 75 80
Leu Trp Val Val Ala Asn Leu Phe Ser Leu Leu Phe Thr Leu Leu Met
85 90 95
Ala Gln Leu Ser Phe Cys Gly Asn Asn Thr Ile Pro His Phe Phe Cys
100 105 110
Asp Leu Ser Val Leu Leu Lys Leu Ser Cys Ser Asp Thr His Ile Val
115 120 125

Glu Asn Leu Leu Leu Ile Val Ser Gly Leu Leu Gly Val Thr Pro Leu
 130 135 140
 Ile Cys Ile Leu Val Ser Tyr Ser Arg Ile Val Ala Thr Val Met Arg
 145 150 155 160
 Ile Pro Ser Ala Lys Gly Lys Arg Lys Thr Phe Ser Thr Cys Gly S r
 165 170 175
 His Leu Thr Val Val Ala Leu Phe Tyr Cys Ala Gly Phe Gly Val Phe
 180 185 190
 Phe Thr Pro Pro Ser Ser His Ser Gly Gly Lys Asp Thr Ala Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2514

<211> 222

<212> PRT

<213> Unknown (3983377-dir-0-8 conceptual translation of range 1-666)

<400>2514

Ala Asn Leu Ser Ser Val Asp Ile Ser Ala Pro Ser Val Ile Val Pro
 1 5 10 15
 Lys Ala Leu Val Asn His Met Leu Gly Ser Lys Ser Ile Ser Tyr Thr
 20 25 30
 Gly Cys Met Thr Gln Ile Tyr Phe Phe Ile Thr Phe Asn Asn Met Asp
 35 40 45
 Gly Phe Leu Leu Ser Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 50 55 60
 His Pro Leu His Tyr Thr Met Met Met Arg Pro Arg Leu Cys Val Leu
 65 70 75 80
 Leu Val Ala Ile Ser Trp Ala Ile Thr Asn Leu His Ala Leu Leu His
 85 90 95
 Thr Leu Leu Met Val Arg Leu Thr Phe Cys Ser His Asn Ala Val His
 100 105 110
 His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys Ser Asp
 115 120 125
 Thr Phe Ile Asn Asp Leu Met Val Phe Thr Ile Gly Gly Leu Val Phe
 130 135 140
 Met Thr Pro Phe Thr Cys Ile Ile Val Ser Tyr Ala Tyr Ile Phe Ser
 145 150 155 160
 Lys Val Leu Lys Leu Lys Ser Ala His Gly Ile Arg Lys Ala Leu Ser
 165 170 175
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ala Ile
 180 185 190
 Leu Gly Ile Tyr Met His Pro Ser Ser Thr Tyr Thr Val Gln Asp Thr
 195 200 205
 Val Ala Thr Val Ile Phe Thr Val Val Thr Pro Met Val Asn
 210 215 220

<210> 2515

<211> 156

<212> PRT

<213> Unknown (902714-dir-0-6 conceptual translation of range 2-469)

<400>2515

Ile Cys His Pro Leu His Tyr Thr Val Met Met Arg Pro Arg Leu Cys
 1 5 10 15
 Val Leu Leu Val Ala Val Ser Trp Val Ile Thr Asn Leu His Ala Leu
 20 25 30
 Leu His Thr Leu Leu Met Val Gln Leu Thr Phe Cys Ser His Asn Ala
 35 40 45
 Val His His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys

50	55	60
Ser Asp Thr Phe Ile Asn Asp Ile Thr Ala Phe Thr Val Gly Gly Leu		
65	70	75
Thr Ser Ile Thr Pro Phe Thr Cys Ile Thr Val Ser Tyr Ala Tyr Ile		
	85	90
Leu Ser Ser Val Leu Lys Phe Pro Ser Ile Gln Gly Ile Arg Lys Ala		
	100	105
Leu Ser Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly		
	115	120
Ala Ile Leu Gly Val Tyr Met His Pro Ser Ser Thr Tyr Ser Leu Gln		
	130	135
Asp Thr Val Ala Thr Ala Phe Phe Thr Val Val Thr		
145	150	155

<210> 2516

<211> 216

<212> PRT

<213> Unknown (OST034-dir-0-8 conceptual translation of range 2-649)

<400>2516

Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val		
1	5	10
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr		
	20	25
Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu		
	35	40
Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn		
	50	55
Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile		
	65	70
Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu		
	85	90
Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys		
	100	105
Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn		
	115	120
Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe		
	130	135
Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg		
	145	150
Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser		
	165	170
His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr		
	180	185
Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala		
	195	200
Val Leu Phe Thr Val Val Thr Pro		
210	215	

<210> 2517

<211> 323

<212> PRT

<213> Unknown (p156-dir-0-12 conceptual translation of range 34-1003)

<400>2517

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu		
1	5	10
Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln Gln His Ile Phe Phe Leu		
	20	25
Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile		
	35	40
		45

Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Ph
 50 55 60
 Phe Leu Ala Ser L u Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr
 65 70 75 80
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
 85 90 95
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Gly Thr Ala Leu Leu
 100 105 110
 Leu Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala Thr Met Ala
 115 120 125
 Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Met Met Ile
 130 135 140
 Met Ser Leu His Arg Cys Ala Leu Leu Val Thr Ala Cys Trp Thr Leu
 145 150 155 160
 Thr Ser Leu Val Ala Met Thr His Thr Phe Leu Ile Phe Arg Leu Ser
 165 170 175
 Phe Cys Ser Lys Ile Leu Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu
 180 185 190
 Met Lys Val Ser Cys Ser Asp Ala Gln Val Asn Glu Leu Val Leu Leu
 195 200 205
 Phe Leu Gly Gly Ala Val Ile Leu Ile Pro Phe Met Leu Ile Leu Val
 210 215 220
 Ser Tyr Ile Arg Ile Val Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln
 225 230 235 240
 Gly Arg Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Val Val
 245 250 255
 Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser
 260 265 270
 Ser Ser Ser Asn Ser Val Lys Glu Asp Thr Val Ala Ala Val Met Tyr
 275 280 285
 Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
 290 295 300
 Lys Asp Met Lys Ala Ala Val Val Arg Leu Leu Lys Gly Arg Val Ser
 305 310 315 320
 Leu Ser Gln

<210> 2518

<211> 320

<212> PRT

<213> Unknown (p38-dir-0-11 conceptual translation of range 34-993)

<400>2518

Ser Asp Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu
 1 5 10 15
 Leu Ser Gly Leu Ser Asp Gln Pro Gln Gln Gln His Ile Leu Phe Leu
 20 25 30
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile
 35 40 45
 Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr
 65 70 75 80
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
 85 90 95
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp
 100 105 110
 Met Asp Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys
 130 135 140

Ala Leu Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Val Ala Met
 145 150 155 160
 Thr His Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Lys Ile Ile
 165 170 175
 Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser
 180 185 190
 Asp Thr Gln Val Ser Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val
 195 200 205
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val
 210 215 220
 Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Val Val Val Ala Leu Phe Phe Gly Thr
 245 250 255
 Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val
 260 265 270
 Asp Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Leu
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Ala Ala
 290 295 300
 Val Val Arg Leu Leu Lys Gly Arg Val Ser Phe Ser Gln Gly Gln Gly
 305 310 315 320

<210> 2519

<211> 317

<212> PRT

<213> Unknown (p27-dir-0-11 conceptual translation of range 34-984)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400>2519

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu
 1 5 10 15
 Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln Gln His Ile Phe Phe Leu
 20 25 30
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile
 35 40 45
 Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Ser Thr Thr
 65 70 75 80
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
 85 90 95
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp
 100 105 110
 Met Asp Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys
 130 135 140
 Ala Phe Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Leu Ala Met
 145 150 155 160
 Thr Arg Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu
 165 170 175
 Pro Gly Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser
 180 185 190
 Asp Ala Gln Val Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val
 195 200 205
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val

210	215	220
Ser Ala Ile Leu Arg	Ala Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe	
225	230	235
Ser Thr Cys Asp Ser	His Leu Val Val Val Ala Leu Phe Phe Gly Thr	240
	245	250
Val Ile Arg Ala Tyr	Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val	255
	260	265
Lys Glu Asp Thr Ala	Ala Ala Val Met Tyr Thr Val Val Thr Pro Leu	270
	275	280
Leu Asn Pro Phe Ile	Tyr Ser Met Arg Asn Lys Asp Met Lys Ala Ala	285
	290	295
Val Val Arg Leu Leu	Lys Gly Arg Val Ser Phe Ser Gln	300
305	310	315

<210> 2520

<211> 242

<212> PRT

<213> Unknown (p80-dir-0-9 conceptual translation of range 5-731)

<400>2520

Thr Asp Ile Phe Phe Thr Ser Thr Thr Val Pro Lys Ala Leu Val Asn	
1 5 10 15	
Ile Gln Thr Gln Ser Thr Ser Ile Ser Tyr Ala Gly Cys Leu Ala Gln	
20 25 30	
Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala	
35 40 45	
Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr	
50 55 60	
Met Met Ile Met Ser Leu Arg Arg Cys Ala Val Leu Val Ala Ala Cys	
65 70 75 80	
Trp Thr Leu Thr Ser Leu Val Ala Met Thr His Thr Phe Leu Ile Ser	
85 90 95	
Gln Leu Ser Phe Cys Ser Lys Ile Ile Pro Asp Phe Phe Cys Asp Leu	
100 105 110	
Gly Pro Leu Met Lys Val Ser Cys Phe Asp Thr Gln Val Asn Glu Leu	
115 120 125	
Val Leu Leu Phe Leu Gly Gly Thr Val Ile Leu Ile Pro Phe Met Leu	
130 135 140	
Val Leu Val Ser Tyr Ile Gln Ile Val Ser Ala Ile Leu Arg Ala Pro	
145 150 155 160	
Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu	
165 170 175	
Val Val Val Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys	
180 185 190	
Pro Ser Ser Ser Ser Ser Ser Ser Val Glu Glu Asp Thr Ala Ala Ala	
195 200 205	
Val Met Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser	
210 215 220	
Leu Arg Asn Lys Asp Met Lys Ala Ala Val Val Arg Leu Leu Lys Gly	
225 230 235 240	
Arg Val	

<210> 2521

<211> 225

<212> PRT

<213> Unknown (3983403-dir-0-8 conceptual translation of range 1-675)

<400>2521

Ala Thr Leu Ser Cys Val Asp Ile Leu Phe Thr Ser Thr Thr Val Pro
1 5 10 15

Lys Ala Leu Val Asn Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala
 20 25 30
 Gly Cys Leu Val Gln Leu Tyr Phe Leu Thr Phe Gly Asp Met Asp
 35 40 45
 Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Ph Val Ala Ile Cys
 50 55 60
 His Pro Leu His Tyr Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu
 65 70 75 80
 Leu Val Thr Val Cys Trp Thr Leu Thr Thr Val Val Ala Met Thr His
 85 90 95
 Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Gln Lys Val Ile Pro
 100 105 110
 Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Ile Ala Cys Ser Glu
 115 120 125
 Thr Arg Ile Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val Ile
 130 135 140
 Leu Ile Pro Phe Leu Leu Ile Leu Met Ser Tyr Ile Arg Ile Val Ser
 145 150 155 160
 Ala Ile Leu Arg Val Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val
 180 185 190
 Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val
 195 200 205
 Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Val Leu
 210 215 220
 Asn
 225

<210> 2522

<211> 217

<212> PRT

<213> Unknown (p144-dir-0-8 conceptual translation of range 5-654)

<400>2522

Asp Asp Ile Leu Leu Val Ser Thr Ile Val Pro Lys Ala Leu Val Asn
 1 5 10 15
 Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala Gly Cys Leu Val Gln
 20 25 30
 Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala
 35 40 45
 Thr Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr
 50 55 60
 Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu Leu Val Thr Val Cys
 65 70 75 80
 Trp Ile Leu Thr Thr Val Val Ala Met Thr His Thr Phe Leu Ile Phe
 85 90 95
 Trp Phe Ser Phe Tyr Ser Lys Lys Val Ile Pro Gly Phe Phe Cys Asp
 100 105 110
 Leu Glu Pro Leu Ile Lys Ile Pro Cys Ser Glu Thr Arg Ile Asn Glu
 115 120 125
 Leu Val Leu Leu Phe Leu Gly Ser Ala Val Val Phe Ile Leu Leu Leu
 130 135 140
 Leu Ile Leu Val Ser Tyr Ile Gln Ile Val Ser Ala Ile Phe Arg Val
 145 150 155 160
 Pro Ser Ala Gln Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His
 165 170 175
 Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu
 180 185 190
 Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val Glu Asp Thr Ala Ala
 195 200 205

Ala Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 2523

<211> 215

<212> PRT

<213> Unknown (p111-d-0-8 conceptual translation of range 2-646)

<220>

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400>2523

Val	Val	Asp	Val	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1				5					10					15	
Asp	Met	Gln	Thr	Gly	Ser	His	Thr	Ile	Ser	Gln	Ala	Asp	Cys	Leu	Ser
			20					25					30		
Gln	Val	Tyr	Phe	Ser	Ile	Leu	Phe	Gly	Asp	Leu	Asp	Asp	Phe	Leu	Leu
		35					40					45			
Ala	Val	Met	Ser	Phe	Asp	Xaa	Tyr	Met	Ala	Ile	Cys	Arg	Pro	Leu	Cys
	50					55					60				
Tyr	Ala	Thr	Ala	Met	Ser	Ser	Gln	Cys	Cys	Val	Leu	Leu	Val	Ala	Thr
65					70					75				80	
Cys	Trp	Val	Ile	Ala	Gln	Leu	Asn	Ser	Leu	Leu	His	Thr	Val	Leu	Leu
				85					90					95	
Ala	Gln	Leu	Thr	Phe	Cys	Ala	Asp	His	Thr	Ile	Pro	His	Phe	Phe	Cys
			100					105					110		
Asp	Leu	Ala	Leu	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Ile	Asn
		115					120					125			
Glu	Leu	Val	Leu	Met	Ser	Met	Gly	Gly	Ala	Gly	Ile	Leu	Ile	Pro	Leu
	130					135					140				
Met	Cys	Ile	Leu	Gly	Ser	Tyr	Ala	Gln	Ile	Ile	Ser	Ala	Ile	Leu	Arg
145					150					155				160	
Met	Pro	Ser	Ala	Gly	Ser	Lys	Arg	Ile	Ala	Phe	Ser	Thr	Ser	Ser	Ser
			165						170					175	
His	Leu	Ala	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Val	Ile	Ser	Glu	Tyr	
		180					185					190			
Leu	Cys	Pro	Ser	Pro	Ser	Gly	Ser	Ser	Asp	Glu	Ser	Ser	Leu	Ala	Ala
		195				200						205			
Val	Leu	Tyr	Ala	Val	Val	Thr									
	210					215									

<210> 2524

<211> 216

<212> PRT

<213> Unknown (2921629-dir-0-8 conceptual translation of range 2-649)

<400>2524

Phe	Val	Asp	Met	Gly	Leu	Thr	Ser	Ser	Thr	Val	Thr	Lys	Met	Leu	Val
1				5					10					15	
Asn	Ile	Gln	Thr	Arg	His	His	Thr	Ile	Thr	Tyr	Thr	Gly	Cys	Leu	Thr
			20					25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Met	Phe	Gly	Asp	Leu	Asp	Ser	Phe	Phe	Leu
		35					40					45			
Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Cys
	50					55					60				
Tyr	Ser	Thr	Val	Met	Arg	Pro	Gln	Val	Cys	Ala	Leu	Met	Leu	Ala	Leu
65					70					75				80	
Cys	Trp	Val	Leu	Thr	Asn	Ile	Val	Ala	Leu	Thr	His	Thr	Phe	Leu	Met
			85						90					95	

Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
 115 120 125
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
 130 135 140
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
 145 150 155 160
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
 180 185 190
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Ile Val Thr Pro
 210 215

<210> 2525

<211> 342

<212> PRT

<213> Unknown (1256388-dir-2-13 conceptual translation of range 379-1402)

<220>

<221> VARIANT

<222> (1)...(342)

<223> Xaa = Any Amino Acid

<400>2525

Phe Xaa Leu Ser Phe Leu Asn Tyr Arg Cys Ser Ile Arg Met Glu Asn
 1 5 10 15
 Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser Gly Phe Pro
 20 25 30
 Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met Tyr Leu Val
 35 40 45
 Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly Ser Asp Pro
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Ala
 65 70 75 80
 Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu Phe Asn Val
 85 90 95
 Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu Thr Gln Met
 100 105 110
 Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Ser
 130 135 140
 Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile Leu Cys Trp
 145 150 155 160
 Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu Met Ala Arg
 165 170 175
 Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe Cys Asp Val
 180 185 190
 Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val Asn Glu Leu
 195 200 205
 Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro Phe Val Ser
 210 215 220
 Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu Arg Ile Gln
 225 230 235 240
 Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu
 245 250 255
 Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val Tyr Leu Phe

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<210> 2526
<211> 216
<212> PRT
<213> Unknown (p101-dir-0-8 conceptual translation of range 2-649)
```

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<210> 2527
<211> 176
<212> PRT
<213> Unknown (3273640-dir-0-7 conceptual translation of range 4-531)
```

1535

```

Asp Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
65          70          75          80
Lys Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
      85          90          95
Ile Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys
      100        105        110
Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
      115        120        125
His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
      130        135        140
Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala
      145        150        155        160
Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

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<210> 2528

<211> 175

<212> PRT

<213> Unknown (3273644-dir-0-7 conceptual translation of range 4-528)

<400>2528

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Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile
      85          90          95
Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys Val
      100        105        110
Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
      115        120        125
Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr Leu
      130        135        140
Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala Val
      145        150        155        160
Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

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<210> 2529

<211> 158

<212> PRT

<213> Unknown (3273656-dir-0-6 conceptual translation of range 4-477)

<400>2529

```

Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Thr Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile

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<210> 2530
<211> 176
<212> PRT
<213> Unknown (3273650-dir-0-7 conceptual translation of range 1-528)
```

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<210> 2531
<211> 157
<212> PRT
<213> Unknown (902676-dir-0-6 conceptual translation of range 2-472)
```

1537

Thr Thr Ile Gly Val Tyr Leu Cys Pro Ser Ser Val Arg Thr Ala Val
 130 135 140
 Lys Glu Lys Ala Ser Ala Val Met Tyr Thr Ala Val Thr
 145 150 155

<210> 2532

<211> 313

<212> PRT

<213> Unknown (p82-dir-0-11 conceptual translation of range 1-939)

<400>2532

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
 20 25 30
 Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
 85 90 95
 Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
 100 105 110
 Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
 130 135 140
 Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145 150 155 160
 Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
 165 170 175
 Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
 180 185 190
 Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
 195 200 205
 Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
 245 250 255
 Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
 260 265 270
 Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
 290 295 300
 Val Asn Arg Lys Ile Thr Ser Ser Ser
 305 310

<210> 2533

<211> 157

<212> PRT

<213> Unknown (902331-dir-0-6 conceptual translation of range 2-472)

<400>2533

Ile Cys His Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys
 1 5 10 15
 Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu

20							25					30				
Leu	His	Thr	Val	Leu	Ile	Ala	Gln	Leu	Ser	Phe	Cys	Ala	Ser	Asn	Ile	
35							40					45				
Ile	His	His	Phe	Leu	Cys	Asp	Leu	Asn	Pro	Leu	Leu	Gln	Leu	Ser	Cys	
50							55					60				
Ser	Asp	Val	Ser	Phe	Asn	Val	Met	Ile	Ile	Phe	Ala	Val	Gly	Asp	Leu	
65							70					75				
Leu	Ala	Leu	Thr	Pro	Leu	Val	Cys	Ile	Leu	Val	Ser	Tyr	Gly	Leu	Ile	
85							90					95				
Phe	Ser	Thr	Val	Leu	Lys	Ile	Thr	Ser	Thr	Gln	Gly	Lys	Gln	Arg	Ala	
100							105					110				
Val	Ser	Thr	Cys	Ser	Cys	His	Leu	Ser	Val	Val	Val	Leu	Phe	Tyr	Gly	
115							120					125				
Thr	Ala	Ile	Ala	Val	Tyr	Phe	Ser	Pro	Ser	Ser	Pro	His	Met	Pro	Glu	
130							135					140				
Ser	Asp	Thr	Leu	Ser	Thr	Ile	Met	Tyr	Ser	Met	Val	Ala				
145							150					155				

44-38861-2534

<211> 217

<212> PRT

<213> Unknown (p152-rev-0-8 conceptual translation of range 2-652)

<400>2534

Phe	Leu	Asp	Ile	Gly	Phe	Ile	Ser	Thr	Ile	Ile	Pro	Lys	Met	Leu	Asp
1				5					10					15	
His	Ile	Ser	Ser	Gly	Ile	Lys	Leu	Ile	Ser	Tyr	Gly	Glu	Cys	Leu	Thr
			20					25					30		
Gln	Leu	Tyr	Phe	Ser	Gly	Leu	Phe	Ala	Asp	Leu	Asp	Asn	Asn	Phe	Leu
		35					40					45			
Leu	Ala	Val	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Ser	His	Pro	Leu
	50					55					60				
His	Tyr	Ala	Leu	Thr	Met	Asn	Ser	Gln	Arg	Cys	Val	Leu	Leu	Val	Ala
65				70						75				80	
Val	Ser	Trp	Val	Ile	Thr	Ile	Leu	His	Ala	Leu	Val	His	Thr	Leu	Leu
				85					90					95	
Val	Thr	Arg	Leu	Ser	Phe	Cys	Gly	Pro	Asn	Ile	Ile	Pro	His	Phe	Phe
			100					105					110		
Cys	Asp	Leu	Val	Pro	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Ser	Thr	Cys	Val
			115				120					125			
Asn	Asp	Leu	Val	Leu	Ile	Leu	Val	Ala	Gly	Thr	Leu	Leu	Ile	Ala	Pro
						135					140				
Phe	Val	Cys	Ile	Leu	Met	Ser	Tyr	Phe	Tyr	Ile	Ala	Leu	Ala	Ile	Leu
145					150					155				160	
Arg	Ile	Asp	Ser	Pro	Arg	Gly	Lys	Gln	Arg	Ala	Phe	Ser	Ser	Cys	Thr
				165					170					175	
Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Ser	Thr	Ala	Ile	Gly	Val
			180					185					190		
Tyr	Leu	Cys	Pro	Pro	Ser	Ser	His	Ser	Asp	Gly	Lys	Asp	Arg	Val	Phe
		195					200					205			
Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro							
	210					215									

<210> 2535

<211> 156

<212> PRT

<213> Unknown (902317-dir-0-6 conceptual translation of range 5-472)

<400>2535

Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val
1 5 10 15

Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu
 20 25 30
 His Thr Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile
 35 40 45
 Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr
 50 55 60
 Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val
 65 70 75 80
 Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile
 85 90 95
 Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe
 100 105 110
 Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr
 115 120 125
 Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys
 130 135 140
 Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr
 145 150 155

<210> 2536

<211> 215

<212> PRT

<213> Unknown (OST226-dir-0-8 conceptual translation of range 2-646)

<400>2536

Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Gln
 1 5 10 15
 Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly Cys Leu Ala
 20 25 30
 Gln Thr Tyr Ser Ser Leu Leu Arg Arg His Glu Asn Phe Ile Leu Ala
 35 40 45
 Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Phe His Tyr
 50 55 60
 Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met Val Val Met Cys
 65 70 75 80
 His Ala Leu Ser His Leu His Ala Met Leu His Thr Phe Leu Met Gly
 85 90 95
 Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His Phe Phe Cys Asp
 100 105 110
 Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr Tyr Leu Asn Thr
 115 120 125
 Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser Gly Ala Leu Ala
 130 135 140
 Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val Val Leu Arg Ile
 145 150 155 160
 Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr Arg Gly Ser His
 165 170 175
 Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser Trp Val Tyr Phe
 180 185 190
 Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg Ile Ile Thr Val
 195 200 205
 Val Tyr Thr Val Val Thr Pro
 210 215

<210> 2537

<211> 319

<212> PRT

<213> Unknown (4190944-dir-20-13 conceptual translation of range 2175-3131)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400>2537

```

Gln Gln Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu
 1           5           10           15
Leu Gly Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val
 20           25           30
Phe Ser Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile
 35           40           45
Thr Leu Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe
 50           55           60
Leu Ser Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val
 65           70           75           80
Pro Lys Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr
 85           90           95
Thr Gly Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met
 100          105          110
Glu Asn Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile
 115          120          125
Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val
 130          135          140
Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu
 145          150          155          160
His Thr Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile
 165          170          175
Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr
 180          185          190
Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val
 195          200          205
Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile
 210          215          220
Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe
 225          230          235          240
Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr
 245          250          255
Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys
 260          265          270
Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn
 275          280          285
Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met
 290          295          300
Lys Trp Met Ser Arg Met Gln Thr Phe Phe Phe Arg Xaa Asn Pro
 305          310          315

```

<210> 2538

<211> 326

<212> PRT

<213> Unknown (4190944-dir-490-12 conceptual translation of range 49118-50095)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2538

```

Ile Cys Tyr Ser Val Ser Leu Ser Leu Gly Glu Pro Thr Thr Met Gly
 1           5           10           15
Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly Leu Ser
 20           25           30

```

Ser Arg Pro Glu Asp Gln Lys Pr Leu Phe Ala Val Phe Leu Pro Ile
 35 40 45
 Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala Ile Arg
 50 55 60
 Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Ile Leu
 65 70 75 80
 Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu
 85 90 95
 Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu Cys Leu
 100 105 110
 Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser Tyr Leu
 115 120 125
 Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe
 130 135 140
 His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Leu Val
 145 150 155 160
 Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile Leu Leu
 165 170 175
 Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe
 180 185 190
 Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val
 195 200 205
 Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro
 210 215 220
 Phe Ser Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu
 225 230 235 240
 Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly
 245 250 255
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Val
 260 265 270
 Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr
 275 280 285
 Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met His Arg
 305 310 315 320
 Met Lys Cys Gln Xaa Lys
 325

<210> 2539

<211> 214

<212> PRT

<213> Unknown (hg23-dir-0-8 conceptual translation of range 4-645)

<400>2539

Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu Val Asn
 1 5 10 15
 Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu Cys Leu Thr Gln
 20 25 30
 Met Tyr Phe Phe Leu Ala Cys Gly Asn Thr Asp Ser Tyr Leu Leu Ala
 35 40 45
 Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe His Tyr
 50 55 60
 Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Val Leu Ser
 65 70 75 80
 Phe Cys Ile Pro His Leu His Ser Leu Leu His Ile Leu Leu Thr Asn
 85 90 95
 Gln Val Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe Cys Asp
 100 105 110
 Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val Lys Glu
 115 120 125

Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro Phe Ser
 130 135 140
 Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu Lys Ile
 145 150 155 160
 Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Leu Tyr Phe
 180 185 190
 Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr Ile Ile
 195 200 205
 Tyr Pro Val Leu Thr Pro
 210

<210> 2540

<211> 316

<212> PRT

<213> Unknown (4190944-dir-624-13 conceptual translation of range 62576-63523)

<400>2540

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu
 20 25 30
 Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val
 145 150 155 160
 Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr
 180 185 190
 Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met
 195 200 205
 Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala
 210 215 220
 Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser
 245 250 255
 Tyr Val Tyr Leu Gln Pro Leu Ser Ser Tyr Thr Val Lys Asp Arg Ile
 260 265 270
 Ala Thr Ile Asn Tyr Thr Val Leu Thr Ser Val Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Gln Lys Leu Ile
 290 295 300
 Asn Lys Ile Lys Ser Gln Met Ser Arg Phe Ser Thr
 305 310 315

<210> 2541

<211> 327

<212> PRT

<213> Unknown (4190944-dir-1371-13 conceptual translation of range 137254-138234)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2541

```

Arg Lys Ser Arg Asp Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser
 1           5           10           15
Gly Phe Ile Leu Leu Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro
          20           25           30
Leu Phe Ala Ile Phe Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn
          35           40           45
Val Leu Ile Ile Pro Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro
          50           55           60
Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr
65           70           75           80
Thr Val Ile Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys
          85           90           95
Val Ile Ser Tyr Val Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala
          100          105          110
Phe Gly Asn Thr Asp Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg
          115          120          125
Leu Val Ala Ile Cys Asn Pro Leu His Tyr Asp Val Val Met Lys Pro
          130          135          140
Arg His Cys Leu Leu Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu
145          150          155          160
His Ser Leu Phe Arg Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala
          165          170          175
Ser His Ile Ile Lys His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys
          180          185          190
Leu Ser Cys Ser Asp Thr Ser Ser Ser Gln Met Val Val Met Thr Glu
          195          200          205
Thr Leu Ala Val Ile Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr
          210          215          220
Leu Arg Ile Met Val Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys
225          230          235          240
Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu
          245          250          255
Phe Tyr Gly Ser Ile Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr
          260          265          270
Ser Val Val Arg Asp Arg Val Ala Thr Val Met Tyr Thr Val Val Thr
          275          280          285
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys
          290          295          300
Arg Gly Leu Lys Lys Leu Gln Asp Arg Ile Tyr Arg Xaa Lys Glu Gln
305          310          315          320
Asn Val Gly Val Ser Xaa Leu
          325

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<210> 2542

<211> 216

<212> PRT

<213> Unknown (hg16-dir-0-8 conceptual translation of range 1-648)

<400>2542


```

Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
 1          5          10          15
Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val Gly Cys Leu Ala
 20          25          30
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35          40          45
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50          55          60
Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu Met Leu Leu Gly
 65          70          75          80
Ser Tyr Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85          90          95
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
100          105          110
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
115          120          125
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
130          135          140
Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
145          150          155          160
Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
165          170          175
His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
180          185          190
Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp Arg Val Ala Thr
195          200          205
Val Met Tyr Thr Val Val Thr Pro
210          215

```

<210> 2543

<211> 323

<212> PRT

<213> Unknown (4190944-dir-1112-13 conceptual translation of range 111405-112373)

<220>

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400>2543

```

Arg Asp Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile
 1          5          10          15
Leu Leu Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala
 20          25          30
Ile Phe Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile
 35          40          45
Ile Leu Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe
 50          55          60
Phe Leu Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile
 65          70          75          80
Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser
 85          90          95
Tyr Val Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn
100          105          110
Thr Asp Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala
115          120          125
Ile Cys Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys
130          135          140
Leu Leu Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu
145          150          155          160

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Phe Arg Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile
 165 170 175
 Ile Lys His Phe Phe Cys Asp Thr Gln Pr Val Leu Lys Leu Ser Cys
 180 185 190
 Ser Asp Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala
 195 200 205
 Val Ile Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile
 210 215 220
 Ile Val Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly
 245 250 255
 Ser Val Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met
 260 265 270
 Lys Gly Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu
 290 295 300
 Lys Lys Leu Arg His Arg Ile Tyr Ser Xaa Lys Glu Gln Asn Val Gly
 305 310 315 320
 Met Ser Lys

<210> 2544

<211> 216

<212> PRT

<213> Unknown (OST046-dir-0-8 conceptual translation of range 2-649)

<400>2544

Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
 1 5 10 15
 Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val Gly Cys Leu Val
 20 25 30
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35 40 45
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60
 Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu Met Leu Leu Gly
 65 70 75 80
 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95
 Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
 100 105 110
 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125
 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140
 Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
 145 150 155 160
 Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr
 180 185 190
 Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly Arg Val Ala Thr
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2545

<211> 216

<212> PRT

<213> Unknown (p100-dir-0-8 conceptual translation of range 2-649)

<400>2545

```

Leu Val Asp Leu Cys Phe Thr Thr Val Ile Val Pro Glu Met Leu Val
 1          5          10          15
Ser Met Leu Met Gln Asn Lys Ala Ile Ser Phe Ala Gln Cys Ile Ala
 20          25          30
Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu
 35          40          45
Ala Ala Met Pro Ile Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu His
 50          55          60
Tyr Thr Thr Thr Met Ser Pro Arg Arg Cys Val Leu Leu Val Ala Met
 65          70          75          80
Ser Trp Val Val Ser His Phe His Ser Leu Val His Thr Leu Leu Met
 85          90          95
Ala Arg Leu Ser Phe Cys Gly Pro Asn Ala Ile His His Phe Phe Cys
100          105          110
Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn
115          120          125
Glu Val Leu Ala Phe Thr Glu Gly Ser Leu Val Ile Met Ser Pro Phe
130          135          140
Leu Phe Ile Val Ile Ser Tyr Val Trp Ile Thr Arg Ala Val Leu Arg
145          150          155          160
Val Pro Ser Gly Arg Gly Arg Tyr Lys Ala Phe Ser Thr Cys Ser Ser
165          170          175
His Ile Thr Val Val Val Leu Phe Tyr Gly Thr Ile Val Ser Val Tyr
180          185          190
Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr
195          200          205
Val Ile Tyr Thr Val Val Thr Pro
210          215

```

<210> 2546

<211> 328

<212> PRT

<213> Unknown (4190944-rev-159-13 conceptual translation of range 16099-17082)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400>2546

```

Phe Gln Ala Gly Xaa Leu Ser Leu Met Met Ser Phe Ala Pro Asn Ala
 1          5          10          15
Ser His Ser Pro Val Phe Leu Leu Leu Gly Phe Ser Arg Ala Asn Ile
 20          25          30
Ser Tyr Thr Leu Leu Phe Phe Leu Phe Leu Ala Ile Tyr Leu Thr Thr
 35          40          45
Ile Leu Gly Asn Val Thr Leu Val Leu Leu Ile Ser Trp Asp Ser Arg
 50          55          60
Leu His Ser Pro Met Tyr Tyr Leu Leu Arg Gly Leu Ser Val Ile Asp
 65          70          75          80
Met Gly Leu Ser Thr Val Thr Leu Pro Gln Leu Leu Ala His Leu Val
 85          90          95
Ser His Tyr Pro Thr Ile Pro Ala Ala Arg Cys Leu Ala Gln Phe Phe
100          105          110
Phe Phe Tyr Ala Phe Gly Val Thr Asp Thr Leu Val Ile Ala Val Met
115          120          125
Ala Leu Asp Arg Tyr Val Ala Ile Cys Asp Pro Leu His Tyr Ala Leu

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130	135	140
Val Met Asn His Gln Arg Cys Ala Cys Leu Leu Ala Leu Ser Trp Val		
145	150	155
Val Ser Ile Leu His Thr Met Leu Arg Val Gly Leu Val Leu Pro Leu		
	165	170
Cys Trp Thr Gly Asp Ala Gly Gly Asn Val Asn Leu Pro His Phe Phe		
	180	185
Cys Asp His Arg Pro Leu Leu Arg Ala Ser Cys Ser Asp Ile His Ser		
	195	200
Asn Glu Leu Ala Ile Phe Phe Glu Gly Gly Phe Leu Met Leu Gly Pro		
	210	215
Cys Ala Leu Ile Val Leu Ser Tyr Val Arg Ile Gly Ala Ala Ile Leu		
225	230	235
Arg Leu Pro Ser Ala Ala Gly Arg Arg Arg Ala Val Ser Thr Cys Gly		
	245	250
Ser His Leu Thr Met Val Gly Phe Leu Tyr Gly Thr Ile Ile Cys Val		
	260	265
Tyr Phe Gln Pro Pro Phe Gln Asn Ser Gln Tyr Gln Asp Met Val Ala		
	275	280
Ser Val Met Tyr Thr Ala Ile Thr Pro Leu Ala Asn Pro Phe Val Tyr		
	290	295
Ser Leu His Asn Lys Asp Val Lys Gly Ala Leu Cys Arg Leu Leu Glu		
305	310	315
Trp Val Lys Val Asp Pro Xaa Leu		
	325	

<210> 2547

<211> 216

<212> PRT

<213> Unknown (hg99-dir-0-8 conceptual translation of range 1-648)

<400>2547

Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro Lys Met Leu Asp	
1	5
Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala Gly Cys Leu Thr	
	20
Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp Ser Cys Leu Leu	
	35
Ala Asp Met Ala Tyr Asp Cys Tyr Val Asp Ile Arg His Pro Leu Pro	
	50
Tyr Asp Thr Arg Met Ser Arg Ala Met Cys Ala Ala Leu Val Gly Met	
65	70
Ala Trp Val Val Ser His Val His Ser Leu Leu Tyr Ile Leu Leu Met	
	85
Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro His Phe Phe Cys	
	100
Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp Asn His His Ile	
	115
Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val Val Thr Pro Phe	
	130
Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala Ala Val Leu Gln	
145	150
Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser Thr Cys Gly Ser	
	165
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr	
	180
Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly Arg Val Ala Thr	
	195
Val Met Tyr Thr Val Val Thr Pro	
	210

<210> 2548

<211> 319

<212> PRT

<213> Unknown (p16-dir-0-11 conceptual translation of range 1-960)

<400>2548

```

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1           5           10           15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
          20           25           30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
          35           40           45
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
          50           55           60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65           70           75           80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
          85           90           95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
          100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
          115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
          130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
          165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
          180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
          195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
          210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
          245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
          260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
          275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
          290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
305          310          315

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<210> 2549

<211> 158

<212> PRT

<213> Unknown (2564509-dir-0-6 conceptual translation of range 1-474)

<400>2549

```

Ile Cys Ser Pro Leu His Tyr Gly Met Val Met Ser Arg Arg Met Cys
 1           5           10           15
Phe Cys Leu Val Ala Ile Ser Trp Leu Val Ile Ala Val His Ser Val
          20           25           30
Leu His Ser Val Leu Thr Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln
          35           40           45
Ile His His Phe Phe Cys Asp Met Thr Pro Leu Leu Lys Leu Ser Cys
          50           55           60

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Ser Asp Thr Ser Val Asn Glu Leu Val Ile Phe Ile Glu Gly Pro Phe
 65 70 75 80
 Ser Val Ala Val Pro Leu Gly Ile Val Leu Val Ser Tyr Val Arg Ile
 85 90 95
 Ile Ser Ala Ile Leu Lys Ile Arg Ser Pro Glu Gly Arg His Arg Ala
 100 105 110
 Phe Ser Thr Cys Ser Ser His Leu Met Val Val Ile Leu Tyr Phe Gly
 115 120 125
 Thr Ile Ile Phe Met Tyr Phe Arg Pro Thr Ser Ser Tyr Ser Leu Asp
 130 135 140
 Tyr Asp Arg Val Val Ser Val Met Tyr Thr Val Val Ala Pro
 145 150 155

<210> 2550

<211> 156

<212> PRT

<213> Unknown (2564511-dir-0-6 conceptual translation of range 1-468)

<400>2550

Asn Pro Leu His Tyr Thr Thr Val Met Ser Lys Lys Val Cys Leu Leu
 1 5 10 15
 Leu Val Gly Met Leu Trp Leu Trp Ala Val Leu Tyr Ser Leu Met His
 20 25 30
 Ile Val Leu Ile Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln Ile Asn
 35 40 45
 His Phe Val Cys Asp Thr Val Pro Leu Phe Lys Leu Ser Cys Ser Asp
 50 55 60
 Thr Ser Thr Asn Gln Leu Val Ile Phe Thr Val Gly Ser Leu Ile Val
 65 70 75 80
 Met Val Pro Phe Leu Ile Val Leu Ile Ser Tyr Ala Arg Ile Val Phe
 85 90 95
 Ala Ile Leu Lys Ile Ser Ser Thr Asp Gly Arg Arg Lys Thr Phe Ser
 100 105 110
 Thr Cys Ser Ser His Leu Thr Val Thr Leu Tyr Phe Gly Thr Ile
 115 120 125
 Met Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Leu Thr Lys Asp
 130 135 140
 Arg Val Ala Ser Val Met Tyr Thr Val Leu Ala Pro
 145 150 155

<210> 2551

<211> 158

<212> PRT

<213> Unknown (2564513-dir-0-6 conceptual translation of range 1-474)

<400>2551

Ile Cys Asp Pro Leu Arg Tyr Thr Val Val Met Ser Lys Arg Ile Cys
 1 5 10 15
 Leu Gln Met Val Ala Gly Ser Trp Val Leu Val Ser Leu His Ser Leu
 20 25 30
 Leu His Thr Val Leu Thr Ala Arg Leu Ser Phe Cys Gly Arg Asn Leu
 35 40 45
 Ile Arg His Phe Phe Cys Glu Met Ser Pro Leu Phe Ala Leu Ser Cys
 50 55 60
 Ser Asp Thr Thr Thr Asn Glu Leu Val Ile Phe Thr Glu Gly Ser Phe
 65 70 75 80
 Ser Leu Ala Leu Pro Phe Leu Leu Ile Leu Phe Ser Tyr Leu Arg Ile
 85 90 95
 Leu Ser Thr Val Leu Arg Ile Arg Ser Val Asp Gly Lys Cys Arg Ala
 100 105 110
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ala Leu Phe Tyr Gly

115 120 125
 Thr Leu Phe Ser Val Tyr Phe Arg Pro Ser Ser Ser His Ser Leu Asp
 130 135 140
 Asn Asp Arg Val Val Ser Ile Met Tyr Thr Ala Ile Thr Pro
 145 150 155

<210> 2552

<211> 315

<212> PRT

<213> Unknown (4808260-rev-1059-13 conceptual translation of range 106061-107005)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2552

Cys Leu Leu Ser Glu Val Met Leu Asn Thr Thr Ser Val Thr Glu Phe
 1 5 10 15
 Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe
 20 25 30
 Val Val Phe Leu Thr Ile Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala
 35 40 45
 Val Leu Met Ile Val Ile Ser Asp Pro Arg Leu His Ser Leu Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val
 65 70 75 80
 Thr Leu Pro Lys Met Leu Gln Asn Phe Leu Ser Thr His Lys Ala Ile
 85 90 95
 Ser Phe Leu Gly Cys Ile Ser Gln Leu His Phe Phe His Phe Leu Gly
 100 105 110
 Ser Thr Glu Ser Met Leu Phe Ala Val Met Ala Phe Asp Leu Ser Val
 115 120 125
 Ala Ile Cys Lys Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Gln Leu
 130 135 140
 Cys Thr Gln Met Ala Ile Thr Ile Trp Val Ile Gly Phe Phe His Ala
 145 150 155 160
 Leu Leu His Ser Val Met Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn
 165 170 175
 Arg Ile His His Phe Leu Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala
 180 185 190
 Cys Gly Asn Thr Glu Leu Asn Gln Trp Leu Leu Ser Thr Val Thr Gly
 195 200 205
 Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr
 210 215 220
 Ile Ile Thr Tyr Leu Phe Phe Lys Thr Arg Ser Cys Ser Met Leu Cys
 225 230 235 240
 Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Ile Leu Phe
 245 250 255
 Tyr Ala Pro Val Leu Phe Thr Tyr Ile His Pro Ala Leu Glu Ser Phe
 260 265 270
 Met Asp Gln Asp Arg Ile Val Ala Ile Met Tyr Thr Val Val Thr Pro
 275 280 285
 Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly
 290 295 300
 Ala Leu Gly Arg Val Ile Arg Arg Leu Xaa Phe
 305 310 315

<210> 2553

<211> 162

<212> PRT

<213> Unknown (1617234-dir-0-6 conceptual translation of range 1-486)

<400>2553

```

Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn
      20           25           30
Ser Leu Ile His Thr Ile Leu Thr Phe Met Leu Pro Phe Cys Gly Ser
      35           40           45
Asn Ala Ile Asp Ser Phe Phe Cys Asp Met Pro Pro Leu Leu Lys Leu
      50           55           60
Ala Cys Thr Asp Thr Leu Val Asn Gln Ile Val Ile Phe Val Thr Gly
      65           70           75           80
Ser Cys Ile Ile Ala Gly Pro Phe Met Leu Thr Val Phe Ser Tyr Val
      85           90           95
Gln Ile Ile Ser Thr Ile Val Ser Ile Arg Ser Ser Ser Arg Lys Lys
      100          105          110
Lys Ala Phe Ser Thr Cys Thr Ser His Ile Thr Ala Val Val Ile Phe
      115          120          125
Tyr Val Pro Ser Ile Cys Ile Tyr Phe Arg Pro Lys Ser Asn Gln Ala
      130          135          140
Met Ile Gln Asp Lys Met Ala Thr Val Ile Cys Ala Val Ile Thr Pro
      145          150          155          160
Leu Leu

```

<210> 2554

<211> 160

<212> PRT

<213> Unknown (4877310-dir-0-6 conceptual translation of range 2-481)

<400>2554

```

Ala Ala Ile Cys Lys Pro Leu His Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Leu Cys Val Cys Leu Ala Leu Gly Cys Trp Gly Val Gly Val Ile Asn
      20           25           30
Ser Thr Ile His Val Phe Phe Thr Phe Gln Leu Pro Phe Cys Arg Ser
      35           40           45
Arg His Ile Asn His Phe Phe Cys Glu Val Pro Pro Phe Phe Arg Leu
      50           55           60
Ser Cys Gln Asp Thr Trp Phe Asn Glu Leu Ala Met Tyr Ile Ser Ala
      65           70           75           80
Cys Ile Ile Ala Ile Cys Ala Phe Phe Leu Thr Leu Ile Ser Tyr Ile
      85           90           95
Tyr Ile Ile Ser Ser Ile Ala Lys Ile Arg Ala Pro Gln Gly Arg Tyr
      100          105          110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ala Val Tyr
      115          120          125
Tyr Gly Thr Ile Met Phe Ile Tyr Leu His Pro His Ser Ala Tyr Ser
      130          135          140
Pro Glu Met Gly Lys Ile Val Ser Ile Ile Tyr Thr Ser Val Thr Pro
      145          150          155          160

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<210> 2555

<211> 160

<212> PRT

<213> Unknown (4877337-dir-0-6 conceptual translation of range 2-481)

<400>2555

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Ile Cys Ser Pro Leu Leu Tyr Phe Thr Lys Met Ser Thr Arg Val Tyr

```


1	5	10	15
Val Gln Leu Leu Thr Val Ala Tyr Val Gly Gly Phe Leu Asn Ala Cys			
20	25	30	
Ser Phe Thr Ile Cys Phe Tyr Tyr Leu Leu Leu Cys Gly Pro Asn Arg			
35	40	45	
Val Asn His Phe Phe Cys Asp Phe Ala Pro Leu Val Glu Phe Ser Cys			
50	55	60	
Ser Asp Ile Ser Ile Pro Ala Val Val Pro Ser Phe Thr Ala Gly Ser			
65	70	75	80
Ile Ile Val Val Thr Val Ile Val Ile Ala Ile Ser Tyr Ile Tyr Ile			
85	90	95	
Leu Ile Thr Ile Leu Lys Met Arg Ser Thr Glu Gly His His Lys Ala			
100	105	110	
Phe Ser Thr Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly			
115	120	125	
Thr Ile Thr Leu Ile Tyr Val Met Pro Lys Ser Ser Phe Ser Thr Asp			
130	135	140	
Gln Asn Lys Val Val Cys Val Phe Tyr Thr Val Val Ile Pro Met Leu			
145	150	155	160

<210> 2556

<211> 315

<212> PRT

<213> Unknown (4680263-dir-1-12 conceptual translation of range 259-1203)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2556

Glu Met Glu Pro Gly Asn Tyr Thr Val Val Thr Glu Phe Ile Leu Leu			
1	5	10	15
Gly Leu Thr Asp Asp Ile Thr Val Ser Val Ile Leu Phe Val Met Phe			
20	25	30	
Leu Ile Val Tyr Ser Val Thr Leu Met Gly Asn Leu Asn Ile Ile Val			
35	40	45	
Leu Ile Arg Thr Ser Pro Gln Leu His Thr Pro Met Tyr Leu Phe Leu			
50	55	60	
Ser His Leu Ala Phe Leu Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro			
65	70	75	80
Ile Met Leu Arg Gly Phe Leu Arg Lys Gly Thr Phe Ile Pro Val Ala			
85	90	95	
Gly Cys Val Ala Gln Leu Cys Ile Val Val Ala Phe Gly Thr Ser Glu			
100	105	110	
Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys			
115	120	125	
Ser Pro Leu Leu Tyr Ser Thr Gln Met Ser Ser Thr Val Cys Ile Leu			
130	135	140	
Leu Val Gly Thr Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Ile Phe			
145	150	155	160
Thr Gly Cys Ser Leu Asn Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn			
165	170	175	
His Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ser Cys Ser His			
180	185	190	
Asp Phe Ser Phe Glu Val Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile			
195	200	205	
Val Val Thr Val Phe Ile Ile Ala Leu Ser Tyr Val Tyr Ile Leu Val			
210	215	220	
Ser Ile Leu Lys Met Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser			
225	230	235	240

Thr Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Phe Gly Thr Ile
 245 250 255
 Thr Phe Ile Tyr Val Met Pro Gln Ser Tyr Ser Thr Asp Gln Asn
 260 265 270
 Lys Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Phe Arg Asn Lys Glu Val Lys Glu Ala Met Lys Lys
 290 295 300
 Leu Ile Ala Lys Thr His Trp Trp Ser Xaa Asn
 305 310 315

<210> 2557

<211> 312

<212> PRT

<213> Unknown (1246533-dir-0-11 conceptual translation of range 1-936)

<400>2557

Met Ala Glu Gly Asn His Thr Leu Ala Ser Glu Phe Ile Leu Val Gly
 1 5 10 15
 Leu Ser Asp His Pro Lys Met Lys Ala Ala Leu Phe Val Val Phe Leu
 20 25 30
 Leu Ile Tyr Val Ile Thr Phe Gln Gly Asn Leu Gly Ile Ile Ile Leu
 35 40 45
 Ile Gln Gly Asp Pro Arg Leu His Thr Ser Met Tyr Phe Phe Leu Ser
 50 55 60
 Ser Leu Ser Val Val Asp Ile Cys Phe Ser Ser Val Ile Ala Pro Arg
 65 70 75 80
 Thr Leu Val Asn Phe Leu Ser Glu Arg Arg Thr Ile Ser Phe Thr Gly
 85 90 95
 Cys Thr Gly Gln Thr Phe Phe Tyr Ile Val Phe Val Thr Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Thr Arg Arg Gln Cys Met Gln Leu
 130 135 140
 Val Val Gly Ser Tyr Ile Gly Gly Ile Leu Asn Ala Ile Ile Gln Thr
 145 150 155 160
 Thr Phe Ile Ile Arg Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Leu Leu Ala Leu Ser Leu Ala Ser Thr
 180 185 190
 Tyr Ile Ser Glu Met Ile Leu Phe Ser Leu Ala Gly Ile Ile Glu Leu
 195 200 205
 Ser Thr Val Thr Ser Ile Leu Val Ser Tyr Ile Phe Ile Ser Cys Ala
 210 215 220
 Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Leu Leu Tyr Gly Thr Thr Ile
 245 250 255
 Phe Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Thr Asp Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Val Glu Arg Ile Thr Val Arg Val
 305 310

<210> 2558

<211> 313

<212> PRT

<213> Unknown (p28-dir-0-11 conceptual translation of range 1-939)

<400>2558

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1          5          10          15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
 20          25          30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35          40          45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65          70          75          80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85          90          95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

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<210> 2559

<211> 117

<212> PRT

<213> Unknown (2695895-dir-0-5 conceptual translation of range 2-351)

<220>

<221> VARIANT

<222> (1)...(117)

<223> Xaa = Any Amino Acid

<400>2559

```

Asp Leu Cys Tyr Ser Thr Val Ile Ala Pro Lys Ala Leu Ala Ile Phe
 1          5          10          15
Leu Ser Lys Asp Lys Lys Ile Ser Tyr Asn Gly His Ala Ala Xaa Phe
 20          25          30
Tyr Phe Leu Cys Cys Val Gly Thr Glu Gly Leu Leu Leu Ala Val Met
 35          40          45

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Ala Tyr Asp His Phe Ser Ala Phe Cys Ser Pro Phe Leu Tyr Pro Val
 50 55 60
 Arg Met Ser Gln Gln Val Cys Val His Leu Val Ile Gly Ser Tyr Ile
 65 70 75 80
 Cys Gly Gly Ile Asn Ser Met Val Gln Thr Gly Phe Thr Phe Ser Leu
 85 90 95
 Asn Phe Cys Gly Glu Asn Xaa Leu Asp His Phe Phe Cys Asp Val Pro
 100 105 110
 Ala Leu Ile Ile Lys Ile
 115

<210> 2560

<211> 216

<212> PRT

<213> Unknown (2921661-dir-0-8 conceptual translation of range 2-649)

<400>2560

Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu
 20 25 30
 Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala
 65 70 75 80
 Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met
 85 90 95
 Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys
 100 105 110
 Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn
 115 120 125
 Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val
 130 135 140
 Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp
 180 185 190
 Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2561

<211> 313

<212> PRT

<213> Unknown (p19-dir-0-11 conceptual translation of range 1-939)

<400>2561

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu
 20 25 30
 Phe Met Tyr Leu Val Met Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35 40 45
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys

65					70					75				80
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly
			85						90				95	
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala
		100						105					110	
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His
		115						120					125	
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu
		130				135					140			
Val	Ser	Ala	Ser	Trp	Ile	Met	Asn	Ala	Leu	Tyr	Ser	Leu	Leu	His Thr
145					150					155				160
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Cys	Ala	Asn	His	Glu	Ile	Pro His
			165						170					175
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Ala	Asp Pro
		180						185					190	
Phe	Thr	Asn	Glu	Leu	Val	Ile	Phe	Ile	Thr	Gly	Gly	Leu	Thr	Gly Leu
		195					200					205		
Ile	Cys	Val	Leu	Cys	Leu	Ile	Ile	Ser	Tyr	Thr	Asn	Val	Phe	Ser Thr
	210					215					220			
Ile	Leu	Lys	Ile	Pro	Ser	Ala	Gln	Gly	Lys	Arg	Lys	Ala	Phe	Ser Thr
225				230						235				240
Cys	Ser	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ser Phe
			245						250					255
Cys	Val	Tyr	Phe	Ser	Pro	Pro	Ser	Thr	Arg	Ser	Ala	Gln	Lys	Asp Thr
		260						265				270		
Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro Phe
	275					280						285		
Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Glu	Ile	Lys	Ser	Ser	Leu	Arg	Lys Leu
	290				295						300			
Ile	Trp	Val	Arg	Lys	Ile	His	Ser	Pro						
305					310									

<210> 2562

<211> 313

<212> PRT

<213> Unknown (p40-dir-0-11 conceptual translation of range 1-938)

<400>2562

Met	Glu	Gly	Lys	Asn	Leu	Thr	Ser	Ile	Ser	Glu	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Glu	Gln	Leu	Glu	Glu	Gln	Lys	Ala	Leu	Leu	Val	Ser	Phe	Leu
		20						25					30		
Phe	Met	Tyr	Leu	Val	Thr	Val	Ala	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Val
	35					40						45			
Ile	Ile	Thr	Asp	Thr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50				55						60				
Asn	Leu	Ser	Leu	Ala	Asp	Ala	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys
65				70					75					80	
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly	
			85						90					95	
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala	
		100						105					110		
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His	
		115					120					125			
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu	
	130					135					140				
Val	Ser	Ala	Ser	Trp	Ile	Met	Asp	Ala	Leu	His	Ser	Leu	Leu	His Thr	
145				150						155				160	
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Tyr	Ala	Asn	His	Glu	Thr	Pro His	
			165						170					175	
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Thr	Asp Pro	

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<210> 2563
<211> 161
<212> PRT
<213> Unknown (293757-dir-0-6 conceptual translation of range 2-484)
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<210> 2564
<211> 313
<212> PRT
<213> Unknown (p39-dir-0-11 conceptual translation of range 1-939)
```

1558

```

Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
65          70          75          80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
      85          90          95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
      100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu
      130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
      165          170          175
Phe Phe Cys Asp Ile Asp Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
      180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
      195          200          205
Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Ile Phe Ser Thr
210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
      245          250          255
Cys Val Tyr Phe Ile Pro Pro Ser Thr Arg Ser Ala Gln Lys Asp Thr
      260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
290          295          300
Ile Trp Val Arg Glu Ile His Ser Pro
305          310

```

<210> 2565

<211> 315

<212> PRT

<213> Unknown (3738097-rev-723-12 conceptual translation of range 72448-73392)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2565

```

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
1          5          10          15
Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu
      20          25          30
Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
      35          40          45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
50          55          60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65          70          75          80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
      85          90          95
Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
100          105          110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115          120          125

```

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
 130 135 140
 Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
 145 150 155 160
 Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
 165 170 175
 Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
 195 200 205
 Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
 210 215 220
 Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
 245 250 255
 Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
 260 265 270
 Phe Ser Val Phe Tyr Thr Asn Val Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
 290 295 300
 Ile Lys Ile Gln Arg Arg Asn Ile Phe Xaa Leu
 305 310 315

<210> 2566

<211> 313

<212> PRT

<213> Unknown (p41-dir-0-11 conceptual translation of range 1-938)

<400>2566

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu
 20 25 30
 Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35 40 45
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Arg Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85 90 95
 Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu
 130 135 140
 Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Asn Ser Leu Ser Phe Cys Thr Asn Arg Glu Ile Pro His
 165 170 175
 Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180 185 190
 Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Val Ala Gly Leu
 195 200 205
 Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Met Asn Val Phe Ser Thr
 210 215 220
 Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Ser Ser Phe Ser Thr
 225 230 235 240

Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245 250 255
 Cys Val Tyr Val Ser Pro Pr Ser Thr Leu Ser Ala Gln Lys Asp Thr
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Ile
 290 295 300
 Ile Trp Val Arg Lys Ile His Ser Pro
 305 310

<210> 2567

<211> 315

<212> PRT

<213> Unknown (2317703-dir-0-13 conceptual translation of range 211-1155)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2567

Met Ala Thr Gly Asn Tyr Cys Val Phe Pro Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Leu Ser Lys Lys Ser Glu Leu Gln Met Pro Leu Phe Val Leu Phe Leu
 20 25 30
 Gly Ile Tyr Ile Val Thr Val Val Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 Ile Arg Leu Ser Ser Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Cys His Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Ala Glu Lys Asn Ile Ile Ser Tyr Thr Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Phe Phe Leu Ile Phe Ala Ile Ala Glu Cys
 100 105 110
 His Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Tyr Gln Ser Tyr Ile Ser Met
 130 135 140
 Ile Ser Gly Val Tyr Ile Ile Gly Val Val Cys Ala Ser Ala His Thr
 145 150 155 160
 Gly Phe Met Ile Arg Ser Gln Phe Cys Asn Leu Asp Val Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Glu Leu Ala His Ser Ser Thr
 180 185 190
 Tyr Val Asn Glu Leu Val Ile Leu Ile Cys Gly Thr Cys Asn Ile Val
 195 200 205
 Val Pro Thr Leu Thr Ile Leu Thr Ser Tyr Ile Phe Ile Ile Ala Thr
 210 215 220
 Ile Leu His Ile Arg Ser Thr Glu Gly Arg Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Ala Ala
 245 250 255
 Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Ser Thr Ala Leu Lys Lys Ile
 290 295 300
 Leu Glu Arg Lys Ser Phe Val Xaa Thr Glu Val

305

310

315

<210> 2568

<211> 114

<212> PRT

<213> Unknown (888-dir-0-5 conceptual translation of range 2-343)

<400>2568

```

Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Ser Asn Thr Leu Cys
 1             5             10             15
Ile Arg Leu Leu Val Leu Ser Leu Leu Gly Gly Leu Leu His Ala Ile
      20             25             30
Ile His Ser Ser Phe Leu Phe Arg Leu Thr Phe Cys Asp Ser Ile Ile
      35             40             45
Val His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Thr Cys
      50             55             60
Thr Asp Pro Ser Ile Asn Tyr Leu Ile Val Phe Ile Phe Ala Gly Ser
      65             70             75             80
Ile Gln Met Phe Thr Ile Leu Ile Val Leu Val Ser Tyr Thr Leu Val
      85             90             95
Leu Phe Thr Ile Leu Arg Lys Lys Ser Leu Gln Gly Ile Lys Lys Ala
      100             105             110
Phe Ser

```

<210> 2569

<211> 159

<212> PRT

<213> Unknown (1514485-dir-0-6 conceptual translation of range 2-478)

<400>2569

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Thr Ile Ser Met Pro Lys Ser
 1             5             10             15
Leu Cys Met Lys Leu Val Ala Gly Ser Tyr Leu Gly Gly Val Leu Asn
      20             25             30
Ser Leu Thr Gln Thr Cys Cys Leu Leu Pro Leu Pro Phe Cys Gly Pro
      35             40             45
Asn Val Ile Asn His Tyr Phe Cys Asp Thr Asn Pro Leu Leu Lys Leu
      50             55             60
Thr Cys Ser Asp Gly Arg Leu Asn Glu Leu Leu Val Thr Phe Asn
      65             70             75             80
Gly Thr Ile Ser Met Thr Val Leu Leu Ile Ile Val Ile Ser Tyr Val
      85             90             95
Tyr Ile Leu Val Ser Ile Leu Ser Ile Arg Ser Ala Arg Gly Arg His
      100             105             110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Leu Thr Val Thr Leu Phe
      115             120             125
Tyr Val Pro Ala Gly Leu Ser His Met Gln Pro Gly Ser Lys Tyr Ser
      130             135             140
Leu Asp Met Glu Lys Val Thr Ala Val Phe Tyr Thr Leu Leu Val
      145             150             155

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<210> 2570

<211> 131

<212> PRT

<213> Unknown (1514487-dir-0-5 conceptual translation of range 2-394)

<400>2570

```

Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser Thr Val Met Thr Lys Arg
 1             5             10             15
Val Cys Met Gln Leu Val Val Gly Ser Tyr Met Gly Gly Leu Leu Asn

```

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<210> 2571
<211> 114
<212> PRT
<213> Unknown (32508-dir-0-5 conceptual translation of range 2-343)
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<210> 2572
<211> 315
<212> PRT
<213> Unknown (p42-dir-0-11 conceptual translation of range 1-945)
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1563

```

Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
130      135      140
Gly Met Leu Val Ala Val Ser Trp Thr Cys Ala Phe Thr Asn Ala Leu
145      150      155      160
Thr His Thr Ile Ala Leu Thr Thr Leu Asn Phe Cys Gly Pro Ser Val
      165      170      175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
      180      185      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Phe Val Ala Ala Ala Phe
      195      200      205
Met Ala Val Val Pro Leu Val Leu Ile Ser Val Ser Tyr Ala His Val
      210      215      220
Val Ala Ala Val Leu Gln Ile His Ser Ala Glu Gly Arg Lys Lys Ala
225      230      235      240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
      245      250      255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
      260      265      270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
      275      280      285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
      290      295      300
Trp Gln Leu Leu Val Gly Lys Arg Ser Leu Thr
305      310      315

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<210> 2573

<211> 315

<212> PRT

<213> Unknown (p176-dir-0-11 conceptual translation of range 1-945)

<400>2573

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
1      5      10      15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val
      20      25      30
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Gly Gly Asn Leu Ser Ile
      35      40      45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ser Pro Met Tyr Phe
      50      55      60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr
      65      70      75      80
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro
      85      90      95
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly
      100      105      110
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Phe Leu Ala
      115      120      125
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
      130      135      140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
      145      150      155      160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
      165      170      175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
      180      185      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
      195      200      205
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val
      210      215      220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
225      230      235      240

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Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Met Phe Tyr Gly
 245 250 255
 Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp
 260 265 270
 Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Val
 275 280 285
 Asn Pro Ile Ile Tyr Arg Phe Arg Asn Pro Glu Val Gln Ser Ala Ile
 290 295 300
 Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala
 305 310 315

<210> 2574

<211> 162

<212> PRT

<213> Unknown (1552397-dir-0-6 conceptual translation of range 1-486)

<400>2574

Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys
 1 5 10 15
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp
 20 25 30
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser
 35 40 45
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu
 50 55 60
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser
 65 70 75 80
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile
 85 90 95
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala
 130 135 140
 Pro Lys Gln Asp Gln Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro
 145 150 155 160
 Leu Leu

<210> 2575

<211> 161

<212> PRT

<213> Unknown (1552399-dir-0-6 conceptual translation of range 1-483)

<400>2575

Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys
 1 5 10 15
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala
 20 25 30
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser
 35 40 45
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly
 65 70 75 80
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val
 85 90 95
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys
 100 105 110
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe

	115		120		125
Tyr	Gly Ser Ile Ile Cys Leu Tyr Met Arg Pro Thr Lys Ser Ile Ser				
130		135		140	
Pro Asn Gln Asp Val Phe Ala Leu Leu Tyr Ala Val Leu Val Pro Met					
145		150		155	160
Leu					

<210> 2576

<211> 160

<212> PRT

<213> Unknown (4877302-dir-0-6 conceptual translation of range 2-481)

<400>2576

Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser Ile Ile Ser Thr Lys					
1	5	10		15	
Val Cys Ile Leu Ala Ala Leu Arg Trp Ser Val Gly Phe Val Cys					
20		25		30	
Thr Leu Pro Cys Thr Val Leu Leu Leu Arg Leu Ser Phe Cys Gly Pro					
35	40		45		
Lys Glu Ile Tyr His Tyr Tyr Cys Asp His Pro Gln Ile Leu Lys Val					
50	55		60		
Ala Cys Asn Asp Thr Ser Leu Asn Tyr Tyr Val Ser Leu Tyr Val Ala					
65	70		75		80
Ala Val Val Ile Val Val Pro Phe Leu Phe Ile Leu Ser Thr Tyr Leu					
85		90		95	
Gly Ile Leu Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg					
100	105		110		
Lys Thr Phe Ser Thr Cys Ser Ser His Leu Val Cys Val Val Ile Phe					
115	120		125		
Tyr Leu Ser Ala Gly Phe Ala Tyr Phe Arg Pro Gln Glu Thr Ser Ala					
130	135		140		
Ser Asp Tyr Ser Ile Met Ala Ser Leu Leu Tyr Ser Thr Leu Ser Pro					
145	150		155		160

<210> 2577

<211> 153

<212> PRT

<213> Unknown (2564501-dir-0-6 conceptual translation of range 1-459)

<400>2577

Lys Pro Leu His Tyr Met Thr Ile Met Ser His Arg Thr Cys Gly Leu					
1	5	10		15	
Leu Val Ala Ala Ser Trp Val Gly Gly Ser Ile His Ser Leu Leu Gln					
20		25		30	
Thr Leu Leu Leu Ala Trp Leu Pro Tyr Cys Gly Pro Asn Met Ile Asp					
35	40		45		
Ser Phe Phe Cys Asp Ala Pro Pro Leu Leu Lys Leu Ala Cys Thr Asp					
50	55		60		
Thr Thr Leu Val Gly Trp Leu Ile Leu Cys Asn Gly Gly Leu Ile Ala					
65	70		75		80
Val Cys Ser Phe Ser Val Leu Val Thr Ser Tyr Thr Phe Ile Ile Arg					
85		90		95	
Thr Pro Arg Thr Gln Leu Ile Glu Gly Lys Arg Arg Ala Leu Ser Thr					
100	105		110		
Cys Gly Ser His Cys Ile Val Val Val Phe Phe Phe Gly Pro Cys Ile					
115	120		125		
Tyr Ile Tyr Leu Arg Pro Ser Ile Ser Ile Phe Leu Asp Lys Val Val					
130	135		140		
Ser Val Phe Tyr Thr Leu Ile Thr Pro					
145	150				

<210> 2578

<211> 152

<212> PRT

<213> Unknown (2564499-dir-0-6 conc ptual translation of range 1-456)

<400>2578

```

Asn Pro Leu Arg Tyr Thr Thr Ile Met Ser Arg Lys Val Cys Ser Leu
 1           5           10           15
Leu Val Leu Ala Cys Trp Val Gly Gly Ala Val His Ser Thr Ala Gln
          20           25           30
Val Leu Leu Val Met Thr Leu Pro Phe Cys Gly Pro Asn Glu Val Gly
          35           40           45
His Phe Phe Cys Asp Ile Pro Pro Leu Phe Pro Leu Val Cys Thr Asp
          50           55           60
Thr Phe Leu Ser Gly Val Leu Ile Met Ser Asn Ser Gly Leu Ile Ser
65          70          75          80
Leu Ala Cys Phe Leu Thr Leu Ile Ile Ser Tyr Thr Leu Ile Leu Leu
          85          90          95
Ala Val Arg Arg Cys Ser Ala Glu Gly Lys Ser Lys Ala Leu Ser Thr
          100          105          110
Cys Gly Thr His Leu Thr Val Val Thr Ile Ala Phe Gly Pro Ser Ile
          115          120          125
Phe Ile Tyr Met Lys Pro Met Asn Leu Gln Val Asp Lys Ile Val Ala
          130          135          140
Leu Phe Phe Val Ile Ile Thr Pro
145          150

```

<210> 2579

<211> 205

<212> PRT

<213> Unknown (hg449-dir-0-7 conceptual translation of range 1-616)

<220>

<221> VARIANT

<222> (1)...(205)

<223> Xaa = Any Amino Acid

<400>2579

```

Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr Asp
 1           5           10           15
Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala Gln
          20           25           30
Ile Phe Leu His Phe Cys Gly Ile Pro Trp Ile Phe Leu Leu Pro Leu
          35           40           45
Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr Thr
          50           55           60
Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe Trp
65          70          75          80
Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val Gln
          85          90          95
Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp Leu
          100          105          110
Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly Val
          115          120          125
Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile Leu
          130          135          140
Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser Ala
145          150          155          160
Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val Phe
          165          170          175

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Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr Lys
 180 185 190
 Asp Lys Leu Val Ala Val Phe Tyr Val Ile Ile Thr Pro
 195 200 205

<210> 2580

<211> 154

<212> PRT

<213> Unknown (902708-dir-0-6 conceptual translation of range 2-463)

<400>2580

Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Ser Arg Pro Val Cys
 1 5 10 15
 Ile Phe Leu Val Gly Ala Ala Val Ile Leu Gly Phe Ile His Gly Ala
 20 25 30
 Ile Gln Thr Leu Phe Met Ala Gln Leu Pro Phe Cys Gly Pro Asn Ile
 35 40 45
 Ile Asn His Phe Met Cys Asp Leu Ile Pro Leu Leu Glu Leu Ala Cys
 50 55 60
 Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser Gly Ser
 65 70 75 80
 Leu Cys Leu Leu Thr Phe Ser Met Leu Val Val Ser Tyr Val Val Ile
 85 90 95
 Pro Arg Ser Leu Arg Asn His Ser Ser Glu Gly Arg Arg Lys Ala Leu
 100 105 110
 Ser Thr Cys Ala Ser His Val Thr Val Val Val Leu Phe Leu Val Pro
 115 120 125
 Cys Ser Tyr Leu Tyr Leu Arg Pro Met Thr Ser Phe Pro Thr Asn Lys
 130 135 140
 Ala Val Thr Val Phe Cys Thr Leu Val Thr
 145 150

<210> 2581

<211> 114

<212> PRT

<213> Unknown (32513-dir-0-5 conceptual translation of range 2-343)

<400>2581

Ile Cys Tyr Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Arg Ile Cys
 1 5 10 15
 Val Ala Leu Ala Val Gly Thr Trp Leu Leu Gly Cys Ile His Ser Ser
 20 25 30
 Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu
 35 40 45
 Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys
 50 55 60
 Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu
 65 70 75 80
 Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile
 85 90 95
 Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala
 100 105 110
 Phe Ser

<210> 2582

<211> 114

<212> PRT

<213> Unknown (32516-dir-0-5 conceptual translation of range 2-343)

<400>2582


```

Ile Cys His Pro Leu Asn Tyr Pr Val Ile Met Asn Arg Gly Val Phe
 1          5          10          15
M t Lys Leu Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr
          20          25          30
Val Gln Thr Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu
          35          40          45
Ile Asn His Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys
          50          55          60
Ala Asp Thr Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu
65          70          75          80
Ile Val Met Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val
          85          90          95
Leu Phe Ala Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala
          100          105          110
Phe Ser

```

<210> 2583

<211> 195

<212> PRT

<213> Unknown (2252615-dir-0-7 conceptual translation of range 1-586)

<400>2583

```

Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr
 1          5          10          15
Ser Cys Val Arg Pro Gln Met Leu Val His Leu Trp Gly Pro His Lys
          20          25          30
Thr Ile Ser Phe Leu Gly Cys Ala Val Gln Leu Phe Ile Phe Leu Leu
          35          40          45
Leu Gly Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg
          50          55          60
Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro
65          70          75          80
Arg Leu Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val
          85          90          95
Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Arg Leu Pro Phe Cys Pro
          100          105          110
His Arg Gln Ile Asp Asp Phe Val Cys Gln Val Pro Ser Leu Ile Arg
          115          120          125
Leu Ser Cys Gly Asp Thr Thr Phe Asn Gly Ile Gln Leu Ala Val Ser
          130          135          140
Ser Val Val Phe Leu Val Val Pro Leu Ala Leu Ile Leu Ile Ser Tyr
145          150          155          160
Gly Ala Ile Ala Arg Ala Val Leu Arg Ile Ser Ser Ala Thr Ala Trp
          165          170          175
Arg Lys Ala Leu Gly Thr Cys Ser Ser His Leu Ala Val Val Thr Leu
          180          185          190
Phe Tyr Ser
          195

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<210> 2584

<211> 106

<212> PRT

<213> Unknown (3328023-dir-0-5 conceptual translation of range 1-318)

<400>2584

```

Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
 1          5          10          15
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro Arg Leu
          20          25          30
Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val Gln Ser

```

	35		40		45		
Ile	Val	Gln	Thr	Pro	Pro	Thr	Leu
50						55	
Arg	Val	Asp	Asp	Phe	Val	Cys	Glu
65						70	
Cys	Gly	Asp	Thr	Thr	Tyr	Asn	Glu
						85	
Phe	Ile	Leu	Val	Val	Pro	Leu	Ser
						100	
							105

<210> 2585

<211> 194

<212> PRT

<213> Unknown (2828696-dir-0-7 conceptual translation of range 1-582)

<400>2585

Tyr	Phe	Phe	Leu	Ser	Asp	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr
1				5					10					15	
Ser	Cys	Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr
			20					25					30		
Ile	Ser	Phe	Leu	Gly	Cys	Ser	Val	Gln	Leu	Phe	Ile	Phe	Leu	Ser	Leu
			35				40					45			
Gly	Thr	Thr	Glu	Cys	Ile	Leu	Leu	Thr	Val	Met	Ala	Phe	Asp	Arg	Tyr
50						55				60					
Val	Ala	Val	Cys	Gln	Pro	Leu	His	Tyr	Ala	Thr	Ile	Ile	His	Pro	Arg
65						70			75						80
Leu	Cys	Trp	Gln	Leu	Ala	Ser	Val	Ala	Trp	Val	Met	Ser	Leu	Val	Gln
			85					90					95		
Ser	Ile	Val	Gln	Lys	Pro	Ser	Thr	Leu	His	Leu	Pro	Phe	Cys	Pro	His
			100					105					110		
Gln	Gln	Ile	Asp	Asp	Phe	Leu	Cys	Glu	Val	Pro	Ser	Leu	Ile	Gly	Leu
			115				120					125			
Ser	Cys	Gly	Asp	Thr	Ser	Tyr	Asn	Glu	Ile	Gln	Leu	Ala	Val	Ser	Ser
			130			135				140					
Val	Ile	Phe	Val	Val	Val	Pro	Leu	Ser	Leu	Ile	Leu	Ala	Tyr	Tyr	Gly
145					150				155						160
Ala	Thr	Ala	Gln	Ala	Val	Leu	Arg	Ile	Asn	Ser	Ala	Thr	Ala	Trp	Arg
			165					170						175	
Lys	Ala	Phe	Gly	Thr	Cys	Ser	Ser	His	Leu	Thr	Val	Val	Thr	Leu	Phe
			180					185					190		
Tyr	Ser														

<210> 2586

<211> 318

<212> PRT

<213> Unknown (4160199-rev-489-12 conceptual translation of range 49035-49987)

<400>2586

Gln	Glu	Gln	Ala	Met	Val	Asn	Gln	Ser	Ser	Thr	Pro	Gly	Phe	Leu	Leu
1				5					10					15	
Leu	Gly	Phe	Ser	Glu	His	Pro	Gly	Leu	Glu	Arg	Thr	Leu	Phe	Val	Val
			20					25					30		
Val	Phe	Thr	Ser	Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Leu	Ile	Ile
			35				40					45			
Leu	Leu	Ser	Ala	Leu	Asp	Pro	Lys	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe
50						55				60					
Leu	Ser	Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Cys	Val
65					70				75						80
Pro	Gln	Met	Leu	Val	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr	Ile	Ser	Phe

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<210> 2587
<211> 320
<212> PRT
<213> Unknown (1041044-dir-3-13 conceptual translation of range 488-1447)
```

400>2587																
Gln	Glu	Gln	Ala	Met	Asp	Asn	Gln	Ser	Ser	Thr	Pro	Gly	Phe	Leu	Leu	
1				5					10					15		
Leu	Gly	Phe	Ser	Glu	His	Pro	Gly	Leu	Gly	Arg	Thr	Leu	Phe	Val	Asp	
			20					25					30			
Val	Ile	Thr	Ser	Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Leu	Ile	Ile	
		35					40					45				
Leu	Leu	Ser	Ala	Leu	Asp	Thr	Lys	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	
	50					55					60					
Leu	Ser	Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Cys	Val	
65					70					75					80	
Pro	Gln	Met	Leu	Ala	Asn	Leu	Trp	Gly	Pro	Lys	Lys	Thr	Ile	Ser	Phe	
				85					90					95		
Leu	Asp	Cys	Ser	Val	Gln	Ile	Phe	Ile	Phe	Leu	Ser	Leu	Gly	Thr	Thr	
			100					105					110			
Glu	Cys	Ile	Leu	Met	Lys	Val	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val	
		115					120					125				
Cys	Gln	Pro	Leu	His	Tyr	Ala	Thr	Ile	Ile	His	Pro	Arg	Leu	Cys	Trp	
	130					135					140					
Gln	Leu	Ala	Ser	Val	Ala	Trp	Val	Ile	Gly	Leu	Val	Gly	Ser	Val	Val	
145					150					155					160	
Gln	Thr	Pro	Ser	Thr	Leu	His	Leu	Pro	Phe	Cys	Pro	Asp	Arg	Gln	Val	
				165					170					175		
Asp	Asp	Phe	Val	Cys	Glu	Val	Pro	Ala	Leu	Ile	Arg	Leu	Ser	Cys	Glu	
		180					185						190			
Asp	Thr	Ser	Tyr	Asn	Glu	Ile	Gln	Val	Ala	Val	Ala	Ser	Val	Phe	Ile	

195	200	205
Leu Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr		
210	215	220
Trp Ala Val Leu Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe		
225	230	235
Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser		
	245	250
Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg		
	260	265
Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn		
	275	280
Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg		
	290	295
Arg Leu Leu Gly Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala		
305	310	315
		320

<210> 2588

<211> 316

<212> PRT

<213> Unknown (3093312-dir-1364-13 conceptual translation of range 136584-137530)

<400>2588

Val Ala Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu		
1	5	10
Leu Gly Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile		
	20	25
Ile Phe Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val		
	35	40
Leu Val Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe		
	50	55
Leu Ser Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val		
	65	70
Pro Gln Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr		
	85	90
Ile Gly Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr		
	100	105
Glu Tyr Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val		
	115	120
Cys His Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu		
	130	135
Gln Leu Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile		
	145	150
Gln Ser Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val		
	165	170
Asp Asp Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr		
	180	185
Asp Thr Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu		
	195	200
Leu Val Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala		
	210	215
Lys Ala Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe		
	225	230
Gly Thr Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr		
	245	250
Val Thr Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp		
	260	265
Gly Lys Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn		
	275	280
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile		
	290	295
		300

Arg Leu Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn
305 310 315

<210> 2589

<211> 348

<212> PRT

<213> Unknown (5262456-dir-612-12 conceptual translation of range 61285-62326)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400>2589

Leu	Ile	Phe	Cys	Pro	Met	Ala	Asn	Thr	Leu	Ser	Ser	Leu	Asn	Ser	Cys
1				5					10				15		
Asn	Val	Phe	Leu	Leu	Val	Leu	Asn	Arg	Val	Met	Gly	Met	Thr	Asn	Ser
		20						25					30		
Ser	Val	Lys	Gly	Asp	Phe	Ile	Leu	Val	Gly	Phe	Ser	His	Gln	Pro	His
		35					40					45			
Leu	Glu	Lys	Ile	Leu	Phe	Val	Ala	Val	Leu	Ile	Ser	Tyr	Leu	Leu	Thr
	50					55					60				
Leu	Val	Gly	Asn	Thr	Val	Ile	Ile	Leu	Ile	Cys	Ser	Val	Asp	Pro	Lys
65					70					75					80
Leu	Lys	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His	Leu	Ser	Leu	Val	Asp
				85					90					95	
Ile	Cys	Phe	Thr	Thr	Ser	Ile	Val	Pro	Gln	Leu	Leu	Trp	Asn	Leu	Lys
			100					105					110		
Gly	Pro	Asp	Lys	Thr	Ile	Thr	Phe	Leu	Gly	Cys	Val	Ile	Gln	Leu	Tyr
		115					120					125			
Ile	Ser	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met
	130					135					140				
Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Lys	Pro	Leu	His	Tyr	Thr	Ala
145					150					155					160
Val	Met	Asn	Pro	Gln	Leu	Cys	Gln	Ala	Leu	Ala	Gly	Val	Ala	Trp	Leu
			165						170					175	
Ser	Gly	Val	Gly	Asn	Thr	Leu	Ile	Gln	Gly	Thr	Val	Thr	Leu	Trp	Leu
			180					185					190		
Pro	Arg	Cys	Gly	His	Arg	Leu	Leu	Gln	His	Phe	Phe	Cys	Glu	Val	Pro
		195				200						205			
Ser	Met	Ile	Lys	Leu	Ala	Cys	Val	Asp	Ile	His	Asp	Asn	Glu	Val	Gln
	210					215					220				
Leu	Phe	Val	Ala	Ser	Leu	Val	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Ile
225					230					235					240
Leu	Leu	Ser	Tyr	Gly	His	Ile	Ala	Lys	Val	Val	Ile	Arg	Ile	Lys	Ser
			245						250					255	
Val	Gln	Ala	Trp	Cys	Lys	Gly	Leu	Gly	Thr	Cys	Gly	Ser	His	Leu	Ile
		260						265					270		
Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ile	Thr	Ala	Val	Tyr	Ile	Gln	Ser
		275					280					285			
Asn	Ser	Ser	Tyr	Ala	His	Ala	His	Gly	Lys	Phe	Ile	Ser	Leu	Phe	Tyr
	290					295					300				
Thr	Val	Val	Thr	Pro	Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn
305					310					315					320
Asn	Asp	Val	Lys	Gly	Ala	Leu	Arg	Leu	Phe	Asn	Arg	Asp	Leu	Gly	Thr
			325						330					335	
Xaa	Lys	Met	Lys	Gln	Ser	Thr	Gln	Arg	Ser	Thr	Phe				
		340						345							

<210> 2590

<211> 312

<212> PRT

<213> Unknown (200153-dir-0-11 conceptual translation of range 1-936)

<400>2590

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1           5           10           15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
          20           25           30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
          35           40           45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
          65           70           75           80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
          85           90           95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
          100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
          115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
          130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
          145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn
          165          170          175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
          180          185          190
Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Val
          195          200          205
Val Pro Val Ser Val Ile Leu Val Ser Tyr Cys Phe Ile Ala Gln Ala
          210          215          220
Val Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala Phe Asn Thr
          225          230          235          240
Cys Val Ser His Leu Val Val Val Phe Leu Phe Tyr Gly Ser Ala Ile
          245          250          255
Tyr Gly Tyr Leu Leu Pro Ala Lys Ser Ser Asn Gln Ser Gln Gly Lys
          260          265          270
Phe Ile Ser Leu Phe Tyr Ser Val Val Thr Pro Met Val Asn Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Leu
          290          295          300
Leu Gly Lys Gly Arg Gly Ala Ser
          305          310

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<210> 2591

<211> 157

<212> PRT

<213> Unknown (902728-dir-0-6 conceptual translation of range 2-472)

<400>2591

```

Val Cys Arg Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys
 1           5           10           15
Trp Val Leu Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val
          20           25           30
Ile Gln Ser Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys
          35           40           45
Val Asp Asn Phe Leu Cys Glu Val Pro Ala Met Ile Lys L u Ala Cys
          50           55           60
Gly Asp Thr Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe

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65		70		75		80
Phe Thr Ala Val	Pro Leu Ser Ile Ile	Leu Val Ser Tyr Cys Phe Ile				
	85	90				
Ala Gln Ala Val	Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala					
	100	105				
Phe Asn Thr Cys Val	Ser His Leu Val Val Phe Leu Phe Tyr Gly					
	115	120				
Ser Ala Ile Tyr Gly Tyr	Leu Leu Pro Ala Lys Ser Ser Asn Gln Asp					
	130	135				
Gln Gly Lys Phe Ile	Ser Leu Phe Tyr Ser Val Val Thr					
145	150	155				

<210> 2592

<211> 312

<212> PRT

<213> Unknown (p146-dir-0-11 conceptual translation of range 1-936)

<400>2592

Met Asp Gly Val	Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1	5 10 15
Ile Ser Asp His	Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
	20 25 30
Phe Ser Tyr Leu	Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
	35 40 45
Ser Arg Leu Glu	Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
	50 55 60
Asn Leu Ser Ser	Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65	70 75 80
Met Leu Ile Asn	Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
	85 90 95
Cys Ile Thr Gln	Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
	100 105 110
Ile Leu Leu Val	Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
	115 120 125
Pro Leu Arg Tyr	Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
	130 135 140
Ala Val Ile Ala	Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
145	150 155 160
Thr Phe Thr Leu	Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
	165 170 175
Phe Leu Cys Glu	Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
	180 185 190
Ser Leu Asn Gln	Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
	195 200 205
Val Pro Leu Ser	Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
	210 215 220
Val Leu Lys Ile	His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
225	230 235 240
Cys Leu Ser His	Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
	245 250 255
Tyr Gly Tyr Leu	Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
	260 265 270
Phe Ile Ser Leu	Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
	275 280 285
Ile Tyr Thr Leu	Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
	290 295 300
Leu Gly Lys Gly	Arg Glu Val Gly
305	310

<210> 2593

<211> 216

<212> PRT

<213> Unknown (2921701-dir-0-8 conceptual translation of range 2-648)

<400>2593

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Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1           5           10           15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20           25           30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35           40           45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50           55           60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65           70           75           80
Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85           90           95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100          105          110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115          120          125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130          135          140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145          150          155          160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165          170          175
His Leu Ile Val Val Ser Leu Phe Lys Gly Thr Ala Val Ser Val Tyr
 180          185          190
Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195          200          205
Leu Phe Tyr Gly Ile Ile Ala Pro
 210          215

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<210> 2594

<211> 216

<212> PRT

<213> Unknown (2921699-dir-0-8 conceptual translation of range 2-649)

<400>2594

```

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1           5           10           15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20           25           30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35           40           45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50           55           60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65           70           75           80
Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85           90           95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100          105          110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115          120          125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130          135          140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145          150          155          160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165          170          175

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His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr
 180 185 190
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195 200 205
 Leu Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 2595

<211> 215

<212> PRT

<213> Unknown (2921706-dir-0-8 conceptual translation of range 2-646)

<220>

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400>2595

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1 5 10 15
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20 25 30
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35 40 45
 Ala Val Thr Ser Leu Ile Gly Cys Ser Tyr Cys Arg Pro Leu His Tyr
 50 55 60
 Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala Ser
 65 70 75 80
 Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr Leu
 85 90 95
 Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys Glu
 100 105 110
 Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn Glu
 115 120 125
 Ala Glu Leu Phe Leu Asp Ser Glu Leu Phe His Leu Ile Pro Leu Thr
 130 135 140
 Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg Ile
 145 150 155 160
 Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser His
 165 170 175
 Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr Leu
 180 185 190
 Xaa Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser Leu
 195 200 205
 Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 2596

<211> 112

<212> PRT

<213> Unknown (1142995-dir-0-5 conceptual translation of range 1-336)

<400>2596

Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln
 1 5 10 15
 Leu Ala Ala Val Ser Trp Ile Ile Gly Phe Gly Asn Ser Val Trp Leu
 20 25 30
 Ser Ile Leu Thr Leu Gln Leu Pro Arg Cys Gly His Tyr Val Ile Asp
 35 40 45
 His Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp
 50 55 60

Val Thr Ala Asn Glu Ala Glu Leu Phe Phe Val Ser Val Phe Phe His
 65 70 75 80
 Leu Thr Pr Leu Ser Leu Ile Leu Thr Ser Tyr Ala Phe Ile Ala Arg
 85 90 95
 Ala Ile Leu Lys Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly
 100 105 110

<210> 2597

<211> 314

<212> PRT

<213> Unknown (3080457-rev-750-12 conceptual translation of range 75137-76079)

<400>2597

Asn Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu
 1 5 10 15
 Val Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe
 20 25 30
 Leu Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu
 35 40 45
 Val Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro
 65 70 75 80
 Gln Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly
 85 90 95
 Gly Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu
 100 105 110
 Cys Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln
 130 135 140
 Leu Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln
 145 150 155 160
 Ser Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp
 165 170 175
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp
 180 185 190
 Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu
 195 200 205
 Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln
 210 215 220
 Ala Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala
 245 250 255
 Ile Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly
 260 265 270
 Lys Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg
 290 295 300
 Leu Leu Gln Arg Val Phe Leu Ile Lys Lys
 305 310

<210> 2598

<211> 343

<212> PRT

<213> Unknown (506841-dir-0-12 conceptual translation of range 60-1090)

<220>

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400>2598

Cys Ile Ile Tyr Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe
 1 5 10 15
 Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe
 20 25 30
 Val Val Phe Leu Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met
 35 40 45
 Ile Ile Leu Val Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Thr Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser
 65 70 75 80
 Thr Val Pro Gln Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile
 85 90 95
 Ser Tyr Gly Gly Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly
 100 105 110
 Ser Thr Glu Cys Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg
 130 135 140
 Cys Leu His Leu Ala Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser
 145 150 155 160
 Val Leu Gln Ser Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys
 165 170 175
 Glu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser
 180 185 190
 Cys Val Asp Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val
 195 200 205
 Leu Phe Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe
 210 215 220
 Ile Val Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys
 225 230 235 240
 Ala Phe Gly Thr Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr
 245 250 255
 Gly Thr Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys
 260 265 270
 Asp Arg Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala
 290 295 300
 Phe Lys Arg Leu Met Lys Arg Ile Ile Leu Ile Gly Lys Xaa Gly Val
 305 310 315 320
 Pro Glu Xaa Xaa Pro Tyr Xaa Tyr Lys Tyr Ile Phe Ile Ala Cys Lys
 325 330 335
 Leu Tyr Cys Phe Leu Leu Cys
 340

<210> 2599

<211> 348

<212> PRT

<213> Unknown (3093312-rev-75-13 conceptual translation of range 7680-8721)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400>2599

Leu Ile Ala Phe Leu Ser Tyr Ile Ph Leu Gly Val Arg Asn Lys Xaa
 1 5 10 15
 Val Ile Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu
 20 25 30
 Leu Gly Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val
 35 40 45
 Leu Leu Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met
 50 55 60
 Met Val Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe
 65 70 75 80
 Leu Thr Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val
 85 90 95
 Pro His Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr
 100 105 110
 Ala Gly Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr
 115 120 125
 Glu Cys Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val
 130 135 140
 Cys Arg Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu
 145 150 155 160
 Arg Met Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu
 165 170 175
 Gln Ser Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val
 180 185 190
 Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala
 195 200 205
 Asp Thr Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile
 210 215 220
 Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala
 225 230 235 240
 Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe
 245 250 255
 Gly Thr Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr
 260 265 270
 Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp
 275 280 285
 Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn
 290 295 300
 Ser Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys
 305 310 315 320
 Arg Leu Met Pro Arg Ile Phe Phe Cys Lys Lys Xaa Arg Ser Thr Pro
 325 330 335
 Ser Val Met Arg Ile Phe Leu Val Phe Pro Tyr Leu
 340 345

<210> 2600

<211> 272

<212> PRT

<213> Unknown (5262456-rev-0-10 conceptual translation of range 184-1000)

<400>2600

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
 20 25 30
 Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35 40 45
 His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
 65 70 75 80

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Leu Val Asn L u Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
      85          90          95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
      100          105          110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
      115          120          125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
      130          135          140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
      145          150          155          160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
      165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
      180          185          190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
      195          200          205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
      210          215          220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
      225          230          235          240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
      245          250          255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
      260          265          270

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<210> 2601

<211> 350

<212> PRT

<213> Unknown (3093312-dir-1027-12 conceptual translation of range 102817-103865)

<220>

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400>2601

```

Phe Leu Ser Gly Asn Arg Lys Xaa Met Met Met Glu Lys Xaa Asn Ala
  1           5           10           15
Ser Ser Glu Gly Tyr Phe Ile Leu Val Gly Phe Ser Asn Trp Pro Tyr
      20           25           30
Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Cys Leu Met Thr
      35           40           45
Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Thr Tyr Leu Asp Ser His
      50           55           60
Leu His Thr Pro Leu Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp
      65           70           75           80
Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val Ser Leu Trp
      85           90           95
Gly Val Glu Lys Thr Ile Ser Tyr Ala Gly Cys Met Val Gln Leu Tyr
      100          105          110
Phe Phe Leu Thr Leu Gly Thr Thr Glu Cys Val Leu Leu Val Val Met
      115          120          125
Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His Tyr Thr Val
      130          135          140
Leu Met His Ser Arg Phe Cys His Leu Leu Ala Val Ala Ser Trp Val
      145          150          155          160
Ser Gly Phe Thr Asn Pro Ala Leu His Ser Ser Phe Thr Phe Trp Val
      165          170          175
Pro Leu Cys Gly His Arg Gln Ile Asp His Phe Phe Cys Glu Val Pro
      180          185          190

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Ala Leu Leu Xaa Leu Ser Phe Val Asn Thr Arg Glu Asn Lys Leu Thr
 195 200 205
 Leu Met Ile Thr Ser Ser Ile Phe Val Leu Leu Leu Thr Leu Ile
 210 215 220
 Phe Thr Ser Tyr Gly Ala Ile Ala Gln Ala Val Leu Arg Met Gln Ser
 225 230 235 240
 Thr Thr Gly Leu Gln Lys Val Phe Gly Thr Cys Gly Ala His His Met
 245 250 255
 Val Val Ser Leu Phe Phe Ile Pro Ala Met Cys Met Tyr Leu Gln Pro
 260 265 270
 Pro Ser Gly Asn Ser Gln Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr
 275 280 285
 Thr Val Val Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 290 295 300
 Lys Asp Val Arg Gly Val Val Lys Arg Leu Arg Gly Trp Glu Xaa Ala
 305 310 315 320
 Cys Val Cys Val Ile Leu Thr Ile Xaa Trp Ser Leu Ser Ser Gln Xaa
 325 330 335
 Phe Ile His Leu Phe Ile Tyr Gln Pro Phe Phe Tyr Ser Leu
 340 345 350

<210> 2602

<211> 205

<212> PRT

<213> Unknown (5262456-dir-273-9 conceptual translation of range 27452-28066)

<400>2602

Gln Lys Ile Ala Lys Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met
 1 5 10 15
 Leu Leu Gly Phe Pro Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly
 20 25 30
 Val Val Phe Phe Phe Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu
 35 40 45
 Ile Leu Leu Pro Leu Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe
 50 55 60
 Phe Leu Arg Asn Leu Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile
 65 70 75 80
 Val Pro Gln Met Leu Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr
 85 90 95
 Phe Gly Gly Cys Ala Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr
 100 105 110
 Val Glu Cys Met Leu Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala
 115 120 125
 Val Cys Lys Pro Leu Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys
 130 135 140
 Gln Gly Leu Val Ala Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met
 145 150 155 160
 Ile Leu Ser Pro Cys Pro Val Ser Leu Pro Arg Cys Gly Asp His His
 165 170 175
 Leu Asp His Tyr Phe Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys
 180 185 190
 Gly Ala Thr Thr Val Met Glu Glu Thr Val Arg Val Lys
 195 200 205

<210> 2603

<211> 210

<212> PRT

<213> Unknown (2924249-rev-741-9 conceptual translation of range 74285-74912)

<220>

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400>2603

```

Ser Val Lys Tyr Leu Asn Glu S r Phe Pro Glu Asp Phe Ile Leu Met
 1          5          10          15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
          20          25          30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
          35          40          45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
          50          55          60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65          70          75          80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
          85          90          95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Ile Glu
          100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
          115          120          125
Lys Pro Pro Arg Tyr Thr Ile Ile Asp His Lys Val Cys Leu His
          130          135          140
Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
145          150          155          160
Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
          165          170          175
Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
          180          185          190
Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
          195          200          205
Glu Leu
          210

```

<210> 2604

<211> 210

<212> PRT

<213> Unknown (4156137-rev-1191-9 conceptual translation of range 119253-119880)

<220>

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400>2604

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1          5          10          15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
          20          25          30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
          35          40          45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
          50          55          60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65          70          75          80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
          85          90          95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Thr Glu
          100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
          115          120          125

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Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Tyr Leu His
 130 135 140
 Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
 145 150 155 160
 Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
 165 170 175
 Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
 180 185 190
 Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
 195 200 205
 Glu Leu
 210

<210> 2605

<211> 216

<212> PRT

<213> Unknown (2921643-dir-0-8 conceptual translation of range 2-649)

<400>2605

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1 5 10 15
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
 20 25 30
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
 35 40 45
 Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg
 50 55 60
 Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr
 65 70 75 80
 Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr
 85 90 95
 Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys
 100 105 110
 Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn
 115 120 125
 Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe
 130 135 140
 Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys
 145 150 155 160
 Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser
 165 170 175
 His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr
 180 185 190
 Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser
 195 200 205
 Val Phe Tyr Ala Ile Leu Thr Pro
 210 215

<210> 2606

<211> 216

<212> PRT

<213> Unknown (2921711-dir-0-8 conceptual translation of range 2-649)

<400>2606

Leu Val Asp Val Ser Cys Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1 5 10 15
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
 20 25 30
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu L u
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg

50	55	60
Tyr Ser Ala Ile Met	His Gly Gly Leu Cys	Ala Arg Leu Ala Ile Thr
65	70	75
Ser Trp Val Ser Gly	Phe Ile Ser Ser Pr	Val Gln Thr Ala Ile Thr
85	90	95
Phe Gln Leu Pro Met	Cys Arg Asn Lys Phe	Ile Asp His Ile Ser Cys
100	105	110
Glu Leu Leu Ala Val	Val Arg Leu Ala Cys	Val Asp Thr Ser Ser Asn
115	120	125
Glu Val Thr Ile Met	Val Ser Ser Ile Val	Leu Leu Met Thr Pro Phe
130	135	140
Cys Leu Val Leu Leu	Ser Tyr Ile Gln Ile	Ile Ser Thr Ile Leu Lys
145	150	155
Ile Gln Ser Arg Gly	Arg Lys Lys Ala Phe	His Thr Cys Ala Ser
165	170	175
His Leu Thr Val Val	Ala Leu Cys Tyr Gly	Val Ala Ile Phe Thr Tyr
180	185	190
Ile Gln Pro His Ser	Ser Pro Ser Val Leu	Gln Glu Lys Leu Phe Ser
195	200	205
Val Phe Tyr Ala Ile	Leu Thr Pro	
210	215	

<210> 2607

<211> 317

<212> PRT

<213> Unknown (1336042-dir-0-11 conceptual translation of range 1-951)

<400>2607

Met Gly Thr Asp Asn	Gln Thr Trp Val	Ser Glu Phe Ile	Leu Leu Gly
1	5	10	15
Leu Ser Ser Asp Trp	Asp Thr Arg Val	Ser Leu Phe Val	Leu Phe Leu
20	25	30	
Val Met Tyr Val Val	Thr Val Leu Gly	Asn Cys Leu Ile	Val Leu Leu
35	40	45	
Ile Arg Leu Asp Ser	Arg Leu His Thr	Pro Met Tyr Phe	Phe Leu Thr
50	55	60	
Asn Leu Ser Leu Val	Asp Val Ser Tyr	Ala Thr Ser Val	Val Pro Gln
65	70	75	80
Leu Leu Ala His Phe	Leu Ala Glu His	Lys Ala Ile Pro	Phe Gln Ser
85	90	95	
Cys Ala Ala Gln Leu	Phe Phe Ser Leu	Ala Leu Gly Gly	Ile Glu Phe
100	105	110	
Val Leu Leu Ala Val	Met Ala Tyr Asp	Arg Tyr Val Ala	Val Cys Asp
115	120	125	
Ala Leu Arg Tyr Ser	Ala Ile Met His	Gly Gly Leu Cys	Ala Arg Leu
130	135	140	
Ala Ile Thr Ser Trp	Val Ser Gly Phe	Ile Ser Ser Pro	Val Gln Thr
145	150	155	160
Ala Ile Thr Phe Gln	Leu Pro Met Cys	Arg Asn Lys Phe	Ile Asp His
165	170	175	
Ile Ser Cys Glu Leu	Leu Ala Val Val	Arg Leu Ala Cys	Val Asp Thr
180	185	190	
Ser Ser Asn Glu Val	Thr Ile Met Val	Ser Ser Ile Val	Leu Leu Met
195	200	205	
Thr Pro Leu Cys Leu	Val Leu Leu Ser	Tyr Ile Gln Ile	Ile Ser Thr
210	215	220	
Ile Leu Lys Ile Gln	Ser Arg Glu Gly	Arg Lys Lys Ala	Phe His Thr
225	230	235	240
Cys Ala Ser His Leu	Thr Val Val Ala	Leu Cys Tyr Gly	Val Ala Ile
245	250	255	
Phe Thr Tyr Ile Gln	Pro His Ser Ser	Pro Ser Val Leu	Gln Glu Lys

	260		265		270											
Leu	Phe	Ser	Val	Phe	Tyr	Ala	Ile	Leu	Thr	Pro	Met	Leu	Asn	Pro	Met	
	275						280					285				
Ile	Tyr	Ser	L	u	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	Gln	Lys	Leu
	290					295						300				
Leu	Trp	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Ala	Thr				
305					310					315						

<210> 2608

<211> 216

<212> PRT

<213> Unknown (2921713-dir-0-8 conceptual translation of range 2-649)

<400>2608

Leu	Val	Asp	Val	Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala
1				5				10					15		
His	Phe	Leu	Ala	Glu	His	Lys	Ala	Thr	Pro	Phe	Gln	Ser	Cys	Ala	Ala
		20						25				30			
Gln	Leu	Phe	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe	Val	Leu	Leu
		35					40				45				
Ala	Val	Met	Thr	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys	Asp	Ala	Leu	Arg
	50					55					60				
Tyr	Ser	Ala	Ile	Met	His	Gly	Gly	Leu	Cys	Ala	Arg	Leu	Ala	Ile	Thr
65					70					75				80	
Ser	Trp	Val	Ser	Gly	Phe	Ile	Ser	Ser	Pro	Val	Gln	Thr	Ala	Ile	Thr
			85						90					95	
Phe	Gln	Leu	Pro	Met	Cys	Arg	Asn	Lys	Phe	Ile	Asp	His	Ile	Ser	Cys
			100					105					110		
Glu	Leu	Leu	Ala	Val	Val	Arg	Leu	Ala	Cys	Val	Asp	Thr	Ser	Ser	Asn
		115					120					125			
Glu	Val	Thr	Ile	Met	Val	Ser	Ser	Val	Val	Leu	Leu	Met	Thr	Pro	Phe
	130					135					140				
Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Gln	Ile	Asn	Ser	Thr	Ile	Leu	Lys
145					150					155					160
Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr	Cys	Ala	Ser
			165						170					175	
His	Leu	Thr	Val	Val	Ala	Leu	Cys	Tyr	Gly	Val	Ala	Ile	Phe	Thr	Tyr
		180						185					190		
Ile	Gln	Pro	His	Ser	Ser	Pro	Ser	Val	Leu	Gln	Glu	Lys	Leu	Phe	Ser
		195					200					205			
Val	Phe	Tyr	Ala	Ile	Leu	Thr	Pro								
	210					215									

<210> 2609

<211> 301

<212> PRT

<213> Unknown (p161-dir-0-11 conceptual translation of range 2-903)

<400>2609

Trp	Val	Ser	Glu	Phe	Ile	Leu	Leu	Gly	Leu	Ser	Ser	Asp	Trp	Asp	Thr
1				5				10					15		
Gln	Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	Val	Met	Tyr	Val	Val	Thr	Val
		20						25				30			
Leu	Gly	Asn	Cys	Leu	Ile	Val	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu	
		35					40				45				
His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val
	50					55					60				
Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala
65					70					75				80	
Glu	His	Lys	Ala	Ile	Ser	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe
			85						90					95	

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Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala
      100                      105                      110
Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg Tyr Ser Ala Ile
      115                      120                      125
Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser
      130                      135                      140
Gly Phe Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe Gln Leu Pro
      145                      150                      155                      160
Met Cys Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala
      165                      170                      175
Val Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile
      180                      185                      190
Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu
      195                      200                      205
Leu Ser Tyr Ile Gln Ile Thr Ser Thr Ile Leu Lys Ile Gln Ser Arg
      210                      215                      220
Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val
      225                      230                      235                      240
Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His
      245                      250                      255
Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser Val Phe Tyr Ala
      260                      265                      270
Ile Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys
      275                      280                      285
Glu Val Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
      290                      295                      300

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<210> 2610

<211> 334

<212> PRT

<213> Unknown (3766130-dir-170-13 conceptual translation of range 17111-18112)

<220>

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400>2610

```

Phe Cys Phe Phe Leu Thr Leu Ser Thr Asp Xaa Tyr Ser Ser His Phe
  1           5           10           15
Xaa Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu
      20           25           30
Gly Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe
      35           40           45
Leu Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu
      50           55           60
Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
      65           70           75           80
Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro
      85           90           95
Gln Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln
      100          105          110
Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu
      115          120          125
Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser
      130          135          140
Asp Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg
      145          150          155          160
Leu Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln
      165          170          175

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Thr Ala Ile Thr Ph  Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp
      180      185      190
His Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp
      195      200      205
Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser Ser Ile Val Leu Leu
      210      215      220
Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser
      225      230      235      240
Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His
      245      250      255
Thr Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Thr Thr
      260      265      270
Ile Phe Thr Tyr Ile Gln Pro His Ser Gly Pro Ser Val Leu Gln Glu
      275      280      285
Lys Leu Ile Ser Val Phe Tyr Ala Ile Val Met Pro Leu Leu Asn Pro
      290      295      300
Val Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp His Lys
      305      310      315      320
Leu Leu Glu Lys Phe Ser Gly Leu Thr Ser Lys Leu Gly Thr
      325      330

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<210> 2611

<211> 298

<212> PRT

<213> Unknown (p172-dir-0-10 conceptual translation of range 2-895)

<400>2611

```

Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val Ser
  1           5           10           15
Leu Phe Val Leu Phe Leu Val Met Cys Met Val Thr Met Leu Gly Asn
      20           25           30
Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro
      35           40           45
Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala
      50           55           60
Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His Lys
      65           70           75           80
Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala
      85           90           95
Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg
      100          105          110
Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His Gly
      115          120          125
Ala Pro Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe Ile
      130          135          140
Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys Thr
      145          150          155          160
Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile Arg
      165          170          175
Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser
      180          185          190
Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr
      195          200          205
Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly Arg
      210          215          220
Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala Leu
      225          230          235          240
Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser Leu
      245          250          255
Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu Thr
      260          265          270

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Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
 275 280 285
 Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
 290 295

<210> 2612

<211> 298

<212> PRT

<213> Unknown (p171-dir-0-10 conceptual translation of range 3-896)

<220>

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400>2612

Ser Asp Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
 1 5 10 15
 Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
 20 25 30
 Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
 35 40 45
 Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
 50 55 60
 Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
 65 70 75 80
 Lys Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
 85 90 95
 Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
 100 105 110
 Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His
 115 120 125
 Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe
 130 135 140
 Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys
 145 150 155 160
 Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile
 165 170 175
 Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val
 180 185 190
 Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser
 195 200 205
 Tyr Ile Xaa Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly
 210 215 220
 Arg Lys Lys Ala Phe His Thr Tyr Ala Ser His Leu Thr Val Val Ala
 225 230 235 240
 Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser
 245 250 255
 Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu
 260 265 270
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
 275 280 285
 Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys
 290 295

<210> 2613

<211> 299

<212> PRT

<213> Unknown (p173-dir-0-11 conceptual translation of range 4-900)

<400>2613

```

Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
 1          5          10          15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met L u Gly
          20          25          30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
          35          40          45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
          50          55          60
Ala Ile Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
65          70          75          80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
          85          90          95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
          100          105          110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His
          115          120          125
Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe
          130          135          140
Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys
145          150          155          160
Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile
          165          170          175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val
          180          185          190
Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser
          195          200          205
Tyr Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly
          210          215          220
Arg Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
225          230          235          240
Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser
          245          250          255
Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu
          260          265          270
Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
          275          280          285
Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
          290          295

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<210> 2614

<211> 300

<212> PRT

<213> Unknown (p142-dir-0-11 conceptual translation of range 2-900)

<400>2614

```

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1          5          10          15
Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
          20          25          30
Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
          35          40          45
Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
          50          55          60
Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
65          70          75          80
His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
          85          90          95
Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
          100          105          110
Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
          115          120          125

```

His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Val His Thr Thr Ile Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Phe Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Met Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255
 Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Ser Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2615

<211> 300

<212> PRT

<213> Unknown (p162-dir-0-10 conceptual translation of range 1-899)

<400>2615

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
 20 25 30
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
 50 55 60
 Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
 65 70 75 80
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
 85 90 95
 Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
 100 105 110
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
 115 120 125
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Ala His Thr Thr Ile Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255

Ser Pro Ser Val Leu Gln Glu Lys Leu Ile S r Leu Phe Tyr Ala Thr
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2616

<211> 300

<212> PRT

<213> Unknown (p160-dir-0-11 conceptual translation of range 3-901)

<400>2616

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
 20 25 30
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
 50 55 60
 Tyr Val Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
 65 70 75 80
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
 85 90 95
 Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
 100 105 110
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
 115 120 125
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Val His Thr Thr Thr Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Lys
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255
 Asn Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2617

<211> 298

<212> PRT

<213> Unknown (p165-dir-0-10 conceptual translation of range 1-893)

<400>2617

Val Ser Glu Phe Ile Ile Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Val Leu

<400>2618															
Val	Ser	Glu	Phe	Ile	Ile	Leu	Gly	Leu	Ser	Ser	Asp	Trp	Asp	Thr	Gln
1				5					10					15	
Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	Val	Met	Tyr	Val	Val	Thr	Val	Leu
			20					25					30		
Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu	His
		35					40					45			
Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val	Ser
	50					55					60				
Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala	Glu
65					70					75					80
His	Lys	Ala	Ile	Pro	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser
				85					90					95	
Leu	Ala	Leu	Gly	Ile	Glu	Phe	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	
			100				105					110			

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Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
115 120 125
His Ala Gly Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
130 135 140
Ser Ile Asn Ser Leu Val His Thr Ala Ile Thr Phe Gln Leu Pro Arg
145 150 155 160
Cys Arg Asn Lys Phe Ile Glu His Ile Ser Cys Glu Ile Leu Ala Val
165 170 175
Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
180 185 190
Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
195 200 205
Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
210 215 220
Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val
225 230 235 240
Ala Leu Xaa Tyr Gly Val Ala Ile Phe Thr Xaa Ile Gln Pro His Ser
245 250 255
Ser Pro Ser Val Ile Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile
260 265 270
Val Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Ile Arg Asn Lys Glu
275 280 285
Val Lys Gly Ala Trp Gln Lys Ile Leu Trp Lys
290 295

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<210> 2619

<211> 299

<212> PRT

<213> Unknown (p174-dir-0-11 conceptual translation of range 4-900)

<400>2619

```

Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
1 5 10 15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
20 25 30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His Thr
35 40 45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
50 55 60
Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
65 70 75 80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
85 90 95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
100 105 110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Val Ile Met His
115 120 125
Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr Ser Trp Val Ser Gly Ser
130 135 140
Ile Asn Ser Arg Met His Thr Thr Ile Thr Phe Gln Leu Pro Met Cys
145 150 155 160
Thr Asn Lys Phe Ile Asp His Ile Phe Cys Glu Ile Leu Ala Leu Ile
165 170 175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Ile Val
180 185 190
Ser Ser Ile Val Leu Leu Met Thr Pro Leu Cys Leu Val Leu Leu Ser
195 200 205
Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly
210 215 220
Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
225 230 235 240

```

Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr Ile His Pro His Ser Ser
 245 250 255
 Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile Leu
 260 265 270
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
 275 280 285
 Lys Gly Ala Trp Lys Lys Leu Leu Trp Lys Phe
 290 295

<210> 2620

<211> 317

<212> PRT

<213> Unknown (1314664-dir-0-11 conceptual translation of range 1-951)

<400>2620

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu
 20 25 30
 Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
 115 120 125
 Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr
 145 150 155 160
 Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met
 195 200 205
 Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile
 245 250 255
 Phe Thr Tyr Ile Gln Pro Arg Ser Ser Pro Ser Val Leu Gln Glu Lys
 260 265 270
 Leu Ile Ser Leu Phe Tyr Ser Val Leu Thr Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Val Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
 290 295 300
 Leu Gly Gln Leu Thr Gly Ile Thr Ser Lys Leu Ala Thr
 305 310 315

<210> 2621

<211> 349

<212> PRT

<213> Unknown (3766130-dir-627-13 conceptual translation of range 62771-63818)

<220>

<221> VARIANT

<222> (1)...(349)

<223> Xaa = Any Amino Acid

<400>2621

```

Leu Leu Ile Leu His Phe His Asp Trp Leu Phe Leu His Leu Xaa Cys
 1           5           10           15
Gly Pro Trp Lys Leu Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val
          20           25           30
Ser Glu Phe Ile Leu Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val
          35           40           45
Ser Leu Phe Ala Leu Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly
          50           55           60
Asn Thr Leu Ile Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
          65           70           75           80
Pro Met Tyr Phe Ser Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr
          85           90           95
Thr Lys Ser Ile Val Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg
          100          105          110
Lys Ser Ile Pro Phe Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu
          115          120          125
Ala Leu Cys Gly Ser Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp
          130          135          140
Arg Tyr Val Ala Val Cys His Pro Leu His Tyr Thr Val Ile Met His
          145          150          155          160
Gly Gly Leu Cys Leu Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe
          165          170          175
Ser Asn Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser
          180          185          190
Arg Phe Ile Asn His Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu
          195          200          205
Ala Cys Val Asp Val Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly
          210          215          220
Phe Leu Val Ile Leu Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala
          225          230          235          240
Cys Ile Val Ala Thr Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys
          245          250          255
Lys Ala Phe Gly Thr Cys Ala Ser His Leu Ile Val Val Cys Met Cys
          260          265          270
Phe Gly Ala Thr Ile Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser
          275          280          285
Ala Glu Glu Glu Lys Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro
          290          295          300
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala
          305          310          315          320
Ala Val Arg Lys Val Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu
          325          330          335
Arg Thr Ser Cys Tyr Leu Ser Ser Lys Pro Lys Arg Arg
          340          345

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<210> 2622

<211> 214

<212> PRT

<213> Unknown (hg27-dir-0-8 conceptual translation of range 1-642)

<400>2622

```

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val
 1           5           10           15
His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala

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      20      25      30
Arg Leu Leu Phe Leu Leu Ile Gly Gly Cys Thr Gln Cys Ala Leu Leu
      35      40      45
Gly Val Met S r Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
      50      55      60
Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala
      65      70      75      80
Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr
      85      90      95
Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys
      100      105      110
Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser
      115      120      125
Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val
      130      135      140
Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys
      145      150      155      160
Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr
      180      185      190
Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val Phe
      195      200      205
Tyr Pro Ile Val Thr Pro
      210

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<210> 2623

<211> 217

<212> PRT

<213> Unknown (p51-dir-0-8 conceptual translation of range 1-651)

<400>2623

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
      1      5      10      15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
      20      25      30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
      35      40      45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
      50      55      60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
      65      70      75      80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
      85      90      95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
      100      105      110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
      115      120      125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
      130      135      140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
      145      150      155      160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly
      165      170      175
Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr
      180      185      190
Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val
      195      200      205
Phe Tyr Ala Ile Val Thr Pro Met Leu
      210      215

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<210> 2624

<211> 158

<212> PRT

<213> Unknown (2564517-dir-0-6 conceptual translation of range 1-474)

<400>2624

```

Ile Ser Phe Pro Leu Arg Tyr Thr Ile Ile Met Ser Arg Ser Ile Cys
 1          5          10          15
Ile Thr Met Val Ser Cys Cys Trp Ile Ser Gly Ser Leu Ile Ala Leu
          20          25          30
Val Val Ile Val Phe Thr Leu Gln Leu Pro Leu Cys Gly Ala Asn Val
          35          40          45
Ile Asn His Phe Phe Cys Glu Ala Thr Thr Leu Val Gly Met Ala Cys
          50          55          60
Val Asp Thr Phe Val Thr Glu Met Val Ile Phe Ser Ala Gly Ile Phe
65          70          75          80
Thr Leu Leu Leu Pro Ser Ile Leu Thr Leu Leu Ser Tyr Ile Cys Ile
          85          90          95
Ile Val Ala Ile Val Gly Ile Arg Ser Ser Ala Gly Arg Tyr Lys Ala
          100          105          110
Phe Ser Thr Cys Ala Ser His Leu Ile Ile Val Thr Ile Phe Tyr Gly
          115          120          125
Thr Ala Ile Phe Gly Tyr Met Lys Pro Val Ser Lys Asn Ser Gly Asn
          130          135          140
Gln Asp Lys Met Thr Ser Val Phe Tyr Thr Val Thr Pro Pro
145          150          155

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<210> 2625

<211> 215

<212> PRT

<213> Unknown (p102-dir-0-8 conceptual translation of range 2-646)

<400>2625

```

Phe Leu Asp Ile Cys Tyr Ile Ser Ala Ser Val Pro Gln Met Ile Val
 1          5          10          15
Asn Cys Leu Val Arg Ile Pro Ile Ile Ser Leu Gly Gln Cys Leu Ala
          20          25          30
Gln Met Cys Ala Gly Leu Tyr Leu Gly Val Val Glu Cys Leu Leu Leu
          35          40          45
Ala Val Met Ala Tyr Asp Arg Cys Ile Ala Ile Gly Asp Pro Leu Arg
50          55          60
Tyr Ser Val Arg Met Gly Pro Gln Leu Cys Ala Gln Leu Ala Gly Ala
65          70          75          80
Ser Trp Val Ser Ala Phe Leu Leu Thr Val Val Pro Val Leu Thr Met
          85          90          95
Pro Leu Glu Phe Cys Gly Gln His Ile Ile Asn His Phe Ser Cys Glu
          100          105          110
Leu Leu Ala Val Leu Lys Leu Ala Cys Asn Asp Leu Trp Ile Tyr Glu
          115          120          125
Leu Leu Ile Met Val Thr Ser Ser Leu Thr Leu Leu Ala Pro Phe Ala
          130          135          140
Phe Ile Leu Ala Ser Tyr Gly Cys Ile Leu Gly Ala Val Leu Lys Met
145          150          155          160
His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
          165          170          175
Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ala Ile Ser Met Tyr Met
          180          185          190
Met Pro Gln Asp Lys Ala Ser Arg Asp Lys Asp Lys Ile Ile Ser Met
          195          200          205
Leu Tyr Gly Ile Val Thr Pro
210          215

```

<210> 2626

<211> 217

<212> PRT

<213> Unknown (2921715-dir-0-8 conceptual translation of range 2-652)

<400>2626

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
145          150          155          160
Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
165          170          175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
180          185          190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
195          200          205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
210          215

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<210> 2627

<211> 217

<212> PRT

<213> Unknown (2921709-dir-0-8 conceptual translation of range 2-652)

<400>2627

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr
1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu

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145 150 155 160
 Gly Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 165 170 175
 Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
 180 185 190
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
 195 200 205
 Ser Leu Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 2628

<211> 157

<212> PRT

<213> Unknown (902194-dir-0-6 conceptual translation of range 2-472)

<400>2628

Ile Cys His Pro Leu His Tyr Ser Val Ile Met Ser Trp Arg Val Cys
 1 5 10 15
 Thr Val Gln Ala Val Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu
 20 25 30
 Val His Val Ile Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu
 35 40 45
 Ile Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys
 50 55 60
 Ala Asp Thr Arg Leu Asn Gln Val Val Ile Phe Ala Ala Ser Val Ser
 65 70 75 80
 Ile Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile
 85 90 95
 Leu Phe Ala Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala
 100 105 110
 Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly
 115 120 125
 Ser Ala Ile Val Met Tyr Met Ala Pro Lys Ser Asn His Pro Glu Glu
 130 135 140
 Gln Gln Lys Ile Leu Ser Leu Phe Tyr Ser Leu Phe Asn
 145 150 155

<210> 2629

<211> 215

<212> PRT

<213> Unknown (OST182-dir-0-8 conceptual translation of range 2-646)

<400>2629

Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met Leu Thr
 1 5 10 15
 Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys Ile Met
 20 25 30
 Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu Ile Leu
 35 40 45
 Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala Val Ala
 65 70 75 80
 Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Leu Val Leu Ile
 85 90 95
 Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Ph Cys Glu
 100 105 110
 Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln
 115 120 125
 Val Val Ile Phe Ala Ala Cys Val Phe Ile Leu Val Gly Pro Leu Cys
 130 135 140

Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile
 145 150 155 160
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His
 165 170 175
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met
 180 185 190
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Lys Val Leu Ser Leu
 195 200 205
 Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 2630

<211> 352

<212> PRT

<213> Unknown (4156187-rev-1021-13 conceptual translation of range 102238-103293)

<220>

<221> VARIANT

<222> (1)...(352)

<223> Xaa = Any Amino Acid

<400>2630

Leu Leu Val Phe Cys Leu Phe Leu Cys Leu Phe Phe Ser Ser Glu Met
 1 5 10 15
 Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu
 20 25 30
 Leu Gly Pro Arg Ile Gln Met Leu Phe Gly Leu Phe Ser Leu Phe
 35 40 45
 Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser
 50 55 60
 Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 65 70 75 80
 Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu
 85 90 95
 Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met
 100 105 110
 Thr Xaa Thr Phe Leu Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu
 115 120 125
 Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
 130 135 140
 Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile
 145 150 155 160
 Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val His Val Ser Leu
 165 170 175
 Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe
 180 185 190
 Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu
 195 200 205
 Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly Pro
 210 215 220
 Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile Leu
 225 230 235 240
 Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 245 250 255
 Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
 260 265 270
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
 275 280 285
 Phe Leu Phe Tyr Ser Ser Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr
 290 295 300

Asn Leu Arg Asn Val Glu Val Lys Gly Ala Leu Arg Arg Ala L u Cys
 305 310 315 320
 Lys Glu Ser His Ser Xaa Glu Val Xaa His Leu Asn Cys Gln Pro Gln
 325 330 335
 Leu Ser Arg Gly Leu Leu Met Pro Asn Tyr Cys Leu Asn Pro Glu Lys
 340 345 350

<210> 2631

<211> 314

<212> PRT

<213> Unknown (4156187-rev-834-13 conceptual translation of range 83640-84581)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400>2631

Glu Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser
 20 25 30
 Leu Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu
 35 40 45
 Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln
 65 70 75 80
 Met Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly
 85 90 95
 Cys Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys
 100 105 110
 Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu
 130 135 140
 Ala Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val
 145 150 155 160
 Val Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His
 165 170 175
 Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr
 180 185 190
 Trp Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val
 195 200 205
 Gly Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile
 245 250 255
 Ile Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys
 260 265 270
 Val Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala
 290 295 300
 Leu Gly Lys Glu Ser His Ser Xaa Leu Val
 305 310

<210> 2632

<211> 223

<212> PRT

<213> Unknown (3983369-dir-0-8 conceptual translation of range 1-669)

<400>2632

```

Ser His Leu Ala Ile Val Asp Met Ala Tyr Ala Cys Asn Thr Val Pro
1      5      10      15
Gln Thr Leu Ile Asn Leu Leu Asp Glu Thr Arg Pro Ile Thr Phe Ala
20      25      30
Gly Cys Met Thr Gln Thr Tyr Leu Phe Leu Thr Phe Ala Ile Thr Glu
35      40      45
Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
50      55      60
His Pro Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Ile
65      70      75      80
Met Ala Ala Val Ser Trp Ile Val Ser Phe Leu Leu Ser Leu Val His
85      90      95
Leu Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn
100     105     110
His Phe Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp
115     120     125
Thr Thr Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Thr Leu
130     135     140
Val Gly Pro Leu Cys Phe Val Leu Val Ser Tyr Thr Arg Ile Leu Val
145     150     155     160
Ala Ile Leu Arg Ile Gln Ser Gly Glu Arg Arg Arg Lys Ala Phe Ser
165     170     175
Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala
180     185     190
Ile Val Met Tyr Met Ala Pro Lys Ser Gln His Pro Gly Glu Gln Gln
195     200     205
Lys Ile Leu Phe Leu Phe Tyr Ser Phe Phe Asn Pro Met Leu Asn
210     215     220

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<210> 2633

<211> 216

<212> PRT

<213> Unknown (OST008-dir-0-8 conceptual translation of range 2-649)

<400>2633

```

Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Ala
1      5      10      15
Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys Ile Met
20      25      30
Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu Ile Leu
35      40      45
Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Phe Gln
50      55      60
Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val Leu Thr
65      70      75      80
Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile Leu Leu
85      90      95
Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu Phe Cys
100     105     110
Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Val Asn
115     120     125
Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly Pro Leu
130     135     140
Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile Leu Lys
145     150     155     160
Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys Ser Ser

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[illegible]

<210> 2634

<211> 310

<212> PRT

<213> Unknown (4156187-dir-87-12 conceptual translation of range 8841-9771)

<400>2634

[illegible]

<210> 2635

<211> 339

<212> PRT

<213> Unknown (4156187-rev-1102-12 conceptual translation of range 110295-111311)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400>2635

```

Ile Cys Phe Xaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1          5          10          15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe
          20          25          30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
          35          40          45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
 50          55          60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
 65          70          75          80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
          85          90          95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
          100          105          110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
          115          120          125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
          130          135          140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
 145          150          155          160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
          165          170          175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
          180          185          190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
          195          200          205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
          210          215          220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
 225          230          235          240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
          245          250          255
Ala Phe Cys Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr
          260          265          270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
          275          280          285
Glu Gln Lys Lys Tyr Leu Leu Phe His Ser Leu Phe Asn Pro Met
          290          295          300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
 305          310          315          320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
          325          330          335
His Cys Asp

```

<210> 2636

<211> 339

<212> PRT

<213> Unknown (4156166-dir-1014-13 conceptual translation of range 101536-102552)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400>2636

```

Ile Cys Phe Yaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1           5           10           15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe
      20           25           30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
      35           40           45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
      50           55           60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
      65           70           75           80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
      85           90           95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
      100           105           110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
      115           120           125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
      130           135           140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
      145           150           155           160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
      165           170           175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
      180           185           190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
      195           200           205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
      210           215           220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
      225           230           235           240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
      245           250           255
Ala Phe Arg Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr
      260           265           270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
      275           280           285
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met
      290           295           300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
      305           310           315           320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
      325           330           335
His Cys Asp

```

<210> 2637

<211> 222

<212> PRT

<213> Unknown (293753-dir-0-8 conceptual translation of range 2-667)

<400>2637

```

Phe Phe Leu Ser His Leu Ala Ile Val Asp Ile Ala Tyr Ala Cys Asn
 1           5           10           15
Thr Val Pro Gln Met Leu Val Asn Leu Leu Asp Pro Val Lys Pro Ile
      20           25           30
Ser Tyr Ala Gly Cys Met Thr Gln Thr Phe Leu Phe Leu Thr Phe Ala
      35           40           45
Ile Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val
      50           55           60

```

Ala Ile Cys His Pro Leu Arg Tyr Ser Ala Ile M t Ser Trp Arg Val
 65 70 75 80
 Cys Ser Thr Met Ala Val Thr Ser Trp Ile Ile Gly Val Leu Leu Ser
 85 90 95
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Val Ser Gln
 100 105 110
 Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala
 115 120 125
 Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val
 130 135 140
 Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys
 145 150 155 160
 Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys
 165 170 175
 Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr
 180 185 190
 Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys
 195 200 205
 Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn
 210 215 220

<210> 2638

<211> 114

<212> PRT

<213> Unknown (892-dir-0-5 conceptual translation of range 2-343)

<400>2638

Ile Cys His Pro Leu Arg Tyr Lys Val Ile Met Ser Arg Trp Met Cys
 1 5 10 15
 Leu Leu Met Val Gly Ile Cys Gly Val Tyr Gly Val Val Gly Ser Leu
 20 25 30
 Cys Tyr Thr Phe Phe Ala Met Arg Leu Pro Tyr Cys Gly Pro Asn Glu
 35 40 45
 Ile Asp His Tyr Phe Cys Glu Val Pro Ala Val Leu Lys Leu Ala Cys
 50 55 60
 Ala Asp Thr Ser Leu Asn Asp Leu Val Asp Phe Ile Thr Gly Phe Asn
 65 70 75 80
 Val Ile Val Val Pro Leu Thr Leu Val Val Ile Val Tyr Ala Asn Ile
 85 90 95
 Phe Ala Thr Ile Met Lys Ile Arg Ser Ala Gln Gly Gln Ile Lys Ala
 100 105 110
 Phe Ser

<210> 2639

<211> 350

<212> PRT

<213> Unknown (2331266-dir-0-13 conceptual translation of range 111-1160)

<220>

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400>2639

Leu Ala Gln Asn Ile Lys Arg Lys Thr Ala Met Asn Ser Val Asn Ala
 1 5 10 15
 Ser Phe Tyr Gln Asn Ile Ser Ile Val Arg Pro Glu Tyr Phe Phe Ile
 20 25 30
 Ser Gly Leu Ser Gly Ile Pro Tyr Ser Ser Tyr Tyr Tyr Ile Phe Leu
 35 40 45

Phe Val Val Tyr Phe Ile S r Val Il Gly Asn Ser Val Val Leu L u
 50 55 60
 Ile Ile Ala Val Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val
 65 70 75 80
 Phe Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro
 85 90 95
 Asn Met Met Lys Thr Phe Leu Phe Asn Ser Gln Tyr Ile Ser Tyr Asn
 100 105 110
 Gly Cys Met Ala Asn Met Phe Phe Val Val Leu Phe Asn Ser Ile Gln
 115 120 125
 Ser Phe Thr Leu Val Ala Leu Ala Tyr Asp Arg Phe Ile Ala Ile Cys
 130 135 140
 Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Thr Ser Met Ile Leu
 145 150 155 160
 Ile Phe Leu Ala Ile Trp Ala Phe Asn Ser Ser Val Val Ala Ser Met
 165 170 175
 Val Ser Met Ile Thr Arg Leu Ser Ile Cys Lys Ser Asn Val Ile Pro
 180 185 190
 Ser Tyr Phe Cys Asp His Gly Pro Ile Phe Arg Leu Ala Cys Asn Asp
 195 200 205
 Ile Lys Ile Asn Glu Phe Phe Ala Phe Phe Ile Ser Ile Leu Tyr Leu
 210 215 220
 Thr Met Pro Met Val Ile Ala Leu Ser Tyr Leu Asn Ile Phe Leu
 225 230 235 240
 Ala Leu Ile Lys Ile Thr Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys
 245 250 255
 Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Phe Phe Leu Pro Leu
 260 265 270
 Leu Cys Thr Tyr Ile Ala Gln Val Leu Leu Ala Leu Thr Pro Asn Ala
 275 280 285
 Arg Val Ile Ser Thr Ser Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn
 290 295 300
 Pro Ile Ile Tyr Val Leu Asn Thr Ala Glu Ile Lys Tyr Ile Ile Arg
 305 310 315 320
 Lys Leu Phe Lys Arg Arg Leu Arg Ser Val Ser Asp Asn Ile Ser Lys
 325 330 335
 Xaa Phe Cys Ser Cys Trp Gly Leu Tyr Gln Ser Lys Lys Lys
 340 345 350

<210> 2640

<211> 353

<212> PRT

<213> Unknown (2331262-dir-1-13 conceptual translation of range 199-1257)

<220>

<221> VARIANT

<222> (1)...(353)

<223> Xaa = Any Amino Acid

<400>2640

Val Gln Asn Thr Lys Cys Lys Val Ala Met Ser Ser Leu Asn Ala Ser
 1 5 10 15
 Phe Ser Leu Asn Ile Ser Val Val Arg Pro Glu Tyr Phe Phe Ile Leu
 20 25 30
 Gly Leu Ser Gly Ile Pro Tyr Ser Asn Leu Tyr Tyr Ile Phe Ile Phe
 35 40 45
 Ile Ile Tyr Phe Ile Thr Val Ile Gly Asn Phe Leu Val Ile Leu Leu
 50 55 60
 Ile Val Leu Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val Phe
 65 70 75 80
 Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro Asn

Leu 1	Ser	Pro	Ser	Leu 5	Lys	Pro	Ser	Cys	Asn 10	Cys	Asp	Pro	Thr	Met 15	Trp
Pro	Asn	Ser	Ser 20	Asp	Ala	Pro	Phe	Leu 25	Leu	Thr	Gly	Phe	Leu 30	Gly	Leu
Glu	Met	Ile 35	His	His	Trp	Ile	Ser 40	Ile	Pro	Phe	Phe 45	Val	Ile	Tyr	Phe
Ser	Ile 50	Ile	Val	Gly	Asn 55	Gly	Thr	Leu	Leu	Phe 60	Ile	Ile	Trp	Ser	Asp
His 65	Ser	Leu	His	Glu 70	Pro	Met	Tyr	Tyr	Phe 75	Leu	Ala	Val	Leu	Ala 80	Ser
Met	Asp	Leu	Gly 85	Met	Thr	Leu	Thr	Thr 90	Met	Pro	Thr	Val	Leu 95	Gly	Val
Leu	Val	Leu	Asn	Gln	Arg	Glu	Ile	Val	His	Gly	Ala	Cys	Phe	Ile	Gln

			100					105					110				
Ser	Tyr	Phe	Ile	His	Ser	Leu	Ala	Ile	Val	Glu	Ser	Gly	Val	Leu	Leu		
		115					120					125					
Ala	Met	Ser	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	Thr	Pro	Leu	His	Tyr		
	130					135					140						
Asn	Ser	Ile	Leu	Thr	Asn	Ser	Arg	Val	Met	Lys	Met	Ala	Leu	Gly	Ala		
145					150					155					160		
Leu	Leu	Arg	Gly	Phe	Val	Ser	Ile	Val	Pro	Pro	Ile	Met	Pro	Leu	Phe		
			165						170					175			
Trp	Phe	Pro	Tyr	Cys	His	Ser	His	Val	Leu	Ser	His	Ala	Phe	Cys	Leu		
		180						185					190				
His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Phe	Asn	Leu		
	195						200					205					
Ile	Tyr	Pro	Val	Val	Leu	Val	Ala	Leu	Thr	Phe	Phe	Leu	Asp	Ala	Leu		
	210						215					220					
Ile	Ile	Ile	Phe	Ser	Tyr	Val	Leu	Ile	Leu	Lys	Lys	Val	Met	Gly	Ile		
225					230					235					240		
Ala	Ser	Gly	Glu	Glu	Arg	Lys	Lys	Ser	Leu	Asn	Thr	Cys	Val	Ser	His		
			245						250					255			
Ile	Ser	Cys	Val	Leu	Val	Phe	Tyr	Ile	Thr	Val	Ile	Gly	Leu	Thr	Phe		
		260						265					270				
Ile	His	Arg	Phe	Gly	Lys	Asn	Ala	Pro	His	Val	Val	His	Ile	Thr	Met		
	275						280						285				
Ser	Tyr	Val	Tyr	Phe	Leu	Phe	Pro	Pro	Phe	Met	Asn	Pro	Ile	Ile	Tyr		
	290					295					300						
Ser	Ile	Lys	Thr	Lys	Gln	Ile	Gln	Arg	Ser	Ile	Leu	Arg	Leu	Leu	Ser		
305					310					315					320		
Lys	His	Ser	Arg	Thr	Xaa	Ile	Leu	Ile	Ile	Asp	Ser	Gln	Val	Leu	Tyr		
			325						330					335			
Tyr	Phe	Trp	Pro	Phe	Ile	Arg	Asn	Lys	Ser	Cys	Leu	Lys	Xaa	Tyr			
			340					345						350			

<210> 2642

<211> 159

<212> PRT

<213> Unknown (4680279-dir-0-6 conceptual translation of range 2-478)

<400>2642

Asn	Pro	Leu	Arg	Tyr	Thr	Ser	Ile	Leu	Thr	Ser	Ala	Arg	Val	Leu	Gln		
1				5					10					15			
Ile	Gly	Leu	Ala	Phe	Ser	Leu	Lys	Asn	Val	Leu	Leu	Ile	Leu	Pro	Phe		
		20						25					30				
Pro	Val	Thr	Leu	Val	Arg	Leu	Arg	Tyr	Cys	Lys	Lys	Asn	Leu	Leu	Ser		
		35					40					45					
His	Ser	Tyr	Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	Ser	Asp		
	50					55				60							
Asn	Lys	Phe	Asn	Val	Ile	Tyr	Gly	Leu	Phe	Val	Ala	Leu	Thr	Gly	Ile		
65					70				75						80		
Leu	Asp	Ile	Thr	Phe	Ile	Phe	Met	Ser	Tyr	Ala	Leu	Ile	Leu	Arg	Ala		
			85						90					95			
Val	Leu	Gly	Ile	Ala	Ser	Gln	Arg	Glu	Arg	Leu	Lys	Val	Leu	Ser	Thr		
		100						105					110				
Cys	Val	Ser	His	Ile	Cys	Ala	Val	Leu	Ile	Phe	Tyr	Val	Pro	Val	Ile		
	115						120					125					
Ser	Leu	Ala	Val	Ile	Tyr	Arg	Leu	Ala	Ser	Arg	Ser	Ser	Pro	Ile	Ser		
	130					135					140						
Lys	Ile	Leu	Met	Ala	Asp	Ile	Phe	Leu	Leu	Val	Pro	Pro	Val	Met			
145					150					155							

<210> 2643

<211> 160

<212> PRT

<213> Unknown (902668-dir-0-6 conceptual translation of range 2-481)

<400>2643

```

Ile Ser Asn Pro Leu Arg Tyr Ala Ser Val Leu Thr Asn Asn Val Ile
 1           5           10           15
Ile Arg Ile Gly Val Ala Ile Thr Thr Arg Ala Thr Leu Ser Leu Leu
 20           25           30
Pro Leu Pro Phe Leu Leu Lys Arg Leu Asn Tyr Cys Pro Gly Lys Ile
 35           40           45
Leu Leu Ser His Ser Phe Cys Phe His Ala Asp Val Met Lys Leu Ala
 50           55           60
Cys Ala Asp Ile Thr Val Asn Ile Leu Tyr Gly Leu Tyr Val Val Leu
 65           70           75           80
Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Val Met Ser Tyr Ser Leu
 85           90           95
Ile Leu His Thr Val Met Gly Leu Ala Ser Pro Arg Glu Arg Val Arg
 100          105          110
Thr Leu Asn Thr Cys Val Ser His Ile Ser Ala Val Leu Val Phe Tyr
 115          120          125
Ile Pro Val Ile Gly Val Ser Met Ile His Arg Phe Gly Lys His Leu
 130          135          140
Pro His Ile Val His Ala Leu Val Ala Tyr Val Tyr Leu Val Val Pro
 145          150          155          160

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<210> 2644

<211> 316

<212> PRT

<213> Unknown (3927807-dir-288-13 conceptual translation of range 29007-29954)

<400>2644

```

Leu Asn Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu
 1           5           10           15
Ala Gly Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro
 20           25           30
Phe Gly Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu
 35           40           45
Leu Val Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe
 50           55           60
Leu Leu Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu
 65           70           75           80
Pro Thr Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe
 85           90           95
Pro Ala Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met
 100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Cys Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala
 130          135          140
Gln Ile Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro
 145          150          155          160
Leu Ile Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu
 165          170          175
Ser His Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr
 180          185          190
Asp Ala Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala
 195          200          205
Ile Leu Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg
 210          215          220
Thr Val Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn

```

225 230 235 240
 Thr Cys Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu
 245 250 255
 Ala Gly Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pr Ile
 260 265 270
 Ser His Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu
 275 280 285
 Asn Pro Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu
 290 295 300
 Leu Arg Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly
 305 310 315

<210> 2645

<211> 316

<212> PRT

<213> Unknown (4761596-dir-254-13 conceptual translation of range 25614-26561)

<400>2645

Phe His Asn Asp Thr Asn Pro Gln Asp Val Trp Tyr Val Leu Ile Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Asp Leu His Ser Trp Ile Ala Ile Pro Ile Cys
 20 25 30
 Ser Met Tyr Ile Val Ala Val Ile Gly Asn Val Leu Leu Ile Phe Leu
 35 40 45
 Ile Val Thr Glu Arg Ser Leu His Glu Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Leu Ala Asp Leu Leu Leu Ser Thr Ala Thr Ala Pro Lys
 65 70 75 80
 Met Leu Ala Ile Phe Trp Phe His Ser Arg Gly Ile Ser Phe Gly Ser
 85 90 95
 Cys Val Ser Gln Met Phe Phe Ile His Phe Ile Phe Val Ala Glu Ser
 100 105 110
 Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Tyr
 115 120 125
 Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ser Ser Val Ile Gly Lys Ile
 130 135 140
 Gly Thr Ala Ala Val Val Arg Ser Phe Leu Ile Cys Phe Pro Phe Ile
 145 150 155 160
 Phe Leu Val Tyr Arg Leu Leu Tyr Cys Gly Lys His Ile Ile Pro His
 165 170 175
 Ser Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Asp Asn Ile
 180 185 190
 Thr Val Asn Ile Ile Tyr Gly Leu Thr Met Ala Leu Leu Ser Thr Gly
 195 200 205
 Leu Asp Ile Leu Leu Ile Ile Ile Ser Tyr Thr Met Ile Leu Arg Thr
 210 215 220
 Val Phe Gln Ile Pro Ser Trp Ala Ala Arg Tyr Lys Ala Leu Asn Thr
 225 230 235 240
 Cys Gly Ser His Ile Cys Val Ile Leu Leu Phe Tyr Thr Pro Ala Phe
 245 250 255
 Phe Ser Phe Phe Ala His Arg Phe Gly Gly Lys Thr Val Pro Arg His
 260 265 270
 Ile His Ile Leu Val Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln Asp Arg Val
 290 295 300
 Val Phe Leu Phe Ser Ser Val Ser Thr Cys Gln His
 305 310 315

<210> 2646

<211> 159

<212> PRT

<213> Unknown (2564519-dir-0-6 conceptual translation of range 1-477)

<400>2646

```

Ile Cys Asn Pro Leu Arg Tyr Ala Val Met Leu Thr Asn Ile Val Ile
 1           5           10           15
Arg Lys Ile Ala Ile Leu Ala Val Val Arg Gly Leu Cys Val Val Ala
          20           25           30
Pro Phe Thr Phe Leu Leu His Arg Leu Pro Tyr Cys Gln Asn Asn Val
          35           40           45
Val Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ala Cys
          50           55           60
Ala Asp Val Thr Val Asn Ser Val Tyr Gly Leu Thr Ile Ala Leu Ser
65           70           75           80
Ile Thr Gly Leu Asp Ala Ala Leu Val Val Ala Ser Tyr Val Leu Ile
          85           90           95
Leu Arg Ala Val Leu Asn Met Asn Ser Met Thr Ala Arg His Lys Ala
          100          105          110
Leu Ser Thr Cys Ala Ser His Val Cys Val Ile Ile Leu Phe Cys Val
          115          120          125
Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Lys Asn Ile Pro
          130          135          140
Leu Asn Val His Ile Phe Val Ala Asn Leu Tyr Ile Leu Leu Pro
145          150          155

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<210> 2647

<211> 158

<212> PRT

<213> Unknown (1644474-dir-0-6 conceptual translation of range 1-474)

<400>2647

```

Lys Pro Leu His Tyr Asn Glu Ile Met Asn Ser Ser Met Phe Leu Lys
 1           5           10           15
Leu Phe Leu Phe Thr Leu Ile Arg Ser Gly Thr Ile Met Ser Thr Leu
          20           25           30
Val Ala Leu Ala Ser Pro Leu Ser Phe Cys Gly Ser Asn Val Ile Tyr
          35           40           45
His Cys Tyr Cys Asp His Met Ala Leu Val Ser Leu Ala Cys Asp Ser
          50           55           60
Ile Ala Gln Asn Gln Thr Met Gly Leu Ile Val Ile Ile Cys Phe Val
65           70           75           80
Gly Ile Asp Thr Ser Val Ile Phe Phe Ser Tyr Val Lys Ile Leu His
          85           90           95
Val Val Leu Gly Thr Ala Ala Gly Glu Asp Arg Trp Lys Ala Phe His
          100          105          110
Thr Cys Gly Thr His Leu Met Val Met Ile Cys Phe Tyr Phe Val Gly
          115          120          125
Ser Val Thr Phe Leu Ser Arg Asn Leu Asn Ile Pro Ile Pro Ile Asp
          130          135          140
Val Asn Thr Phe Leu Gly Val Met Tyr Ile Val Phe Pro Ala
145          150          155

```

<210> 2648

<211> 161

<212> PRT

<213> Unknown (4877304-dir-0-6 conceptual translation of range 2-484)

<400>2648

```

Leu Ala Ile Cys Tyr Pro Leu His Tyr Ser Ala Leu Met Thr Asn Lys
 1           5           10           15

```

His Ala Ile Arg Leu Ser Cys Leu Cys Trp Ile Ile Gly Phe Leu Ile
 20 25 30
 Leu Ile Met Asn Leu Cys Phe Ile Arg Gln Thr Leu Phe Cys Gly Pro
 35 40 45
 Asn Glu Val Pro His Tyr Phe Cys Asp Tyr S r Ala Val Ala Ala Leu
 50 55 60
 Ala Cys Asn Asp Ile Ser Ile Tyr Ala Ala Val Gly Phe Ala Ile Ala
 65 70 75 80
 Met Cys Val Ile Cys Ser Val Leu Leu Cys Leu Val Tyr Ser Tyr Val
 85 90 95
 Lys Ile Val Ala Ser Val Leu Lys Ile Ala Ser Thr Asp Gly Arg Gln
 100 105 110
 Lys Ala Phe Ser Thr Cys Val Ser His Leu Phe Val Val Ser Val Phe
 115 120 125
 Ser Ile Leu Ala Ala Phe Val Phe Val Ser Tyr Arg Ile Glu Glu Phe
 130 135 140
 Ser Glu Asp Ala Arg Met Ile Ile His Val Val Gln Asn Thr Phe Pro
 145 150 155 160
 Ser

<210> 2649

<211> 168

<212> PRT

<213> Unknown (5262456-dir-284-6 conceptual translation of range 28407-28908)

<220>

<221> VARIANT

<222> (1)...(168)

<223> Xaa = Any Amino Acid

<400>2649

Gly Phe Trp Leu Gly Cys Tyr Leu Trp Phe Met Val Val Leu Thr Leu
 1 5 10 15
 Ala Ile Arg Leu Arg Pro Phe Gly Leu Gly Gly Phe Leu Leu Lys Xaa
 20 25 30
 Thr Ile Glu Xaa Gly Ala Cys Pro Arg Xaa Val Met Leu Leu Leu Cys
 35 40 45
 Gln Lys Pro Tyr Leu His Cys Val Val Val Val Phe Ile Phe Leu
 50 55 60
 Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala Val Ala
 65 70 75 80
 Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe Gly Thr
 85 90 95
 Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr Val Arg
 100 105 110
 Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu Gly Lys
 115 120 125
 Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn Pro Tyr
 130 135 140
 Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu Ile Gly
 145 150 155 160
 Lys Glu Lys Gly Ser Gly Asp Thr
 165

<210> 2650

<211> 312

<212> PRT

<213> Unknown (3941546-dir-0-12 conceptual translation of range 37-972)

<400>2650

```

Asn Val Ser Phe Tyr Asn Ph Lys Cys Thr Leu Ser Glu Leu Thr Gln
 1          5          10          15
Pro Gln Arg Val Val Leu Ile Trp Val Phe Thr Ile Ile Ile Thr Ile
 20          25          30
Thr Val Val Gly Asn Ile Leu Thr Ile Val Ser Ile Leu Tyr Phe Arg
 35          40          45
Gln Leu Gln Thr Arg Thr Asn Val Leu Ala Leu Ser Leu Ala Leu Ala
 50          55          60
Asp Phe Leu Val Gly Cys Leu Ile Met Pro Phe Ser Val Met Arg Thr
 65          70          75          80
Ala Tyr Ser Cys Trp Phe Tyr Gly Gln Leu Met Cys Arg Ile His Thr
 85          90          95
Trp Leu Asp Tyr Thr Phe Thr Thr Cys Ser Ile Phe Asn Leu Ala Cys
100          105          110
Ile Ser Ile Asp Arg Tyr Val Ala Ile Ser Asp Pro Leu Arg Tyr Asp
115          120          125
Gln Arg Val Thr Tyr Arg Ile Leu Ala Val Met Leu Thr Ile Cys Trp
130          135          140
Gly Asn Ile Ile Pro Tyr Gly Val Ser Tyr Met Leu Lys Leu Asn Ile
145          150          155          160
Asn Gly Ile Glu Ser Val Val Ala Ala Lys Ser Cys Pro Asp Asn Cys
165          170          175
Ser Val Phe Met Asn Val Pro Phe Gly Leu Ala Asn Ser Met Gly Ala
180          185          190
Tyr Val Leu Pro Met Leu Phe Ile Met Ala Ala Tyr Ser Arg Ile Tyr
195          200          205
Val Met Ala Arg Asn Gln Ala Lys Arg Ile Ser Ser Leu Gly Asp Gln
210          215          220
Val Arg Ala Ser Asn Ala Ser Asp Leu Thr Met Gln Ser Lys Trp Asn
225          230          235          240
Ala Met Lys Arg Asp His Asn Ala Thr Lys Thr Leu Gly Met Ile Met
245          250          255
Val Val Leu Phe Ile Val Trp Leu Pro Phe Ile Val Val Val Ala Thr
260          265          270
Glu Pro Val Ile Gly Tyr Arg Met Asp Ser Thr Val Trp Asp Val Ala
275          280          285
Asn Trp Phe Thr Tyr Phe Asn Ser Arg Met Asn Pro Ile Leu Phe Ala
290          295          300
Ser Phe Asn Asn Ser Phe Arg Ser
305          310

```

<210> 2651

<211> 314

<212> PRT

<213> Unknown (17-2 (HGMP07I 400671 OL1A 438389 P30953 OLF1 1804351A S20572) Parmentier-M 92)

<400>2651

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20          25          30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35          40          45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65          70          75          80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85          90          95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser

```

100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2652

<211> 312

<212> PRT

<213> Unknown (17-4 (OLFR1 425221 482560 A48413 HSHGM07EG) Schurmans-S 93)

<400>2652

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala

210	215	220
Ile Leu Arg Ile Pr	Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr	
225	230	235
Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys		240
	245	250
Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val		255
	260	265
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		270
	275	280
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu		285
	290	295
Asp Lys His Phe Lys Arg Leu Thr		300
305	310	

<210> 2653

<211> 315

<212> PRT

<213> Unknown (17-40 (OL1E 516320 2209308A 1588713))

<400>2653

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile	
1	5
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val	10
	20
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Arg Gly Asn Leu Ser Ile	25
	35
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Thr Pro Met Tyr Phe	40
	50
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr	55
65	70
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro	75
	85
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly	90
	100
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Phe Leu Ala	105
	115
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln	120
	130
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu	135
145	150
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Val	155
	165
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys	170
	180
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile	185
	195
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val	200
	210
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala	215
225	230
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly	235
	245
Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp	250
	260
Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Leu	265
	275
Asn Pro Ile Ile Tyr Ser Phe Arg Asn Pro Asp Val Gln Ser Ala Ile	280
	290
Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala	295
305	310
	315

<210> 2654
 <211> 323
 <212> PRT
 <213> Unknown (17-93)

<400>2654

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
      20      25      30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
      35      40      45
Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
      65      70      75      80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
      85      90      95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
      100     105     110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
      115     120     125
Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
      130     135     140
Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
      145     150     155     160
Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
      165     170     175
Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
      180     185     190
Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
      195     200     205
Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
      210     215     220
Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
      225     230     235     240
Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
      245     250     255
Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
      260     265     270
Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
      275     280     285
Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
      290     295     300
Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
      305     310     315     320
Phe Leu Leu

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<210> 2655
 <211> 316
 <212> PRT
 <213> Unknown (FAT11 (HUMORLMHC A57069 601919 1097174 1362875) Fan-W 95)

<400>2655

```

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1      5      10      15
Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
      20      25      30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
      35      40      45

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Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
 85 90 95
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
 165 170 175
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
 195 200 205
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
 210 215 220
 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
 225 230 235 240
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
 245 250 255
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
 260 265 270
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
 290 295 300
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
 305 310 315

<210> 2656

<211> 254

<212> PRT

<213> Unknown (H8 (432510) Selbie-LA 92)

<400>2656

Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Gly Phe
 1 5 10 15
 Ile Ser Thr Ile Ile Pro Lys Met Leu Asp His Ile Ser Ser Gly Ile
 20 25 30
 Lys Leu Ile Ser Tyr Gly Glu Cys Leu Thr Gln Leu Tyr Phe Ser Gly
 35 40 45
 Leu Phe Ala Asp Leu Asp Asn Asn Phe Leu Leu Ala Val Met Ala Ile
 50 55 60
 Asp Arg Tyr Val Ala Ile Ser His Pro Leu His Tyr Ala Leu Thr Met
 65 70 75 80
 Asn Ser Gln Arg Cys Val Leu Leu Val Ala Val Ser Trp Val Ile Thr
 85 90 95
 Ile Leu His Ala Leu Val His Thr Leu Leu Val Thr Arg Leu Ser Phe
 100 105 110
 Cys Gly Pro Asn Ile Ile Pro His Phe Phe Cys Asp Leu Val Pro Leu
 115 120 125
 Leu Lys Leu Ala Cys Ser Ser Thr Cys Val Asn Asp Leu Val Leu Ile
 130 135 140
 Leu Val Pro Gly Thr Leu Leu Ile Ala Pro Ph Val Cys Ile Leu Met
 145 150 155 160

Ser Tyr Phe Tyr Ile Ala Leu Ala Ile Leu Arg Ile Asp Ser Pro Arg
 165 170 175
 Gly Lys Gln Arg Ala Phe Ser Ser Cys Thr Ser His Leu Ser Val Val
 180 185 190
 Ser Leu Phe Tyr Ser Thr Ala Ile Gly Val Tyr Leu Cys Pro Pro Ser
 195 200 205
 Ser His Ser Asp Gly Lys Asp Arg Val Phe Ser Val Met Tyr Thr Val
 210 215 220
 Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp
 225 230 235 240
 Met Lys Gly Ala Leu Gly Lys Leu Leu Gly Ile Lys Thr Ser
 245 250

<210> 2657

<211> 195

<212> PRT

<213> Unknown (G3 (432509) Selbie-LA 92)

<400>2657

Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Asp Leu Gln Pro Val
 1 5 10 15
 Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu
 20 25 30
 Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Pro Asp Ile Gly
 50 55 60
 Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp Thr Gln Ser His
 65 70 75 80
 Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu
 85 90 95
 Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr
 100 105 110
 Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile Val
 115 120 125
 Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser
 130 135 140
 Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Leu Thr Ile
 145 150 155 160
 Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp Pro Ser Gln Leu
 165 170 175
 Leu Lys Leu Ala Cys Ser Asp Ser Val Leu Thr Asn Ile Phe Ile Tyr
 180 185 190
 Ser Ile Gly
 195

<210> 2658

<211> 314

<212> PRT

<213> Unknown (HsOLF1 (1336041 HSU56420) Issel-Tarver-L 97 11q11)

<400>2658

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
 20 25 30
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
 35 40 45
 Leu Leu Ile Arg Il Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val

65		70		75		80										
Pro	Lys	Met	Leu	Val	Asn	Phe	L	u	Ser	Glu	Asn	Lys	Ser	Ile	Ser	Tyr
			85						90						95	
Tyr	Gly	Cys	Ala	Leu	Gln	Phe	Tyr	Phe	Phe	Cys	Thr	Phe	Ala	Asp	Thr	
			100					105						110		
Glu	Ser	Phe	Ile	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	
		115					120					125				
Cys	Asn	Pro	Leu	Leu	Tyr	Thr	Val	Val	Met	Ser	Arg	Gly	Ile	Cys	Met	
	130					135					140					
Arg	Leu	Ile	Val	Leu	Ser	Tyr	Leu	Gly	Gly	Asn	Met	Ser	Ser	Leu	Val	
145					150					155					160	
His	Thr	Ser	Phe	Ala	Phe	Ile	Leu	Lys	Tyr	Cys	Asp	Lys	Asn	Val	Ile	
			165						170					175		
Asn	His	Phe	Phe	Cys	Asp	Leu	Pro	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Thr	
		180						185					190			
Asp	Thr	Thr	Ile	Asn	Glu	Trp	Leu	Leu	Ser	Thr	Tyr	Gly	Ser	Ser	Val	
		195					200					205				
Glu	Ile	Ile	Cys	Phe	Ile	Ile	Ile	Ile	Ile	Ser	Tyr	Phe	Phe	Ile	Leu	
	210					215					220					
Leu	Ser	Val	Leu	Lys	Ile	Arg	Ser	Phe	Ser	Gly	Arg	Lys	Lys	Thr	Phe	
225				230						235					240	
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ser	Val	Thr	Ile	Tyr	Gln	Gly	Thr	
			245						250					255		
Leu	Leu	Phe	Ile	Tyr	Ser	Arg	Pro	Ser	Tyr	Leu	Tyr	Ser	Pro	Asn	Thr	
		260					265						270			
Asp	Lys	Ile	Ile	Ser	Val	Phe	Tyr	Thr	Ile	Phe	Ile	Pro	Val	Leu	Asn	
	275						280					285				
Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Asp	Ala	Ala	Glu	
	290					295					300					
Lys	Val	Leu	Arg	Ser	Lys	Val	Asp	Ser	Ser							
305					310											

<210> 2659

<211> 317

<212> PRT

<213> Unknown (HsOLF3 (1336043 HSU56421) Issel-Tarver-L 97 7q35)

<400>2659

Met	Gly	Thr	Asp	Asn	Gln	Thr	Trp	Val	Ser	Glu	Phe	Ile	Leu	Leu	Gly	
1				5				10					15			
Leu	Ser	Ser	Asp	Trp	Asp	Thr	Arg	Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	
			20				25					30				
Val	Met	Tyr	Val	Val	Thr	Val	Leu	Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	
	35					40					45					
Ile	Arg	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	
	50				55					60						
Asn	Leu	Ser	Leu	Val	Asp	Val	Ser	Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	
65				70				75						80		
Leu	Leu	Ala	His	Phe	Leu	Ala	Glu	His	Lys	Ala	Ile	Pro	Phe	Gln	Ser	
			85					90					95			
Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser	Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe	
		100					105						110			
Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys	Asp	
	115					120					125					
Ala	Leu	Arg	Tyr	Ser	Ala	Ile	Met	His	Gly	Gly	Leu	Cys	Ala	Arg	Leu	
	130				135						140					
Ala	Ile	Thr	Ser	Trp	Val	Ser	Gly	Phe	Ile	Ser	Ser	Pro	Val	Gln	Thr	
145				150					155					160		
Ala	Ile	Thr	Phe	Gln	Leu	Pro	Met	Cys	Arg	Asn	Lys	Phe	Ile	Asp	His	
			165					170						175		
Ile	Ser	Cys	Glu	Leu	Leu	Ala	Val	Val	Arg	Leu	Ala	Cys	Val	Asp	Thr	

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<210> 2660
<211> 312
<212> PRT
<213> Unknown (OLFMF gi|2370145|gnl|PID|e334200 olfactory receptor protein)
```

<400>2660																
Met	Ser	Gly	Thr	Asn	Gln	Ser	Ser	Val	Ser	Glu	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Leu	Ser	Arg	Gln	Pro	Gln	Gln	Gln	His	Leu	Leu	Phe	Val	Phe	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Ala	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ser	
		35					40					45				
Val	Ser	Ile	Asp	Ser	Cys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ser	Phe	Val	Asp	Ile	Cys	Phe	Ser	Phe	Thr	Thr	Val	Pro	Lys	
65					70					75					80	
Met	Leu	Ala	Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	
				85					90					95		
Cys	Leu	Thr	Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Asn	
			100					105					110			
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	
			115				120					125				
Pro	Leu	His	Tyr	Thr	Ala	Lys	Met	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	
	130					135						140				
Val	Ala	Gly	Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	
145					150					155					160	
Leu	Leu	Met	Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	
				165					170					175		
Phe	Phe	Cys	Asp	Val	Thr	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asn	Thr	
			180					185					190			
His	Leu	Asn	Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	
		195					200					205				
Thr	Pro	Phe	Leu	Cys	Ile	Leu	Ala	Ser	Tyr	Met	His	Ile	Thr	Cys	Thr	
	210					215						220				
Val	Leu	Lys	Val	Pro	Ser	Thr	Lys	Gly	Arg	Trp	Lys	Ala	Phe	Ser	Thr	
225					230					235					240	
Cys	Gly	Ser	His	Leu	Ala	Val	Val	Leu	Leu	Phe	Tyr	Ser	Thr	Ile	Ile	
				245					250					255		
Ala	Val	Tyr	Phe	Asn	Pro	Leu	Ser	Ser	His	Ser	Ala	Glu	Lys	Asp	Thr	
			260					265					270			
Met	Ala	Thr	Val	Leu	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	
		275					280					285				
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Tyr	Leu	Lys	Gly	Ala	Leu	Lys	Lys	Val	

290 295 300
 Ile Gly Arg Val Val Phe Ser Val
 305 310

<210> 2661

<211> 315

<212> PRT

<213> Unknown (OLFMF2 gi|2808536|emb|AJ003145|HSAJ03145 Homo sapiens mRNA for)

<400>2661

Val Gln Thr Tyr Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu
 1 5 10 15
 Leu Leu Gly Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val
 20 25 30
 Phe Phe Leu Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile
 35 40 45
 Ile Leu Ala Ile Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe
 85 90 95
 Ser Gly Cys Leu Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met
 100 105 110
 Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val
 115 120 125
 Cys Arg Pro Leu His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala
 130 135 140
 Leu Leu Val Thr Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu
 145 150 155 160
 His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile
 165 170 175
 Pro His Ile Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser
 180 185 190
 Asp Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Leu Val
 195 200 205
 Thr Ile Thr Pro Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr
 210 215 220
 Cys Val Val Leu Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr
 245 250 255
 Ile Met Ser Pro Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg
 260 265 270
 Asp Ile Ala Ala Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val
 290 295 300
 Lys Val Val Ala Val Lys Phe Phe Ser Val Gln
 305 310 315

<210> 2662

<211> 313

<212> PRT

<213> Unknown (CFDTMT)

<400>2662

Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala Leu Phe Leu

```
<210> 2663
<211> 309
<212> PRT
<213> Unknown (CfOLF4 (CFU53682) Issel-Tarver-L 97)
```

<400>2663																
Met	Glu	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Pro	Glu	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Phe	Ser	Glu	Glu	Pro	Lys	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu	
			20					25					30			
Ser	Met	Tyr	Leu	Val	Thr	Ile	Leu	Gly	Asn	Leu	Leu	Leu	Ile	Leu	Ala	
		35				40						45				
Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala	
	50					55					60					
Asn	Leu	Ser	Phe	Val	Asp	Ile	Cys	Phe	Thr	Cys	Thr	Thr	Ile	Pro	Lys	
65				70						75				80		
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Arg	Lys	Val	Ile	Thr	Tyr	Glu	Ser	
			85					90						95		
Cys	Ile	Ile	Gln	Met	Tyr	Phe	Phe	Glu	Leu	Phe	Ala	Gly	Ile	Asp	Asn	
			100					105					110			
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Tyr	
		115					120					125				
Pro	Leu	His	Tyr	Met	Val	Ile	Met	Asn	Pro	Gln	Leu	Cys	Ser	Leu	Leu	

130	135	140
Leu Leu Val Ser Trp	Ile Met Ser Ala Leu His Ser Leu Leu Gln Thr	
145	150	155
Leu Met Val Leu Arg Leu Ser Phe Cys Thr His Phe Gln Ile Pro His		160
	165	170
Phe Phe Cys Glu Leu Asn Gln Met Ile Gln Leu Ala Cys Ser Asp Thr		175
	180	185
Phe Leu Asn Asn Met Met Leu Tyr Phe Ala Ala Ile Leu Leu Gly Val		190
	195	200
Ala Pro Leu Val Gly Val Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser		205
	210	215
Ile Arg Gly Ile Ser Ser Ala His Ser Lys Tyr Lys Ala Phe Ser Thr		220
225	230	235
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu		240
	245	250
Gly Val Tyr Leu Ser Ser Ala Ala Pro Gln Ser Thr His Thr Ser Ser		255
	260	265
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe		270
	275	280
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Asn Val Phe		285
	290	295
Phe Arg Gly Lys Pro		300
305		

<210> 2664

<211> 317

<212> PRT

<213> Unknown (CfOLF3 (CFU53681) Issel-Tarver-L 97)

<400>2664

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly	
1	5
Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu	
	20
Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu	
	35
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr	
	50
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln	
65	70
Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser	
	85
Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe	
	100
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp	
	115
Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu	
	130
Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr	
145	150
Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His	
	165
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr	
	180
Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met	
	195
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr	
	210
Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr	
225	230
Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile	
	235

```
<210> 2665
<211> 311
<212> PRT
<213> Unknown (CfOLF2 (1314663 CFU53680) Issel-Tarver-L 97)
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```
<210> 2666
<211> 311
<212> PRT
<213> Unknown (CfOLF1 (1314661 CFU53679) Issel-Tarver-L 97)
```

<400>2666

```

Met Asp Gly Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Phe
 1          5          10          15
Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Val Phe Leu Thr
          20          25          30
Leu Tyr Gly Ile Ile Leu Thr Gly Asn Ile Gly Leu Met Met Leu Ile
          35          40          45
Arg Thr Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
          50          55          60
Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Ala Ile Val Pro Lys Met
          65          70          75          80
Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Leu Tyr Gly Cys
          85          90          95
Ala Leu Gln Phe Tyr Phe Ser Cys Ala Phe Ala Asp Thr Glu Ser Phe
          100          105          110
Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Val Trp Leu Ile
          130          135          140
Val Leu Ser Tyr Ile Gly Gly Asn Met Ser Ser Leu Val His Thr Ser
          145          150          155          160
Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile Asn His Phe
          165          170          175
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
          180          185          190
Val Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val Glu Ile Phe
          195          200          205
Cys Phe Ile Val Ile Val Ile Ser Tyr Tyr Phe Ile Leu Arg Ser Val
          210          215          220
Leu Arg Ile Arg Ser Ser Ser Gly Arg Lys Lys Thr Phe Ser Thr Cys
          225          230          235          240
Ala Ser His Leu Thr Ser Val Ala Ile Tyr Gln Gly Thr Leu Leu Phe
          245          250          255
Ile Tyr Ser Arg Pro Thr Tyr Leu Tyr Thr Pro Asn Thr Asp Lys Ile
          260          265          270
Ile Ser Val Phe Tyr Thr Ile Ile Ile Pro Val Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Lys Arg Ala Val
          290          295          300
Arg Leu Lys Val Asp Ser Ser
          305          310

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<210> 2667

<211> 155

<212> PRT

<213> Unknown (DRU42392)

<400>2667

```

Asn Pro Leu Arg Tyr Pro Ala Val Met Thr Ser Asn Met Val Val His
 1          5          10          15
Leu Ser Ala Ala Ala Trp Gly Val Ala Val Val Leu Val Gly Ile Leu
          20          25          30
Ile Gly Leu Thr Val Arg Leu Ser Phe Cys Arg Ser Val Ile Glu Asn
          35          40          45
Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Ser Thr
          50          55          60
Ala Ile Asn Asn Ile Tyr Gly Leu Ser Phe Thr Val Val Leu Leu Thr
          65          70          75          80
Ser Ser Leu Gly Ser Ile Ala Leu Thr Tyr Leu Arg Ile Ala Ile Val
          85          90          95

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Cys Phe Lys Ser Lys Asn Lys Ala Thr Asn Ser Lys Ala Ile Lys Thr
 100 105 110
 Cys Ser Thr His Leu Ala Val Tyr Leu Ile Met Met Val Ser Gly Leu
 115 120 125
 Thr Thr Ile Thr Leu His Arg Phe Pro Glu Leu Ser Asp Ser Arg Lys
 130 135 140
 Leu Ser Ser Ile Ile Lys His Ile Val Pro Pro
 145 150 155

<210> 2668

<211> 155

<212> PRT

<213> Unknown (DRU42394)

<400>2668

Asn Pro Leu Arg Tyr Gln Thr Ile Met Thr Asn Lys Thr Val Ile Thr
 1 5 10 15
 Leu Ser Ala Leu Ala Trp Gly Ile Ala Leu Leu Phe Ile Ser Ile Leu
 20 25 30
 Ile Gly Leu Thr Leu Arg Leu Ser Arg Cys Arg Thr Phe Ile Ser Asn
 35 40 45
 Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Asp Val
 50 55 60
 Thr Ile Asn Asn Leu Tyr Gly Leu Ile Tyr Thr Val Leu Leu Phe Gly
 65 70 75 80
 Ser Ser Met Gly Ser Ile Ala Val Thr Tyr Ile Lys Ile Thr Ala Val
 85 90 95
 Cys Leu Val Thr Lys Ser Lys Met Leu Asn Ser Arg Ala Leu Lys Thr
 100 105 110
 Cys Ser Thr His Leu Ser Leu Tyr Leu Ile Met Leu Ile Ser Gly Leu
 115 120 125
 Ile Ile Ile Val Leu His Arg Phe Pro Ala Tyr Ser Asp Tyr Arg Lys
 130 135 140
 Ile Ala Ser Leu Leu Phe His Ile Ile Pro Ser
 145 150 155

<210> 2669

<211> 157

<212> PRT

<213> Unknown (DRU42395)

<400>2669

Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Ser Ser Ile Thr Leu
 1 5 10 15
 Ile Leu Ser Ala Lys Trp Ala Phe Asn Ser Ser Ile Val Ala Leu Met
 20 25 30
 Val Ser Leu Ile Thr Arg Ile Ser Phe Cys Asp Ser Asn Val Ile Gln
 35 40 45
 Ser Tyr Phe Cys Asp His Gly Pro Val Tyr Arg Leu Ala Cys Asn Asp
 50 55 60
 Asn Ser Ile Asn Arg Phe Met Gly Ser Phe Ile Thr Cys Leu Tyr Leu
 65 70 75 80
 Val Val Pro Leu Gly Ile Ile Ile Leu Ser Tyr Ile Gly Ile Phe Leu
 85 90 95
 Ala Leu Asn Lys Ile Thr Thr Trp Glu Ser Arg Leu Lys Ala Leu Lys
 100 105 110
 Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Tyr Phe Leu Pro Met
 115 120 125
 Ser Cys Thr Tyr Ile Ala Ala Trp Leu Leu Ala Leu Ala Pro Asn Ala
 130 135 140
 Arg Val Ile Thr Thr Ser Leu Ala Tyr Thr Ile Ser Gln

145

150

155

<210> 2670

<211> 150

<212> PRT

<213> Unknown (DRU42396)

<400>2670

```

Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Val Ile Val Asn Asn
 1           5           10           15
Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe Met Phe Asn Ser Ile
          20           25           30
Ile Val Ala Ser Met Val Ser Leu Val Thr Asn Ile Ser Phe Cys Lys
          35           40           45
Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His Gly Pro Met Phe Arg
          50           55           60
Met Ala Cys Asn Asp Asn Asn Ile Asn Lys Ile Met Gly Phe Leu Tyr
65          70          75          80
Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val Ile Phe Leu Ser Tyr
          85          90          95
Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala Thr Trp Glu Arg Arg
          100         105         110
Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu Leu Leu Val Gly Ile
          115         120         125
Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr Ser Leu Leu Leu Phe
          130         135         140
Ser Thr Ser Asn Ser Arg
145          150

```

<210> 2671

<211> 158

<212> PRT

<213> Unknown (DRU42397 (odorant receptor 8; 1644478) Weth-F 96)

<400>2671

```

Asn Pro Leu Arg Tyr Pro Asn Ile Val Thr Lys Trp Asn Ile Phe Tyr
 1           5           10           15
Leu Cys Leu Ile Ser Trp Val Ile Ala Asn Val Thr Pro Leu Met Met
          20           25           30
Val Ile Arg Ala Tyr Pro Leu Pro Tyr Cys Ala Glu Asn Thr Ile Ile
          35           40           45
Gln Cys Tyr Cys Asp His Ile Ser Ile Thr Ser Leu Ala Cys Thr Asn
          50           55           60
Arg Ala Pro Tyr Ser Ile Pro Ala Phe Val Leu Ala Met Val Ala Leu
65          70          75          80
Leu Thr Pro Leu Ala Phe Ile Val Phe Ser Tyr Cys Ala Ile Ile Leu
          85          90          95
Ala Val Leu Arg Ile Ser Ser Thr Gln Ala Arg Leu Lys Thr Phe Ser
          100         105         110
Thr Cys Ser Pro Gln Leu Ile Ile Ala Leu Tyr Phe Leu Pro Arg
          115         120         125
Cys Phe Ile Tyr Leu Ser Ser Asn Ile Gly Ile Tyr Phe Ser Thr Asp
          130         135         140
Leu Arg Leu Ala Ile Ile Met Met Tyr Ser Leu Phe Pro Pro
145          150          155

```

<210> 2672

<211> 155

<212> PRT

<213> Unknown (DRU42398 (1151131))

<400>2672

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Arg Pro Leu Glu Tyr His Ser Ile Met Thr Asp Gln Arg Ile Ile Glu
 1           5           10           15
Cys Ile Leu Phe Cys Trp Leu Thr Pro Phe Phe Cys Met Ala Val Leu
      20           25           30
Ile Gly Leu Thr Ala Arg Leu Thr Leu Cys Gly Ser Ala Ile Glu Lys
      35           40           45
Leu Tyr Cys Glu Asn Trp Ser Val Val Lys Leu Ser Cys Phe Ser Thr
      50           55           60
Thr Val Asn Asn Val Val Gly Tyr Val Ile Ile Val Tyr Phe Gly
65           70           75           80
His Ala Val Leu Ile Phe Cys Ser Tyr Ile Tyr Leu Val Val Lys Cys
      85           90           95
Arg Lys Ser Thr Glu Ser Arg His Lys Phe Ile Gln Thr Cys Val Pro
      100           105           110
His Leu Leu Ala Leu Leu Asn Val Thr Val Ala Leu Leu Phe Asp Val
      115           120           125
Leu Tyr Ser Arg Tyr Gly Ser Lys Ser Leu Pro Gln Asp Leu Arg Asn
      130           135           140
Phe Met Ser Leu Glu Phe Leu Leu Val Pro Pro
145           150           155

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<210> 2673

<211> 174

<212> PRT

<213> Unknown (DRU44439)

<400>2673

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Met Ala Tyr Asp Arg Leu Ile Ala Ile Cys Trp Pro Leu Arg Tyr Ser
 1           5           10           15
Thr Ile Asn Thr Asn Leu Arg Met Leu Leu Ile Ile Ala Leu Ile Trp
      20           25           30
Ile Leu Val Thr Leu Leu Asp Ile Phe Pro Val Ile Phe Ala Ser Arg
      35           40           45
Leu Pro Tyr Cys Ser Ser Arg Ala Val Leu Ser Cys Cys Cys Glu His
      50           55           60
Gly Pro Val Tyr Arg Leu Ala Cys Thr Asp Thr Thr Tyr Asn Arg Gln
65           70           75           80
Leu Gly Thr Val Lys Thr Met Ile Thr Leu Leu Gly Pro Leu Phe Phe
      85           90           95
Ile Val Phe Thr Tyr Val Ile Val Val Ile Ala Val Met Arg Ile Ala
      100           105           110
Ser Val Thr Gln Arg Trp Lys Ala Phe His Thr Cys Leu Thr His Met
      115           120           125
Met Leu Val Met Leu Tyr Tyr Met Pro Ile Ile Ile Ala Cys Val Leu
      130           135           140
Gly Asn Leu Arg Leu Val Gln Asn Val Asp Leu Leu Thr Ala Ile Leu
145           150           155           160
Thr Arg Ser Val Thr Val Pro Ala Met Leu Asn Pro Ile Ile
      165           170

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<210> 2674

<211> 173

<212> PRT

<213> Unknown (DRU44440)

<400>2674

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Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
 1           5           10           15
Ser Ile Val Asn Asn Ser Asn Met Ile Leu Il Phe Ser Ala Ile Trp
      20           25           30

```

Ala Phe Asn Ser Ser Val Val Ala Leu Met Val Ser Leu Ile Asp Arg
 35 40 45
 Leu Ser Phe Cys Glu Ser Asn Met Ile Gln Ser Tyr Phe Cys Asp His
 50 55 60
 Gly Pro Val Tyr Arg Leu Ala Cys Ser Asp Ile Ser Lys Asn Lys Ile
 65 70 75 80
 Met Ala Tyr Val Ile Ser Ala Met Tyr Ile Ile Ala Pro Met Val Val
 85 90 95
 Ile Val Phe Ser Tyr Leu Gly Ile Phe Leu Ala Leu Ile Lys Ile Thr
 100 105 110
 Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
 115 120 125
 Leu Leu Val Gly Ile Phe Phe Leu Pro Leu Phe Cys Thr Tyr Leu Ala
 130 135 140
 Gln Leu Leu Leu Ser Leu Asn Pro Asn Ala Arg Val Ile Ser Thr Ser
 145 150 155 160
 Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
 165 170

<210> 2675

<211> 173

<212> PRT

<213> Unknown (DRU44441)

<400>2675

Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
 1 5 10 15
 Val Ile Val Asn Asn Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe
 20 25 30
 Met Phe Asn Ser Ile Ile Val Ala Ser Met Val Ser Leu Val Thr Asn
 35 40 45
 Ile Ser Phe Cys Lys Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His
 50 55 60
 Gly Pro Met Phe Arg Met Ala Cys Asn Asp Asn Ile Ile His Glu Ile
 65 70 75 80
 Met Gly Phe Leu Tyr Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val
 85 90 95
 Ile Phe Leu Ser Tyr Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala
 100 105 110
 Thr Trp Glu Arg Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
 115 120 125
 Leu Phe Val Gly Ile Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr
 130 135 140
 Ser Leu Leu Leu Phe Ser Thr Ser Asn Ser Arg Val Ile Ser Thr Ser
 145 150 155 160
 Leu Ala Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
 165 170

<210> 2676

<211> 344

<212> PRT

<213> Unknown (ICTORDA (fish1 L09217 1079242) Ngai-J 93)

<400>2676

Met Thr Ser Val Leu Asn Ala Leu Ser Ala Asn Ala Thr Phe Ile Arg
 1 5 10 15
 Pro Ser Thr Phe Tyr Ile Asn Gly Phe Tyr Asn Ile Pro His Thr Lys
 20 25 30
 Tyr Tyr Tyr Ala Phe Leu Cys Ile Ala Tyr Ala Val Thr Val Leu Gly
 35 40 45
 Asn Ser Phe Ile Met Cys Thr Ile Tyr Leu Ala Arg Ser Leu His Thr

50 55 60
 Ala Lys Tyr Ile Thr Val Phe Asn Leu Ala Leu Ser Asp Leu Gly Gly
 65 70 75 80
 Ser Ser Ala Leu Ile Pro Lys Leu Ile Asp Thr Phe Leu Phe Glu Asn
 85 90 95
 Gln Val Ile Ser Tyr Glu Ala Cys Leu Ala Asn Met Phe Phe Val Leu
 100 105 110
 Phe Phe Met Thr Val Gln Ser Leu Thr Leu Leu Val Met Ala Tyr Asp
 115 120 125
 Arg Val Val Ala Ile Cys Phe Pro Leu Arg Tyr Asn Val Ile Val Thr
 130 135 140
 Lys Glu Ala Met Thr Leu Ile Ile Val Ile Thr Trp Ile Phe Ser Ile
 145 150 155 160
 Ser Ile Ile Ala Leu Leu Val Ala Leu Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Arg Ser Val Ile Ile Asn Ser Tyr Phe Cys Asp His Gly Pro Ile Leu
 180 185 190
 Ile Leu Ala Cys Asn Asp Lys Phe Ile Asn Arg Val Met Ala Ile Gly
 195 200 205
 Cys Phe Val Val Leu Asp Cys Val Pro Phe Leu Leu Ile Ile Val Ser
 210 215 220
 Tyr Ile Cys Ile Gly Ile Ala Leu Met Asn Ile Ser His Gly Leu Glu
 225 230 235 240
 Arg Arg Lys Ala Met Lys Thr Cys Thr Ser His Leu Ile Leu Val Ala
 245 250 255
 Leu Phe Tyr Leu Pro Phe Ile Gly Thr Asn Ile Thr Ser Leu Thr Ser
 260 265 270
 Ser Ile Asn Ala Asn Asp Arg Ile Leu Asn Ser Thr Leu Thr Gln Ile
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Lys Thr Glu Glu
 290 295 300
 Val Met Gln Ala Val Lys Val Leu Tyr Lys Arg Ala Lys Ala Val Val
 305 310 315 320
 Ile Cys Asp Ile Pro Asn Gly Gln Val Phe Gln Pro Trp Val Gly Val
 325 330 335
 Asp Ser Lys Lys Lys Lys Thr Phe Cys
 340

<210> 2677

<211> 321

<212> PRT

<213> Unknown (ICTORDB (fish3 L09218 1079244) Ngai-J 93)

<400>2677

Met Ala Asp Asn Ile Thr Ser Ile Leu Ser Leu Thr Ser Thr Asn Ala
 1 5 10 15
 Thr Phe Ile Arg Pro Ser Thr Phe Tyr Ile Thr Gly Leu Tyr Asn Ile
 20 25 30
 Pro His Ala Lys Tyr Tyr Tyr Leu Phe Leu Cys Phe Val Tyr Thr Val
 35 40 45
 Thr Phe Leu Gly Asn Ser Phe Ile Met Gly Thr Ile Tyr Leu Ala Arg
 50 55 60
 Ser Leu His Thr Ala Lys Tyr Ile Ala Val Phe Asn Leu Ala Leu Ser
 65 70 75 80
 Asp Leu Cys Gly Ser Ser Ala Leu Ile Pro Lys Leu Leu Asp Met Leu
 85 90 95
 Leu Phe Glu Asn Gln Ser Ile Ser Tyr Glu Ala Cys Leu Ser Asn Met
 100 105 110
 Phe Phe Val Tyr Cys Phe Met Thr Leu Gln Cys Leu Thr Leu Leu Ala
 115 120 125
 Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Tyr Pro Leu Arg Tyr His

130	135	140
Ala Ile Val Thr Lys	Ala Ala Met Ile Phe Ile	Ile Gly Ala Met Trp
145	150	155
Val L u Ser Val Ser	Val Asn Ala Val Leu Val	Ala Leu Ile Thr Arg
165	170	175
Leu Ser Phe Cys Arg	Ser Thr Thr Val Tyr Ser Tyr	Phe Cys Asp His
180	185	190
Gly Pro Ile Tyr Lys	Leu Ala Cys Asn Asp Asn Thr	Ile Asn Ser Ile
195	200	205
Met Gly Asn Val Cys	Thr Ala Thr Leu Leu Tyr Phe	Pro Leu Ile Leu
210	215	220
Ile Ile Ala Ser Tyr	Val Cys Ile Gly Phe Ala	Leu Gln Lys Ile Ala
225	230	235
His Gly Val Glu Gln	Val Lys Ala Met Lys Thr	Cys Thr Ser His Leu
245	250	255
Ile Leu Val Ala Met	Phe Tyr Leu Pro Ile Ile	Ser Val Tyr Thr Val
260	265	270
Ala Leu Thr Thr Arg	Ile Asp Thr Asn Ile Arg	Ile Ile Asn Thr Ala
275	280	285
Leu Thr Gln Thr Ile	Pro Pro Met Leu Asn Pro	Ile Ile Tyr Thr Leu
290	295	300
Lys Thr Glu Glu Val	Met Gln Ala Ile Lys Leu	Tyr Lys His Ile
305	310	315
Arg		320

<210> 2678

<211> 328

<212> PRT

<213> Unknown (ICTORDC (fish32A L09219 1079245) Ngai-J 93)

<400>2678

Met Ser Ala Leu Asn	Ser Ser Leu Leu Gln	Asn Val Ser Phe	Val Arg
1	5	10	15
Pro Glu Tyr Phe	Ile Ser Gly Phe	Ser Gly Ile Pro	Phe Ser Gln
20	25	30	
Tyr Tyr Phe Ala	Phe Leu Ile Phe	Ile Tyr Ile Ile	Ser Leu Cys Gly
35	40	45	
Asn Ser Ile Val	Leu Phe Met Ile	Leu Val Asp Arg	Thr Leu His Ile
50	55	60	
Pro Lys Tyr Met	Gly Ile Phe Asn	Leu Ala Leu Ser	Asp Phe Gly Glu
65	70	75	80
Thr Asn Val Leu	Ile Pro Ser Leu	Val Lys Thr Leu	Phe Phe Asp Ser
85	90	95	
Gln Tyr Ile Ser	Tyr Asp Ala Cys	Leu Ala Asn Met	Phe Leu Thr Phe
100	105	110	
Phe Phe Ser Ser	Gly Gln Ala Leu	Thr Leu Val Ala	Leu Ala Tyr Asp
115	120	125	
Arg Phe Ile Ala	Ile Cys Leu Pro	Leu Arg Tyr Asn	Ala Ile Val Asn
130	135	140	
Asn Ser Phe Met	Phe Ala Ser Leu	Thr Ala Ile Trp	Ile Phe Asn Val
145	150	155	160
Val Met Asn Gly	Thr Leu Val Val	Leu Ile Thr Arg	Leu Ser Phe Cys
165	170	175	
Lys Thr Asn Glu	Ile Lys Ser Phe	Phe Cys Asp His	Gly Pro Val Tyr
180	185	190	
Thr Ile Ala Cys	Asn Asp Asn Ser	Ile Asn Ser Phe	Met Ala Lys Leu
195	200	205	
Cys Thr Ala Val	Tyr Leu Tyr Ala	Pro Leu Thr Ala	Ile Val Phe Ser
210	215	220	
Tyr Leu Gly Ile	Leu Leu Ala Leu	Thr Lys Ile Thr	Thr Trp Glu Ser

225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255
 Val Ph Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2679

<211> 328

<212> PRT

<213> Unknown (ICTORDD (fish22 fish202 L09220 1079243) Ngai-J 93)

<400>2679

Met Pro Glu Gly Asn Ile Thr Asn Val Lys Asn Phe Val Ile Leu Gly
 1 5 10 15
 Phe Pro Gly Leu Pro Pro Asn Tyr Tyr Gly Leu Val Ser Val Val Met
 20 25 30
 Phe Phe Val Tyr Val Cys Thr Leu Ile Gly Asn Cys Thr Phe Phe Thr
 35 40 45
 Leu Phe Leu Arg Glu Lys Ser Leu Gln Lys Pro Met Tyr Tyr Ile Met
 50 55 60
 Leu Asn Leu Ala Ala Ser Asp Val Leu Phe Ser Thr Thr Thr Leu Pro
 65 70 75 80
 Lys Ile Ile Ala Arg Tyr Trp Phe Gly Asp Gly Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Phe Ile Gln Met Gln Phe Val His Tyr Phe Ala Thr Val Asn
 100 105 110
 Ala Leu Val Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
 115 120 125
 Asn Pro Leu Arg Tyr Val Asn Ile Val Lys Glu Ser Thr Ile Leu Gly
 130 135 140
 Leu Cys Val Val Ser Trp Leu Leu Ala Glu Pro Thr Val Leu Thr Thr
 145 150 155 160
 Val Ile Arg Ala Thr Ser Leu Pro Tyr Cys Ala Ser Asn Thr Val Ile
 165 170 175
 Gln Cys Tyr Cys Asp His Val Ser Val Thr Lys Leu Ala Cys Ile Asp
 180 185 190
 Arg Thr Pro Tyr Ala Phe Pro Ala Leu Val Ser Ala Leu Val Met Leu
 195 200 205
 Leu Thr Pro Leu Ala Phe Ile Leu Phe Ser Tyr Gly Ser Ile Ile Val
 210 215 220
 Thr Val Phe Arg Thr Ser Ser Thr Arg Gly Arg Leu Lys Thr Leu Ser
 225 230 235 240
 Thr Cys Ser Ser Gln Leu Ile Ile Ile Thr Leu Phe Phe Leu Pro Arg
 245 250 255
 Cys Leu Asn Tyr Leu Ser Ser Ser Leu Gly Ile His Ile Asn Ala Asp
 260 265 270
 Ile Gln Ile Leu Val Ile Met Leu Tyr Ser Leu Leu Pro Pro Met Ile
 275 280 285
 Asn Pro Val Ile Tyr Cys Leu Arg Thr Lys Glu Ala Lys Glu Cys Leu
 290 295 300
 Lys Arg Ser Leu Asn Arg Ser Ser Phe Val Gln Phe Leu Lys Ile Asn
 305 310 315 320
 Val Gln Val Ser Thr Leu Ser Asn

325

<210> 2680

<211> 317

<212> PRT

<213> Unknown (ICTORDE (fish47 L09221 1079249) Ngai-J 93)

<400>2680

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Met Asn Ser Thr Asn Ser Thr Asp Ser Phe Asp Lys Gly Phe Tyr Leu
 1          5          10          15
Ile Ala Tyr Asn Ser Leu Gly Asn Lys Asn Tyr Leu Ile Leu Ala Leu
          20          25          30
Gly Ile Ile Tyr Leu Ile Thr Leu Leu Cys Asn Phe Thr Leu Leu Ala
          35          40          45
Ile Ile Leu Met Asn Ser Ser Leu Gln Asn Pro Lys Phe Leu Ala Val
          50          55          60
Phe Asn Leu Ala Val Val Asp Ile Ser Ile Asn Ser Val Ile Ile Pro
65          70          75          80
Gln Met Val Pro Val Phe Val Phe Asn Leu Asn His Ile Ser Phe Glu
          85          90          95
Ser Cys Phe Ser Gln Met Phe Phe Met His Phe Phe Gly Asp Met Glu
          100          105          110
Ser Phe Ser Leu Ala Leu Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys
          115          120          125
Phe Pro Leu Arg Tyr Pro Thr Ile Asn Thr Asn Met Arg Met Val Leu
          130          135          140
Ile Ile Ala Ser Leu Trp Phe Leu Val Phe Leu Ile Glu Leu Tyr Pro
          145          150          155          160
Val Ala Leu Ala Ser Gly Leu Ser Tyr Cys Arg Ser Arg Val Val Pro
          165          170          175
Ser Cys Cys Cys Glu His Gly Pro Val Tyr Asn Leu Ala Cys Gly Asp
          180          185          190
Ile Ser Tyr Asn Lys Arg Leu Ala Leu Ala Lys Thr Leu Val Val Leu
          195          200          205
Leu Gly Pro Leu Thr Phe Ile Ile Cys Ser Tyr Val Ile Val Val Val
          210          215          220
Ala Val Leu Arg Ile Ala Ser Pro Thr Gln Cys Trp Lys Ala Phe Asn
          225          230          235          240
Thr Cys Leu Thr His Met Ile Leu Val Leu Ile Tyr Tyr Leu Pro Ile
          245          250          255
Ile Leu Ala Tyr Ile Leu Gly Asn Leu Lys Leu Leu Gln Ser Ala Asp
          260          265          270
Leu Tyr Thr Ala Gly Leu Thr Val Cys Val Thr Leu Pro Ala Met Leu
          275          280          285
Asn Pro Ile Ile Tyr Ser Leu Lys Thr Glu Glu Leu Gln Asp Lys Leu
          290          295          300
Leu Lys Phe Ile Lys Pro Gln Lys Val Ser Asn Thr Val
          305          310          315

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<210> 2681

<211> 313

<212> PRT

<213> Unknown (ICTORDF (fish8 L09222 1079250) Ngai-J 93)

<400>2681

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Met Leu Ala Pro Val Gln Asn Ile Ser Phe Thr Thr Phe Thr Leu Thr
 1          5          10          15
Gly Phe His Asp Leu Gly Glu Trp Gly Pro Ile Leu Ser Ile Pro Tyr
          20          25          30
Leu Leu Met Phe Leu Leu Ser Ser Thr Ser Asn Leu Thr Leu Ile Tyr
          35          40          45

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1635

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Leu Ile Ile Ser Gln Arg Ala Leu His Ser Pro Met Cys Ile Leu Ile
 50                      55                      60
Gly Leu Met Ala Val Val Asp Leu Ser Met Pro Ile Phe Cys Val Pro
65                      70                      75                      80
Asn Met Leu Leu Ser Phe Leu Phe Asn Trp Lys Gly Ile Ser Leu Val
                      85                      90                      95
Gly Cys Leu Val Gln Met Phe Cys Ile His Cys Ala Gly Thr Phe Gln
                      100                      105                      110
Ser Thr Ile Leu Leu Trp Met Ala Leu Asp Arg Phe Phe Ala Ile Cys
                      115                      120                      125
Arg Pro Leu Tyr Tyr Gln Lys Tyr Met Gly Met Pro Asn Phe Leu Lys
                      130                      135                      140
Phe Ile Ile Phe Pro Val Ile Arg Asn Leu Phe Phe Ile Thr Thr Ile
145                      150                      155                      160
Val Ser Trp Ala Gly Lys Leu Thr Phe Cys Glu Thr Asn Glu Ile Asp
                      165                      170                      175
His Cys Val Cys Glu His Met Ala Leu Val Gln Leu Ala Cys Gly Asp
                      180                      185                      190
Ile Ser Ile Asn Asn Ala Leu Gly Leu Leu Thr Val Phe Leu Thr Ile
                      195                      200                      205
Thr Ala Asp Phe Ile Phe Ile Thr Ile Ser Tyr Ile Val Ile Leu Val
                      210                      215                      220
Ser Ile Leu Arg Ser Gly Lys Ala Cys Leu Lys Ala Val Asn Thr Cys
225                      230                      235                      240
Ile Thr His Ile Ile Val Met Thr Val Ser Leu Thr Phe Ala Leu Ile
                      245                      250                      255
Ala Phe Leu Ser Tyr Arg Ile Arg Asn Phe Ser Pro Ser Ser Arg Val
                      260                      265                      270
Phe Leu Ser Thr Met Tyr Leu Phe Ile Pro Ser Cys Phe Asn Pro Ile
                      275                      280                      285
Ile Tyr Gly Val Arg Thr Lys Glu Ile Arg Glu Gln Phe Leu Lys Leu
290                      295                      300
Met Lys Tyr Val Lys Val Phe Pro Lys
305                      310

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<210> 2682

<211> 328

<212> PRT

<213> Unknown (ICTORDG (fish32D L09223 1079248) Ngai-J 93)

<400>2682

```

Met Asn Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1                      5                      10                      15
Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
20                      25                      30
Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
35                      40                      45
Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
50                      55                      60
Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu
65                      70                      75                      80
Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
                      85                      90                      95
Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe
100                      105                      110
Phe Phe Phe Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
115                      120                      125
Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
130                      135                      140
Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu
145                      150                      155                      160

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Val Met Ile Gly Thr Leu Val Val Leu Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2683

<211> 328

<212> PRT

<213> Unknown (ICTORDH (fish32C L09224 1079247) Ngai-J 93)

<400>2683

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Ile Gly Glu
 65 70 75 80
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Thr Asn Met Phe Phe Thr Phe
 100 105 110
 Phe Phe Ser Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu
 145 150 155 160
 Val Ile Phe Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255

Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2684

<211> 328

<212> PRT

<213> Unknown (ICTORDII (fish32B L09225 1079246) Ngai-J 93)

<400>2684

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu
 65 70 75 80
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe
 100 105 110
 Phe Phe Ala Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Val Thr Leu Ile Ala Ile Trp Val Phe Asn Val
 145 150 155 160
 Val Ile Ile Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Tyr Phe
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2685

<211> 313

<212> PRT

<213> Unknown (o11 (RATOL1RECE L34074) Guillaume-D_94)

<400>2685

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Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe Ile Leu Leu Gly
1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Phe Leu
20          25          30
Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met Ile Ile Leu Val
35          40          45
Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
50          55          60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
65          70          75          80
Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile Ser Tyr Gly Gly
85          90          95
Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Ser Thr Glu Cys
100          105          110
Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu Ala Ile Cys Arg
115          120          125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg Cys Leu His Leu
130          135          140
Ala Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
145          150          155          160
Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys Glu Val Asp His
165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
180          185          190
Thr Ala Asn Glu Ala Glu Leu Phe Ile Ser Val Leu Phe Leu Leu
195          200          205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
210          215          220
Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Thr Ala Ile
245          250          255
Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
260          265          270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala Phe Lys Arg Leu
290          295          300
Met Lys Arg Ile Ile Leu Ile Gly Lys
305          310

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<210> 2686

<211> 333

<212> PRT

<213> Unknown (F3 (RATOLFP15 A23701) Buck-L 91)

<400>2686

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Met Asp Ser Ser Asn Arg Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
1          5          10          15
Phe Val Glu Asn Lys Asp Leu Gln Pro Leu Ile Tyr Gly Leu Phe Leu
20          25          30
Ser Met Tyr Leu Val Thr Val Ile Gly Asn Ile Ser Ile Ile Val Ala
35          40          45
Ile Ile Ser Asp Pro Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50          55          60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

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65					70					75				80
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Asn	Asn	Val	Ile	Thr	Tyr	Ala
				85					90					95
Cys	Ile	Thr	Gln	Ile	Tyr	Phe	Phe	Leu	Leu	Phe	Val	Glu	Leu	Asp
			100					105					110	
Phe	Leu	Leu	Thr	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
			115					120					125	
Pro	Met	His	Tyr	Thr	Val	Ile	Met	Asn	Tyr	Lys	Leu	Cys	Gly	Phe
			130					135					140	
Val	Leu	Val	Ser	Trp	Ile	Val	Ser	Val	Leu	His	Ala	Leu	Phe	Gln
			145					150						160
Leu	Met	Met	Leu	Ala	Leu	Pro	Phe	Cys	Thr	His	Leu	Glu	Ile	Pro
			165					170						175
Tyr	Phe	Cys	Glu	Pro	Asn	Gln	Val	Ile	Gln	Leu	Thr	Cys	Ser	Asp
			180					185						190
Phe	Leu	Asn	Asp	Leu	Val	Ile	Tyr	Phe	Thr	Leu	Val	Leu	Leu	Ala
			195					200						205
Val	Pro	Leu	Ala	Gly	Ile	Phe	Tyr	Ser	Tyr	Phe	Lys	Ile	Val	Ser
			210					215						220
Ile	Cys	Ala	Ile	Ser	Ser	Val	His	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
			225					230						240
Cys	Ala	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Cys	Thr	Gly
			245					250						255
Gly	Val	Tyr	Leu	Ser	Ser	Ala	Ala	Asn	Asn	Ser	Ser	Gln	Ala	Ser
			260					265						270
Thr	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Val	Asn	Pro
			275					280						285
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Ser	Val	Leu	Lys	Lys
			290					295						300
Leu	Cys	Glu	Glu	Val	Ile	Arg	Ser	Pro	Pro	Ser	Leu	Leu	His	Phe
			305					310						320
Leu	Val	Leu	Cys	His	Leu	Pro	Cys	Phe	Ile	Phe	Cys	Tyr		
			325						330					

<210> 2687

<211> 313

<212> PRT

<213> Unknown (F5 (RATOLFPROC M64377 RNOLFP17 OLF5 P23266 B23701) Buck-L 91)

<400>2687

Met	Ser	Ser	Thr	Asn	Gln	Ser	Ser	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly
1				5				10						15	
Leu	Ser	Arg	Gln	Pro	Gln	Gln	Gln	Gln	Leu	Leu	Phe	Leu	Leu	Phe	Leu
			20					25						30	
Ile	Met	Tyr	Leu	Ala	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala
			35					40						45	
Ile	Gly	Thr	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
			50					55						60	
Asn	Leu	Ser	Phe	Val	Asp	Val	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys
			65					70						80	
Val	Leu	Ala	Asn	His	Ile	Leu	Gly	Ser	Gln	Ala	Ile	Ser	Phe	Ser	Gly
			85					90						95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Ala	Val	Phe	Gly	Asn	Met	Asp	Asn
			100					105						110	
Phe	Leu	Leu	Ala	Val	Met	Ser	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His
			115					120						125	
Pro	Leu	His	Tyr	Thr	Thr	Lys	Met	Thr	Arg	Gln	Leu	Cys	Val	Leu	Leu
			130					135						140	
Val	Val	Gly	Ser	Trp	Val	Val	Ala	Asn	Met	Asn	Cys	Leu	Leu	His	Ile
			145					150						160	
Leu	Leu	Met	Ala	Arg	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Met	Ile	Pro	His


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<210> 2688
<211> 311
<212> PRT
<213> Unknown (F6 (RATOLEPROD RNOLFPO1 M64378) Buck-L 91)
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Met 1	Ala	Trp	Ser	Thr 5	Gly	Gln	Asn	Leu	Ser 10	Thr	Pro	Gly	Pro	Phe 15	Ile
Leu	Leu	Gly	Phe 20	Pro	Gly	Pro	Arg	Ser 25	Met	Arg	Ile	Gly	Leu 30	Phe	Leu
Leu	Phe	Leu 35	Val	Met	Tyr	Leu	Leu 40	Thr	Val	Val	Gly	Asn 45	Leu	Ala	Ile
Ile	Ser 50	Leu	Val	Gly	Ala	His 55	Arg	Cys	Leu	Gln	Thr 60	Pro	Met	Tyr	Phe
Phe 65	Leu	Cys	Asn	Leu	Ser 70	Phe	Leu	Glu	Ile	Trp 75	Phe	Thr	Thr	Ala	Cys 80
Val	Pro	Lys	Thr 85	Leu	Ala	Thr	Phe	Ala	Pro 90	Arg	Gly	Gly	Val	Ile 95	Ser
Leu	Ala	Gly	Cys 100	Ala	Thr	Gln	Met	Tyr 105	Phe	Val	Phe	Ser	Leu 110	Gly	Cys
Thr	Glu	Tyr 115	Phe	Leu	Leu	Ala	Val 120	Met	Ala	Tyr	Asp	Arg 125	Tyr	Leu	Ala
Ile	Cys 130	Leu	Pro	Leu	Arg	Tyr 135	Gly	Gly	Ile	Met	Thr 140	Pro	Gly	Leu	Ala
Met 145	Arg	Leu	Ala	Leu	Gly 150	Ser	Trp	Leu	Cys	Gly 155	Phe	Ser	Ala	Ile	Thr 160
Val	Pro	Ala	Thr 165	Leu	Ile	Ala	Arg	Leu	Ser 170	Phe	Cys	Gly	Ser	Arg 175	Val
Ile	Asn	His 180	Phe	Phe	Cys	Asp	Ile	Ser 185	Pro	Trp	Ile	Val	Leu 190	Ser	Cys
Thr	Asp	Thr 195	Gln	Val	Val	Glu	Leu 200	Val	Ser	Phe	Gly	Ile 205	Ala	Phe	Cys
Val	Ile 210	Leu	Gly	Ser	Cys	Gly 215	Ile	Thr	Leu	Val	Ser 220	Tyr	Ala	Tyr	Ile
Ile 225	Thr	Thr	Ile	Ile	Lys 230	Ile	Pro	Ser	Ala	Arg 235	Gly	Arg	His	Arg	Ala 240
Phe	Ser	Thr	Cys 245	Ser	Ser	His	Leu	Thr	Val 250	Val	Leu	Ile	Trp 255	Tyr	Gly
Ser	Thr	Ile	Phe 260	Leu	His	Val	Arg	Thr 265	Ser	Val	Glu	Ser	Ser 270	Leu	Asp
Leu	Thr	Lys	Ala	Ile	Thr	Val	Leu	Asn	Thr	Ile	Val	Thr	Pro	Val	Leu

275 280 285
 Asn Pr Phe Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Leu
 290 295 300
 Arg Arg Thr Val Lys Gly Lys
 305 310

<210> 2689

<211> 317

<212> PRT

<213> Unknown (F12 (RATOLFPROG OLF2 P23268 M64381 D23701) Buck-L 91)

<400>2689

Met Glu Ser Gly Asn Ser Thr Arg Arg Phe Ser Ser Phe Phe Leu Leu
 1 5 10 15
 Gly Phe Thr Glu Asn Pro Gln Leu His Phe Leu Ile Phe Ala Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Met
 35 40 45
 Ala Ile Ile Thr Gln Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ala Asn Leu Ser Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro
 65 70 75 80
 Lys Met Leu Val Asn Ile Tyr Thr Gln Ser Lys Ser Ile Thr Tyr Glu
 85 90 95
 Asp Cys Ile Ser Gln Met Cys Val Phe Leu Val Phe Ala Glu Leu Gly
 100 105 110
 Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Arg Cys
 115 120 125
 His Pro Leu Cys Tyr Thr Val Ile Val Asn His Arg Leu Cys Ile Leu
 130 135 140
 Leu Leu Leu Leu Ser Trp Val Ile Ser Ile Phe His Ala Phe Ile Gln
 145 150 155 160
 Ser Leu Ile Val Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro
 165 170 175
 His Phe Phe Cys Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp
 180 185 190
 Asn Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala
 195 200 205
 Ala Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser
 210 215 220
 Ser Ile His Ser Ile Ser Thr Val Gln Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly
 245 250 255
 Leu Gly Val Tyr Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala
 260 265 270
 Ala Ser Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ala Leu Glu Arg
 290 295 300
 Leu Leu Glu Gly Asn Cys Lys Val His His Trp Thr Gly
 305 310 315

<210> 2690

<211> 310

<212> PRT

<213> Unknown (I3 (RATOLFPROK OLF0 P23269 M64385 RNOLFP08 E23701) Buck-L 91)

<400>2690

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro
 1 5 10 15

Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
 20 25 30
 Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
 35 40 45
 Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
 65 70 75 80
 Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
 85 90 95
 Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
 100 105 110
 Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
 115 120 125
 His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
 130 135 140
 Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
 145 150 155 160
 Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
 165 170 175
 Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
 180 185 190
 Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
 195 200 205
 Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
 210 215 220
 Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
 245 250 255
 Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
 260 265 270
 Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
 290 295 300
 Ser Met Lys Ile Thr Leu
 305 310

<210> 2691

<211> 312

<212> PRT

<213> Unknown (I8 (RATOLFFROM M64387 RNOLFP09) Buck-L 91)

<400>2691

Met Asn Asn Lys Thr Val Ile Thr His Phe Leu Leu Leu Gly Leu Pro
 1 5 10 15
 Ile Pro Pro Glu His Gln Gln Leu Phe Phe Ala Leu Phe Leu Ile Met
 20 25 30
 Tyr Leu Thr Thr Phe Leu Gly Asn Leu Leu Ile Val Val Leu Val Gln
 35 40 45
 Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu Lys Leu Leu
 65 70 75 80
 Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala Gly Cys Leu
 85 90 95
 Thr Gln Ile Phe Phe Phe Leu Leu Phe Gly Tyr Leu Gly Asn Phe Leu
 100 105 110
 Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
 115 120 125

His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys Leu Leu Leu
 130 135 140
 Val Phe Trp Ile Met Thr Ser S r His Ala Met Met His Thr Leu Leu
 145 150 155 160
 Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu Asn Phe Phe
 165 170 175
 Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val
 180 185 190
 Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile Val Ile Pro
 195 200 205
 Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser Ser Ile Leu
 210 215 220
 Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
 245 250 255
 Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly Ser Ala Met
 260 265 270
 Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Gln Ala Leu Ile Arg Val Thr Cys
 290 295 300
 Ser Lys Lys Ile Ser Leu Pro Trp
 305 310

<210> 2692

<211> 314

<212> PRT

<213> Unknown (I9 (RATOLFPRON OLF9 H23701 M64388 RNOLFP10 P23272) Buck-L 91)

<400>2692

Met Thr Arg Arg Asn Gln Thr Ala Ile Ser Gln Phe Phe Leu Leu Gly
 1 5 10 15
 Leu Pro Phe Pro Glu Tyr Gln His Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Ile Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His
 165 170 175
 Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr
 180 185 190
 His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val
 195 200 205
 Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr
 225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
 260 265 270
 Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile
 290 295 300
 Met Cys Lys Lys Gln Ile Pro Ser Phe Leu
 305 310

<210> 2693

<211> 312

<212> PRT

<213> Unknown (I14 (RATOLFFPROQ OLF4 I23701 P23273 M64391 RNOLFP14) Buck-L 91)

<400>2693

Met Thr Gly Asn Asn Gln Thr Leu Ile Leu Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Pro Ser Glu Tyr His Leu Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Ile Ile Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Val Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser
 100 105 110
 Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys Ala Ser Leu
 130 135 140
 Val Leu Leu Leu Trp Met Leu Thr Met Thr His Ala Leu Leu His Thr
 145 150 155 160
 Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His
 165 170 175
 Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile
 195 200 205
 Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser
 210 215 220
 Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Phe
 245 250 255
 Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile
 260 265 270
 Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val
 290 295 300
 Ile Cys Thr Lys Lys Ile Ser Leu
 305 310

<210> 2694

<211> 314

<212> PRT

<213> Unknown (I15 (RATOLFFPROR A37286 M64391 RNOLFP16) Buck-L 91)

<400>2694

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Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
 1          5          10          15
Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
 20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Ile Leu
 35          40          45
Ile His Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
 85          90          95
Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
 100         105         110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115         120         125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130         135         140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145         150         155         160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
 165         170         175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180         185         190
His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
 195         200         205
Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
 210         215         220
Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
 225         230         235         240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245         250         255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
 260         265         270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275         280         285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
 290         295         300
Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
305         310

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<210> 2695

<211> 309

<212> PRT

<213> Unknown (RNOLP4 (517366 631861 1083741 S51356) Gat-U 94)

<400>2695

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Met Met Gly Thr Gly Asn His Ser Ala Val Val Val Phe Val Leu Val
 1          5          10          15
Gly Leu Thr Lys Gln Pro Glu Leu Leu Leu Pro Leu Phe Phe Leu Phe
 20          25          30
Leu Val Ile Tyr Val Leu Thr Val Val Gly Asn Leu Gly Met Ile Leu
 35          40          45
Leu Ile Ile Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu
 50          55          60
Ser Ser Leu Ser Phe Val Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro
 65          70          75          80
Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Phe Ile Thr Tyr Ser

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<210> 2696
<211> 318
<212> PRT
<213> Unknown (TB641 (RNU50949 1256393) Thomas-MB 96)

1647

195 200 205
 Gly Val Val Ala Ala Ser Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala
 210 215 220
 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
 225 230 235 240
 Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr
 245 250 255
 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Ser
 260 265 270
 Phe Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275 280 285
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Asn Ser Ala Leu
 290 295 300
 Lys Arg Leu Arg Ala Gly Arg Gly Asn Val Gly Gly Asp Lys
 305 310 315

<210> 2697

<211> 315

<212> PRT

<213> Unknown (TB567 (RNU50948 1256391) Thomas-MB 96)

<400>2697

Met Thr Gln Arg Asn Ala Thr Glu Val Thr Asp Phe Tyr Leu Leu Gly
 1 5 10 15
 Phe Gly Val Gln Gln Asn Thr Gln Cys Val Leu Phe Ile Val Phe Phe
 20 25 30
 Val Ile Tyr Val Thr Ser Met Val Gly Asn Thr Gly Met Ile Leu Leu
 35 40 45
 Ile Asn Thr Asn Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 Asn Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65 70 75 80
 Met Leu Gln Ser Phe Met Val Glu Asp Cys Ser Ile Ser Tyr Thr Gly
 85 90 95
 Cys Val Ile Gln Leu Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
 100 105 110
 Tyr Leu Leu Ala Val Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Arg Gln Val Cys Leu Leu Leu
 130 135 140
 Val Ala Leu Ser Tyr Leu Met Gly Ser Ile Asn Ser Ser Val His Thr
 145 150 155 160
 Gly Phe Thr Phe Ser Leu Ser Tyr Cys Asn Ser Lys Asn Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Val Pro Ile Ile Ser Leu Ser Cys Ser Asn Thr
 180 185 190
 Asp Ile Asn Ile Met Leu Leu Ile Val Phe Val Gly Phe Asn Leu Thr
 195 200 205
 Phe Thr Val Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met Ala Ala
 210 215 220
 Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Tyr Met Tyr Leu Gln Pro His Ser Asp Asn Ser Glu Glu Asn Met Lys
 260 265 270
 Val Ala Ser Val Phe Tyr Gly Ile Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Ala Met
 290 295 300
 Ser Arg Arg Phe Leu Arg Met Lys Ser Asn Pro

305

310

315

<210> 2698

<211> 311

<212> PRT

<213> Unknown (TB334 (RNU50947 1256389) Thomas-MB 96)

<400>2698

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Met Glu Asn Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser
 1          5          10          15
Gly Phe Pro Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met
          20          25          30
Tyr Leu Val Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly
 35          40          45
Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu
 50          55          60
Ser Phe Ala Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu
 65          70          75          80
Phe Asn Val Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu
          85          90          95
Thr Gln Met Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe
          100          105          110
Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          115          120          125
His Tyr Ser Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile
          130          135          140
Leu Cys Trp Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu
          145          150          155          160
Met Ala Arg Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe
          165          170          175
Cys Asp Val Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val
          180          185          190
Asn Glu Leu Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro
          195          200          205
Phe Val Ser Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu
          210          215          220
Arg Ile Gln Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser
          225          230          235          240
Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val
          245          250          255
Tyr Leu Phe Pro Ser Ser Val Glu Thr Thr Glu Lys Asp Val Ala Ala
          260          265          270
Ala Ala Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Lys Arg Leu Leu Ser
          290          295          300
His Arg Arg Ile Leu Ser Ser
305          310

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<210> 2699

<211> 312

<212> PRT

<213> Unknown (OR12 (423700 S29708) Raming-K 93)

<400>2699

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Met Ile Met Asn Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Pro Pro Glu His Trp His Leu Phe Tyr Thr Leu Leu Leu
          20          25          30
Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45

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Ile Leu Leu Asp Ser Asn Leu His Ile Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Asn Gln Asp Thr Ser Ile Thr Tyr Thr Gly
          85          90          95
Cys Leu Thr Gln Met Tyr Phe Ser Met Val Phe Ala Gly Met Glu Ile
          100          105          110
Phe Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu
          115          120          125
Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Phe Cys Val Cys Leu
          130          135          140
Gly Ser Leu Ser Trp Val Phe Asn Val Leu Tyr Ser Met Leu His Thr
145          150          155          160
Leu Leu Leu Ala Arg Leu Ser Phe Cys Lys Asp Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Tyr Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly Leu Leu Ile Val
          195          200          205
Ile Pro Phe Leu Leu Ile Val Met Thr Tyr Val Gln Ile Val Cys Ser
          210          215          220
Ile Leu Lys Val Pro Ser Thr Arg Ala Ile Tyr Lys Ile Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Thr Val Ser Leu Phe Tyr Gly Thr Val Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ala Met Met Ile Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala Leu Val Arg Val
          290          295          300
Leu Ile Lys Lys Lys Ile Ser Leu
305          310

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<210> 2700

<211> 304

<212> PRT

<213> Unknown (OR14 (423701) Raming-K 93)

<400>2700

```

Ser Val Thr Glu Phe Ile Leu Ala Gly Leu Thr Asp Gln Pro Gly Leu
 1          5          10          15
Arg Met Pro Leu Phe Phe Leu Phe Leu Gly Phe Tyr Met Val Thr Val
          20          25          30
Val Gly Asn Leu Ile Gly Leu Phe Leu Ile Gly Leu Asn Ser His Leu
          35          40          45
His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Val Val Asp Phe
          50          55          60
Cys Phe Ser Ser Thr Ile Ile Pro Lys Met Leu Met Ser Phe Ile Ser
65          70          75          80
Lys Lys Asn Ile Ile Ser His Ser Gly Cys Met Thr Gln Leu Phe Phe
          85          90          95
Phe Cys Phe Phe Val Val Ser Glu Thr Phe Ile Leu Ser Ala Met Ala
          100          105          110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Met Tyr Thr Val Thr
          115          120          125
Met Ser Pro Gln Val Cys Leu Leu Leu Leu Gly Ala Tyr Val Met
          130          135          140
Gly Phe Ser Glu Ala Met Ala His Thr Gly Asn Leu Met Asn Leu Thr
145          150          155          160

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Phe Cys Ala Asp Asn Leu Val Asn His Phe Met Cys Asp Ile Leu Pro
 165 170 175
 Leu Leu Glu Leu Ser Cys Asn Ser Thr Phe Ile Asn Glu Leu Val Val
 180 185 190
 Phe Ile Val Val Ala Ile Asp Ile Ala Val Pro Ile Val Ser Ile Phe
 195 200 205
 Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile Leu Arg Met His Ser Thr
 210 215 220
 Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Val
 225 230 235 240
 Val Cys Leu Leu Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Leu Pro
 245 250 255
 Ser Ile Leu Pro Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr
 260 265 270
 Ile Val Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 275 280 285
 Asp Val Lys Val Ala Leu Arg Lys Thr Leu Gly Lys Ile Ile Leu Ser
 290 295 300

<210> 2701

<211> 307

<212> PRT

<213> Unknown (OR18 (423702) Raming-K 93)

<400>2701

Met Gly Glu Asn Asn Asn Ile Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asp Pro Asp Gly Arg Lys Ala Leu Phe Val Ile Phe Phe Leu Ile
 20 25 30
 Tyr Ile Val Thr Met Met Gly Asn Leu Leu Ile Val Val Thr Val Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
 50 55 60
 Ser Leu Leu Asp Ala Leu Phe Ser Thr Ala Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Ala Asp Leu Leu Tyr Asp Gln Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Ser Gln Leu Phe Ile Glu His Leu Phe Gly Gly Val Asp Ile Val Ile
 100 105 110
 Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Ala Ile Met Asn Arg Arg Val Cys Ile Thr Leu Leu Ile
 130 135 140
 Phe Ala Trp Thr Gly Gly Phe Thr His Ser Leu Ile Gln Ile Val Phe
 145 150 155 160
 Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
 165 170 175
 Cys Asp Met Ser Pro Leu Leu Val Leu Ala Cys Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Ile Ala Asn Gly Gly Val Asn Cys Ile Val Ile
 195 200 205
 Phe Thr Leu Leu Leu Gly Ser Tyr Gly Ile Ile Leu Arg Ser Leu Lys
 210 215 220
 Thr Gln Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Leu Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
 245 250 255
 Ala Arg Pro Val Tyr Asn Phe Pro Ile Asp Lys Cys Ile Thr Val Phe
 260 265 270
 Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285

Asn Ser Glu Ile Lys Ser Cys Met Lys Lys Leu Trp Cys Lys Met Leu
 290 295 300
 His Ala Asp
 305

<210> 2702

<211> 314

<212> PRT

<213> Unknown (OR5 (423703 444281) Raming-K 93)

<400>2702

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Pro Pro Glu His Gln His Val Gly Tyr Ala Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
 195 200 205
 Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Pro Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
 260 265 270
 Val Met Ser Leu Met Tyr Thr Leu Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Ile Ile
 290 295 300
 Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
 305 310

<210> 2703

<211> 305

<212> PRT

<213> Unknown (OR37 (423699 S29711 265086) Raming-K 93)

<400>2703

Leu Leu Leu Gly Leu Ser Gly Tyr Pro Lys Thr Glu Ile Leu Tyr Phe
 1 5 10 15
 Val Ile Val Leu Val Met Tyr Leu Val Ile His Thr Gly Asn Gly Val

20	25	30
Leu Ile Ile Ala Ser Ile Phe Asp S r His Leu His Thr Pro Met Tyr		
35	40	45
Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser		
50	55	60
Ser Val Pro Ser Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile		
65	70	75
Ser Phe Ser Gly Cys Thr Val Gln Met Phe Val Gly Phe Ala Met Gly		
85	90	95
Ser Thr Glu Cys Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val		
100	105	110
Ala Ile Cys Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Glu Val		
115	120	125
Tyr Val Ser Met Ala Ser Ala Ser Trp Phe Ser Gly Gly Ile Asn Ser		
130	135	140
Val Val Gln Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn		
145	150	155
Val Ile Asn His Phe Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala		
165	170	175
Cys Ala Asp Ile Ser Leu Asn Ile Val Thr Met Val Ile Ser Asn Met		
180	185	190
Ala Phe Leu Val Leu Pro Leu Leu Leu Ile Phe Phe Ser Tyr Val Leu		
195	200	205
Ile Leu Tyr Thr Ile Leu Arg Met Asn Ser Ala Ser Gly Arg Arg Lys		
210	215	220
Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr		
225	230	235
Gly Thr Ile Phe Ser Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Thr		
245	250	255
Gly Lys Asp Lys Phe Gln Thr Ser Asp Lys Ile Ile Ser Leu Phe Tyr		
260	265	270
Gly Val Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn		
275	280	285
Lys Asp Val Lys Ala Ala Val Lys Tyr Ile Leu Lys Gln Lys Tyr Ile		
290	295	300

Pro
305

<210> 2704

<211> 314

<212> PRT

<213> Unknown (RNOLFREC (1504112) Raming-K 93)

<400>2704

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly	
1	15
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu	
20	30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu	
35	45
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser	
50	60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys	
65	75
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly	
85	95
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn	
100	110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe	
115	125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu	

130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu L u Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
 195 200 205
 Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
 260 265 270
 Val Met Ser Leu Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Arg Ile
 290 295 300
 Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
 305 310

<210> 2705

<211> 314

<212> PRT

<213> Unknown (1906335A (444281) Raming-K 93)

<400>2705

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
 195 200 205
 Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile

	245		250		255										
Pro	Leu	Tyr	Leu	Cys	Pro	Ser	Ser	Asn	Asn	Ser	Thr	Val	Lys	Glu	Thr
	260		265		270										
Val	Met	Ser	Leu	Met	Tyr	Thr	Leu	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe
	275		280		285										
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Lys	Gly	Ala	Met	Glu	Ile	Ile
	290		295		300										
Phe	Cys	Lys	Arg	Lys	Ile	Gln	Leu	Asn	Leu						
305			310												

<210> 2706

<211> 185

<212> PRT

<213> Unknown (PTE01 (544449) Abe-K 93)

<400>2706

Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Ser	Phe	Thr
1			5						10					15	
Ser	Thr	Thr	Leu	Pro	Lys	Met	Ile	Val	Asp	Ile	Gln	Thr	Asn	Asn	Arg
			20					25					30		
Ala	Ile	Ser	Tyr	Ser	Gly	Cys	Leu	Thr	Gln	Met	Ser	Phe	Phe	Met	Leu
			35				40					45			
Phe	Gly	Cys	Leu	Asp	Ser	Leu	Leu	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg
			50			55				60					
Phe	Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Gln	Val	Ile	Met	Asn	Pro
65					70				75					80	
Arg	Leu	Cys	Gly	Leu	Val	Phe	Leu	Ser	Ile	Leu	Ile	Ser	Leu	Leu	
				85				90					95		
Val	Ser	Gln	Leu	His	Asn	Ser	Val	Val	Leu	Gln	Leu	Thr	Tyr	Phe	Lys
			100					105					110		
Ser	Val	Asp	Ile	Ser	His	Phe	Phe	Cys	Asp	Pro	Ser	Leu	Leu	Leu	Asn
			115				120					125			
Leu	Ala	Cys	Ser	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Val	Met	Tyr	Phe	Val
			130			135					140				
Gly	Ala	Ile	Ser	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Phe	Phe	Ser	Tyr
145					150					155				160	
Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	Arg	Met	Pro	Ser	Pro	Gly	Gly	Lys
				165				170					175		
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser							
			180					185							

<210> 2707

<211> 168

<212> PRT

<213> Unknown (PTE03 (544450) Abe-K 93)

<400>2707

Thr	Thr	Val	Pro	Lys	Met	Leu	Ile	Asn	Leu	Gln	Lys	Gln	Asn	Lys	Ala
1				5					10					15	
Ile	Ser	Tyr	Ala	Gly	Cys	Ile	Thr	Gln	Leu	Ser	Phe	Val	Leu	Leu	Phe
			20					25					30		
Ala	Gly	Met	Glu	Asn	Phe	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr
			35			40						45			
Val	Ala	Ile	Cys	Lys	Pro	Leu	Arg	Tyr	Thr	Ala	Ile	Met	Lys	Ala	His
			50			55				60					
Leu	Cys	Leu	Val	Met	Thr	Leu	Leu	Ser	Leu	Cys	Ile	Ser	Ile	Val	Asp
65					70				75					80	
Ala	Leu	Leu	His	Gly	Leu	Met	Ile	Leu	Arg	Leu	Ser	Phe	Cys	Thr	Phe
			85					90					95		
Leu	Glu	Ile	Pro	His	Tyr	Phe	Cys	Glu	Leu	Tyr	Gln	Val	Ile	Lys	Leu
			100					105					110		

Ser Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Thr Met Thr
 115 120 125
 Ser Thr Leu Gly Gly Val Pro Leu Gly Gly Ile Ile Phe Ser Tyr Phe
 130 135 140
 Lys Ile Ile Ser Ser Ile Leu Arg Met Pro Ser Ser Gly Ser Arg His
 145 150 155 160
 Arg Ala Phe Ser Thr Cys Gly Ser
 165

<210> 2708

<211> 234

<212> PRT

<213> Unknown (PTE33 (544451) Abe-K 93)

<400>2708

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Val Asp Ile Tyr Phe Ile
 1 5 10 15
 Ser Gly Thr Ile Pro Lys Ile Leu Val Asn Met Gln Ser Lys Thr Lys
 20 25 30
 Asp Ile Ser Tyr Ile Glu Cys Leu Thr Gln Val Tyr Phe Phe Asn Thr
 35 40 45
 Phe Val Gly Met Asp Asp Val Leu Arg Thr Leu Met Ala Tyr Asp Arg
 50 55 60
 Phe Val Ala Ile Cys Met Pro Leu Lys Tyr Thr Val Ile Met Asn Pro
 65 70 75 80
 Arg Val Cys Thr Leu Leu Val Leu Met Phe Trp Ile Ile Met Phe Cys
 85 90 95
 Ile Ser Leu Ile His Val Leu Leu Met Asn Glu Leu Asn Phe Ser Arg
 100 105 110
 Gly Thr Lys Ile Pro His Phe Phe Cys Glu Leu Ala Gln Val Leu Lys
 115 120 125
 Val Ser Asn Ser Asp Thr His Ile Asn Asn Ile Phe Met Tyr Val Leu
 130 135 140
 Ser Ser Leu Leu Gly Val Ile Pro Met Thr Gly Ile Leu Met Ser Tyr
 145 150 155 160
 Ser Gln Ile Val Ser Ser Leu Leu Arg Met Ser Ser Thr Val Ser Lys
 165 170 175
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Cys Val Val Cys Leu
 180 185 190
 Phe Tyr Gly Ser Val Ile Gly Val Tyr Phe Ser Ser Ser Val Val Leu
 195 200 205
 Ser Thr Gln Arg Ile Met Val Ala Ser Leu Met Tyr Thr Val Ile Ser
 210 215 220
 Pro Met Phe Asn Pro Phe Ile Tyr Ser Leu
 225 230

<210> 2709

<211> 234

<212> PRT

<213> Unknown (PTE38 (544452) Abe-K 93)

<400>2709

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Asn Asp Ile Cys Ile Ile
 1 5 10 15
 Thr Thr Thr Ile Pro Lys Met Leu Met Asn Val Gln Ser His Asp Gln
 20 25 30
 Ser Ile Thr Tyr Leu Gly Cys Leu Ser Gln Val Tyr Leu Ile Val Asn
 35 40 45
 Phe Gly Ser Ile Glu Ser Cys Leu Leu Ala Val Met Ala Tyr Asp Arg
 50 55 60
 Tyr Val Ala Ile Cys His Pro Leu Lys Tyr Thr Val Ile Met Asn His


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<210> 2710
<211> 234
<212> PRT
<213> Unknown (PTE45 (544453) Abe-K 93)
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[illegible]

1657

<212> PRT

<213> Unknown (PTE58 (544454) Abe-K 93)

<400>2711

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Leu Leu Met Cys Asn Leu Cys Phe Ala Asp Ile Cys Phe Thr Ser Ala
 1           5           10           15
Ser Ile Pro Thr Asn Leu Val Asn Ile Gln Thr Lys Asn Lys Val Ile
           20           25           30
Thr Tyr Glu Gly Cys Ile Ser Gln Val Tyr Phe Phe Ile Leu Phe Gly
           35           40           45
Val Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val
           50           55           60
Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Asn Arg Arg Leu
65           70           75           80
Cys Gly Leu Leu Val Leu Gly Ser Trp Val Thr Thr Ala Leu Asn Ser
           85           90           95
Leu Leu Gln Ser Ser Met Ala Leu Arg Leu Ser Phe Cys Thr Asp Leu
           100          105          110
Lys Ile Pro His Phe Val Cys Glu Leu Asn Gln Leu Val Leu Leu Ala
           115          120          125
Cys Asn Asp Thr Phe Pro Asn Asp Met Val Met Tyr Phe Ala Ala Val
           130          135          140
Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys
145           150          155          160
Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ser Gln Gly Lys Tyr Lys
           165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr
           180          185          190
Ser Thr Leu Leu Gly Val Tyr Leu Ser Ser Ser Phe Thr Gln Asn Ser
           195          200          205
His Ser Thr Ala Arg Ala Ser Val Met Tyr Ser Val Val Thr Pro Met
           210          215          220
Leu Asn Pro Phe Ile Tyr Phe Phe
225           230

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<210> 2712

<211> 312

<212> PRT

<213> Unknown (RATGUST27 (D12820 P34987 A46750) Abe-K 93)

<400>2712

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Met Ile Leu Asn Cys Asn Pro Phe Ser Gly Leu Phe Leu Ser Met Tyr
 1           5           10           15
Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser Ser
           20           25           30
Asn Ser His Leu His Asn Leu Met Tyr Phe Phe Leu Ser Asn Leu Ser
           35           40           45
Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
           50           55           60
Asn Ile His Ser Gln Thr Lys Asp Ile Ser Tyr Ile Glu Cys Leu Ser
65           70           75           80
Gln Val Tyr Phe Leu Thr Thr Phe Gly Gly Met Asp Asn Phe Leu Leu
           85           90           95
Thr Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys His Pro Leu Asn
           100          105          110
Tyr Thr Val Ile Met Asn Leu Gln Leu Cys Ala Leu Leu Ile Leu Met
           115          120          125
Phe Trp Leu Ile Met Phe Cys Val Ser Leu Ile His Val Leu Leu Met
           130          135          140
Asn Glu Leu Asn Phe Ser Arg Gly Thr Glu Ile Pro His Phe Phe Cys
145           150          155          160

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Glu Leu Ala Gln Val Leu Lys Val Ala Asn Ser Asp Thr His Ile Asn
 165 170 175
 Asn Val Phe Met Tyr Val Val Thr Ser Leu Leu Gly Leu Ile Pro Met
 180 185 190
 Thr Gly Ile Leu Met Ser Tyr Ser Gln Ile Ala Ser Ser Leu Leu Lys
 195 200 205
 Met Ser Ser Ser Val Ser Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 210 215 220
 His Leu Cys Val Val Ser Leu Phe Tyr Gly Ser Ala Thr Ile Val Tyr
 225 230 235 240
 Phe Cys Ser Ser Val Leu His Ser Thr His Lys Lys Met Ile Ala Ser
 245 250 255
 Leu Met Tyr Thr Val Ile Ser Pro Met Leu Asn Pro Phe Ile Tyr Ser
 260 265 270
 Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Lys Leu Phe Ile Arg
 275 280 285
 Val Ala Ser Cys Pro Leu Trp Ser Lys Asp Phe Arg Pro Lys Phe Ile
 290 295 300
 Leu Lys Pro Glu Arg Gln Ser Leu
 305 310

<210> 2713

<211> 222

<212> PRT

<213> Unknown (K7 (MUSODORECA L14566 293754 464305 C40745) Ressler-KJ 93)

<400>2713

Phe Phe Leu Ser His Leu Ala Ile Val Asp Ile Ala Tyr Ala Cys Asn
 1 5 10 15
 Thr Val Pro Gln Met Leu Val Asn Leu Leu Asp Pro Val Lys Pro Ile
 20 25 30
 Ser Tyr Ala Gly Cys Met Thr Gln Thr Phe Leu Phe Leu Thr Phe Ala
 35 40 45
 Ile Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val
 50 55 60
 Ala Ile Cys His Pro Leu Arg Tyr Ser Ala Ile Met Ser Trp Arg Val
 65 70 75 80
 Cys Ser Thr Met Ala Val Thr Ser Trp Ile Ile Gly Val Leu Leu Ser
 85 90 95
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Val Ser Gln
 100 105 110
 Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala
 115 120 125
 Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val
 130 135 140
 Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys
 145 150 155 160
 Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys
 165 170 175
 Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr
 180 185 190
 Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys
 195 200 205
 Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn
 210 215 220

<210> 2714

<211> 222

<212> PRT

<213> Unknown (M50 (MUSODORECB L14567 293756 P34986 OLF5) Buck 93)

<400>2714

```

Tyr Phe Leu Ser Thr Met Ser Phe Leu Glu Ala Trp Tyr Ile Ser Val
 1           5           10           15
Thr Val Pro Lys Met Leu Ala Gly Phe Leu Phe His Pro Asn Thr Ile
      20           25           30
Ser Phe Leu Gly Cys Met Thr Gln Leu Tyr Phe Phe Met Ser Leu Ala
      35           40           45
Cys Thr Glu Cys Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys Trp Pro Leu Arg Tyr Pro Val Met Thr Thr Gly Phe
65           70           75           80
Cys Val Gln Leu Thr Ile Ser Ser Trp Val Ser Gly Phe Thr Ile Ser
      85           90           95
Met Ala Lys Val Tyr Phe Leu Ser Arg Val Ala Phe Cys Gly Asn Asn
      100          105          110
Val Leu Asn His Phe Phe Cys Asp Val Ser Pro Ile Leu Lys Leu Ala
      115          120          125
Cys Met Asn Leu Ser Met Ala Glu Thr Val Asp Phe Ala Leu Ala Ile
      130          135          140
Val Ile Leu Ile Phe Pro Leu Ser Ala Thr Val Leu Ser Tyr Gly Phe
145          150          155          160
Ile Val Ser Thr Val Leu Gln Ile Pro Ser Ala Thr Gly Gln Arg Lys
      165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Val Ile Phe Tyr
      180          185          190
Thr Ala Val Ile Phe Met Tyr Val Arg Pro Arg Ala Ile Ala Ser Phe
      195          200          205
Asn Ser Asn Lys Leu Ile Ser Ala Ile Tyr Ala Val Phe Thr
      210          215          220

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<210> 2715

<211> 161

<212> PRT

<213> Unknown (K18 (MUSODORECC L14568 293758 B40745) Buck 93)

<400>2715

```

Arg Tyr Val Ala Ile Cys Lys Pro Leu Thr Tyr Lys Val Ile Met Ser
 1           5           10           15
Pro Lys Ile Cys Cys Leu Leu Ile Phe Ser Ser Tyr Leu Met Gly Phe
      20           25           30
Ala Ser Ala Met Ala His Thr Gly Cys Met Ile Arg Leu Ser Phe Cys
      35           40           45
Asp Ser Asn Ile Ile Asn His Tyr Met Cys Asp Ile Phe Pro Leu Leu
      50           55           60
Pro Leu Ser Cys Ser Ser Thr Tyr Val Asn Glu Leu Met Ser Ser Val
65           70           75           80
Val Val Gly Ser Ala Ile Ile Leu Cys Cys Leu Ile Ile Leu Ile Ser
      85           90           95
Tyr Ala Met Ile Leu Phe Asn Ile Ile His Met Ser Ser Gly Lys Gly
      100          105          110
Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser
      115          120          125
Leu Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala
      130          135          140
Lys Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu
145          150          155          160
Val

```

<210> 2716

<211> 222

<212> PRT

<213> Unknown (K4 (MUSODORECD L14569 293760 464303 OLF4 P34983) Ressler-KJ 93)

<400>2716

```

Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys Gln Ser Thr Val
 1           5           10           15
Val Ile Pro Lys Met Leu Val Ser Phe Leu Thr Glu Met Asn Ile Ile
      20           25           30
Ser Tyr Ser Glu Cys Met Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly
      35           40           45
Ile Ala Gly Cys Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys Asn Pro Leu Leu Tyr Asn Val Thr Met Ser Tyr Gln Ile
      65           70           75           80
Tyr Ser Ser Leu Ile Ser Gly Val Tyr Ile Phe Ala Val Ile Cys Ser
      85           90           95
Ser Phe Asn Thr Gly Phe Met Leu Arg Thr Gln Phe Cys Asn Leu Asp
      100          105          110
Val Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Leu Leu Asn Leu Ala
      115          120          125
Ser Ser Asn Thr Tyr Ile Asn Glu Ile Leu Ile Leu Phe Phe Ala Thr
      130          135          140
Leu Asn Ser Phe Val Pro Val Leu Thr Ile Ile Thr Ser Tyr Ile Phe
      145          150          155          160
Ile Ile Val Thr Ile Leu Ser Ile His Ser Arg Glu Gly Lys Phe Lys
      165          170          175
Ala Phe Ser Thr Cys Ser Thr His Ile Ser Ala Val Ala Ile Phe Tyr
      180          185          190
Gly Ser Gly Ala Phe Thr Tyr Leu Gln Pro Ser Ser Leu Asn Ser Met
      195          200          205
Gly Gln Ala Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val
      210          215          220

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<210> 2717

<211> 312

<212> PRT

<213> Unknown (olf3 (MUSOR3X OR3 M84005 200154 P23275 A46247) Nef 92)

<400>2717

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1           5           10           15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
      20           25           30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
      35           40           45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
      65           70           75           80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
      85           90           95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
      130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
      145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn

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Met 1	Gln	Arg	Asn	Asn 5	Phe	Thr	Glu	Val	Ile 10	Glu	Phe	Val	Phe	Leu 15	Gly
Phe	Ser	Ser	Phe	Gly	Lys	His	Gln	Ile	Thr	Leu	Phe	Val	Val	Phe	Leu
			20					25					30		
Thr	Ile	Tyr	Ile	Leu	Thr	Leu	Ala	Gly	Asn	Ile	Ile	Ile	Val	Thr	Ile
		35					40					45			
Thr	His	Ile	Asp	His	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55				60					
Met	Leu	Ala	Ser	Ser	Glu	Thr	Val	Tyr	Thr	Leu	Val	Ile	Val	Pro	Arg
65					70					75					80
Met	Leu	Ser	Ser	Leu	Ile	Phe	Tyr	Asn	Leu	Pro	Ile	Ser	Leu	Ala	Gly
				85					90					95	
Cys	Ala	Thr	Gln	Met	Phe	Phe	Phe	Val	Thr	Leu	Ala	Thr	Asn	Asn	Cys
			100					105					110		
Phe	Leu	Leu	Thr	Ala	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn
			115				120					125			
Pro	Leu	Arg	Tyr	Thr	Ile	Ile	Met	Ser	Lys	Gly	Met	Cys	Ala	Leu	Leu
	130					135					140				
Val	Cys	Gly	Ser	Leu	Gly	Thr	Gly	Leu	Val	Met	Ala	Val	Leu	His	Val
145					150					155					160
Pro	Ala	Met	Phe	His	Leu	Pro	Phe	Cys	Gly	Thr	Val	Val	Glu	His	Phe
				165					170					175	
Phe	Cys	Asp	Ile	Tyr	Pro	Val	Met	Lys	Leu	Ser	Cys	Val	Asp	Thr	Thr
			180					185					190		
Val	Asn	Glu	Ile	Ile	Asn	Tyr	Gly	Val	Ser	Ser	Phe	Val	Ile	Leu	Val
		195					200					205			
Pro	Ile	Gly	Leu	Ile	Phe	Ile	Ser	Tyr	Val	Leu	Ile	Val	Ser	Ser	Ile
	210					215					220				
Leu	Lys	Ile	Val	Ser	Thr	Glu	Gly	Gln	Lys	Lys	Ala	Phe	Ala	Thr	Cys
225					230					235					240
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Val	His	Tyr	Gly	Cys	Ala	Ser	Ile
				245					250					255	
Ala	Tyr	Leu	Lys	Pro	Lys	Ser	Glu	Ser	Ser	Val	Glu	Lys	Asp	Leu	Leu
			260					265				270			
Leu	Ser	Val	Thr	Tyr	Thr	Ile	Ile	Thr	Pro	Leu	Leu	Asn	Pro	Val	Val

275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val
 290 295 300
 Gly Arg Asn Thr Ser
 305

<210> 2719

<211> 332

<212> PRT

<213> Unknown (GGCOR2GEN)

<400>2719

Met Leu Val Leu Cys Phe Ser Ala Ser Leu Leu Ser Asn Cys Asn Cys
 1 5 10 15
 Val Val Met Met Ala Lys Gly Asn His Ser Ser Ile Thr Glu Phe Val
 20 25 30
 Leu Leu Gly Phe Ser Glu Lys Arg Ala Ile Gln Ala Val Leu Phe Met
 35 40 45
 Gly Phe Leu Leu Ile Tyr Leu Ile Thr Leu Leu Gly Asn Val Gly Met
 50 55 60
 Ile Thr Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe
 65 70 75 80
 Phe Leu Ser Ser Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Thr Ile
 85 90 95
 Thr Pro Arg Val Leu Ser Asp Leu Pro Ala Ser Gln Lys Val Ile Ser
 100 105 110
 His Ser Ala Cys Leu Ala Gln Phe Tyr Phe Tyr Ala Val Phe Ala Thr
 115 120 125
 Thr Glu Cys Tyr Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
 130 135 140
 Ile Cys Ser Pro Leu Leu Tyr Val Phe Ser Met Ser Ser Arg Val Cys
 145 150 155 160
 Val Leu Leu Val Ala Gly Ser Tyr Leu Val Gly Val Val Asn Ala Thr
 165 170 175
 Ile His Thr Gly Leu Ala Leu Gln Leu Ser Phe Cys Gly Pro Asn Ile
 180 185 190
 Ile Asn His Phe Tyr Cys Asp Gly Pro Pro Leu Tyr Ala Ile Ser Cys
 195 200 205
 Thr Asp Pro Thr Thr Asn Glu Ile Ala Ile Phe Leu Val Val Gly Phe
 210 215 220
 Asn Met Leu Ile Thr Ser Val Thr Ile Phe Ile Ser Tyr Thr Tyr Ile
 225 230 235 240
 Leu Phe Ala Val Leu Arg Met His Thr Ala Ala Gly Lys Arg Lys Thr
 245 250 255
 Phe Ser Thr Cys Ala Ser His Leu Ala Thr Val Thr Leu Phe Tyr Ala
 260 265 270
 Ser Ala Gly Ser Met Tyr Ser Arg Pro Ser Ser Arg His Ser Gln Asp
 275 280 285
 Leu Asp Lys Val Ala Ser Val Phe Tyr Thr Met Val Thr Pro Met Leu
 290 295 300
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asp Val Leu
 305 310 315 320
 Gly Lys Val Met Gly Arg Lys Ser Val Ser Asp Lys
 325 330

<210> 2720

<211> 312

<212> PRT

<213> Unknown (GGCOR3GEN)

<400>2720

```

Met Ala Leu Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1          5          10          15
Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
          20          25          30
Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
          35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
          50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
          85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
          100          105          110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
          130          135          140
Val Lys Gly Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
145          150          155          160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
          165          170          175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
          180          185          190
Thr Leu Asn Glu Leu Leu Val Ile Phe Gly Ser Leu Phe Val Met
          195          200          205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
          210          215          220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
          245          250          255
Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
          260          265          270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
          290          295          300
Thr Ala Thr Ser Ile Trp Leu His
305          310

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<210> 2721

<211> 312

<212> PRT

<213> Unknown (GGCOR4GEN)

<400>2721

```

Met Ala Glu Gly Asn His Thr Leu Ala Ser Glu Phe Ile Leu Val Gly
 1          5          10          15
Leu Ser Asp His Pro Lys Met Lys Ala Ala Leu Phe Val Val Phe Leu
          20          25          30
Leu Ile Tyr Val Ile Thr Phe Gln Gly Asn Leu Gly Ile Ile Ile Leu
          35          40          45
Ile Gln Gly Asp Pro Arg Leu His Thr Ser Met Tyr Phe Phe Leu Ser
          50          55          60
Ser Leu Ser Val Val Asp Ile Cys Phe Ser Ser Val Ile Ala Pro Arg
65          70          75          80
Thr Leu Val Asn Phe Leu Ser Glu Arg Arg Thr Ile Ser Phe Thr Gly
          85          90          95
Cys Thr Gly Gln Thr Phe Phe Tyr Ile Val Phe Val Thr Thr Glu Cys
          100          105          110

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Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Thr Arg Arg Gln Cys Met Gln Leu
 130 135 140
 Val Val Gly Ser Tyr Ile Gly Gly Ile Leu Asn Ala Ile Ile Gln Thr
 145 150 155 160
 Thr Phe Ile Ile Arg Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Leu Leu Ala Leu Ser Leu Ala Ser Thr
 180 185 190
 Tyr Ile Ser Glu Met Ile Leu Phe Ser Leu Ala Gly Ile Ile Glu Leu
 195 200 205
 Ser Thr Val Thr Ser Ile Leu Val Ser Tyr Ile Phe Ile Ser Cys Ala
 210 215 220
 Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Leu Leu Tyr Gly Thr Thr Ile
 245 250 255
 Phe Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Thr Asp Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Val Glu Arg Ile Thr Val Arg Val
 305 310

<210> 2722

<211> 318

<212> PRT

<213> Unknown (GGCOR1)

<400>2722

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1 5 10 15
 Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
 20 25 30
 Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
 35 40 45
 Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
 50 55 60
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Thr Glu Ser
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
 130 135 140
 Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
 145 150 155 160
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Ile
 180 185 190
 Ala Ile Ser Glu Leu Leu Val Ile Ser Gly Ser Leu Phe Val Met
 195 200 205
 Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
 210 215 220

Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
 245 250 255
 Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
 260 265 270
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
 290 295 300
 Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln
 305 310 315

<210> 2723

<211> 312

<212> PRT

<213> Unknown (GGCOR2)

<400>2723

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1 5 10 15
 Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
 20 25 30
 Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
 35 40 45
 Ile Gly Met Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
 50 55 60
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ala Thr Phe Leu Glu Glu Arg Arg Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Trp
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
 130 135 140
 Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
 145 150 155 160
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
 165 170 175
 Phe Phe Cys Asp Asn Arg Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
 180 185 190
 Thr Leu Asn Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
 195 200 205
 Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
 210 215 220
 Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
 245 250 255
 Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
 260 265 270
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
 290 295 300
 Thr Ala Thr Ser Val Trp Leu His
 305 310

<210> 2724

<211> 318

<212> PRT

<213> Unknown (GGCOR3)

<400>2724

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1           5           10           15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
           20           25           30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Arg Leu
           35           40           45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
           50           55           60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65           70           75           80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
           85           90           95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
           100          105          110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
           115          120          125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
           130          135          140
Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
145          150          155          160
Cys Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His
           165          170          175
Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ile
           180          185          190
Ala Ile Ser Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
           195          200          205
Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
           210          215          220
Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
           245          250          255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
           260          265          270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
           275          280          285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
           290          295          300
Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln
305          310          315

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<210> 2725

<211> 312

<212> PRT

<213> Unknown (GGCOR4)

<400>2725

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1           5           10           15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
           20           25           30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
           35           40           45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
           50           55           60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys

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65					70					75				80
Met	Leu	Ala	Thr	Phe	Leu	Glu	Glu	Arg	Lys	Thr	Ile	Ser	Tyr	Ile
				85					90					95
Cys	Ile	Leu	Gln	Tyr	Phe	Ser	Phe	Val	Leu	Leu	Thr	Val	Thr	Glu
			100					105					110	S r
Leu	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
		115					120					125		Lys
Pro	Leu	Leu	Tyr	Pro	Ser	Ile	Met	Thr	Lys	Ala	Val	Cys	Trp	Arg
	130					135					140			Leu
Val	Lys	Gly	Leu	Tyr	Ser	Leu	Ala	Phe	Leu	Asn	Ser	Leu	Val	His
145					150					155				160
Ser	Gly	Leu	Leu	Lys	Leu	Ser	Phe	Cys	Ser	Ser	Asn	Val	Val	Asn
				165					170					175
Phe	Phe	Cys	Asp	Asn	Ser	Pro	Leu	Phe	Gln	Ile	Ser	Ser	Ser	Thr
			180					185					190	
Thr	Leu	Asn	Glu	Leu	Leu	Val	Phe	Ile	Phe	Gly	Ser	Leu	Phe	Ala
		195					200					205		Met
Ser	Ser	Ile	Ile	Thr	Ile	Leu	Ile	Ser	Tyr	Val	Phe	Ile	Ile	Leu
	210					215					220			Thr
Val	Val	Arg	Ile	Arg	Ser	Lys	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
225					230					235				240
Cys	Thr	Ser	His	Leu	Met	Ala	Val	Ser	Leu	Phe	His	Gly	Thr	Val
			245						250					255
Phe	Met	Tyr	Leu	Arg	Pro	Val	Lys	Leu	Phe	Ser	Leu	Asp	Thr	Asp
		260					265					270		Lys
Ile	Ala	Ser	Leu	Phe	Tyr	Thr	Val	Val	Ile	Pro	Met	Leu	Asn	Pro
	275					280					285			Leu
Ile	Tyr	Ser	Trp	Arg	Asn	Lys	Glu	Val	Lys	Asp	Ala	Leu	Arg	Arg
	290				295					300				Val
Ile	Ala	Thr	Asn	Val	Trp	Ile	His							
305					310									

<210> 2726

<211> 312

<212> PRT

<213> Unknown (GGCOR5)

<400>2726

Met	Ala	Leu	Gly	Asn	Cys	Thr	Thr	Pro	Thr	Thr	Phe	Ile	Leu	Ser	Gly
1				5					10					15	
Leu	Thr	Asp	Asn	Pro	Arg	Leu	Gln	Met	Pro	Leu	Phe	Met	Val	Phe	Leu
		20						25					30		
Ala	Ile	Tyr	Thr	Ile	Thr	Leu	Leu	Ala	Asn	Leu	Gly	Leu	Ile	Ala	Leu
	35					40						45			
Ile	Ser	Val	Asp	Phe	His	Leu	Gln	Thr	Pro	Met	Tyr	Ile	Phe	Leu	Gln
	50					55					60				
Asn	Leu	Ser	Phe	Thr	Asp	Ala	Ala	Tyr	Ser	Thr	Val	Ile	Thr	Pro	Lys
65					70					75					80
Met	Leu	Ala	Thr	Phe	Leu	Glu	Glu	Arg	Arg	Thr	Ile	Ser	Tyr	Val	Gly
			85						90					95	
Cys	Ile	Leu	Gln	Tyr	Phe	Ser	Phe	Val	Leu	Leu	Thr	Ser	Ser	Glu	Cys
		100						105					110		
Leu	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys
	115						120					125			
Pro	Leu	Leu	Tyr	Pro	Ala	Ile	Met	Thr	Lys	Ala	Val	Cys	Trp	Arg	Leu
	130					135					140				
Val	Glu	Gly	Leu	Tyr	Ser	Leu	Ala	Phe	Leu	Asn	Ser	Leu	Val	His	Thr
145					150					155					160
Ser	Gly	Leu	Leu	Lys	Leu	Ser	Phe	Cys	Ser	Ser	Asn	Val	Val	Asn	His
			165						170					175	
Phe	Phe	Cys	Asp	Asn	Ser	Pro	Leu	Phe	Gln	Ile	Ser	Ser	Ser	Ser	Thr

<210> 2727
<211> 312
<212> PRT
<213> Unknown (GGCOR6)

Met	Ala	Ser	Gly	Asn	Cys	Thr	Thr	Pro	Thr	Thr	Phe	Ile	Leu	Ser	Gly
1				5					10					15	
Leu	Thr	Asp	Asn	Pro	Gly	Leu	Gln	Met	Pro	Leu	Phe	Met	Val	Phe	Leu
			20					25					30		
Ala	Ile	Tyr	Thr	Ile	Thr	Leu	Leu	Thr	Asn	Leu	Gly	Leu	Ile	Ala	Leu
		35					40					45			
Ile	Ser	Ile	Asp	Leu	Gln	Leu	Gln	Thr	Pro	Met	Tyr	Ile	Phe	Leu	Gln
	50					55					60				
Asn	Leu	Ser	Phe	Thr	Asp	Ala	Val	Tyr	Ser	Thr	Val	Ile	Thr	Pro	Lys
65					70					75					80
Met	Leu	Ala	Thr	Phe	Leu	Glu	Glu	Thr	Lys	Thr	Ile	Ser	Tyr	Val	Gly
				85					90					95	
Cys	Ile	Leu	Gln	Tyr	Phe	Ser	Phe	Val	Leu	Leu	Thr	Val	Arg	Glu	Cys
			100					105					110		
Leu	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	Lys
		115					120					125			
Pro	Leu	Leu	Tyr	Pro	Ala	Ile	Met	Thr	Lys	Ala	Val	Cys	Trp	Arg	Leu
	130					135					140				
Val	Lys	Gly	Leu	Tyr	Ser	Leu	Ala	Phe	Leu	Asn	Phe	Leu	Val	His	Thr
145					150					155					160
Ser	Gly	Leu	Leu	Lys	Leu	Ser	Phe	Cys	Ser	Ser	Asn	Val	Val	Asn	His
				165					170					175	
Phe	Phe	Cys	Asp	Asn	Ser	Pro	Leu	Phe	Gln	Ile	Ser	Ser	Ser	Ser	Thr
			180					185					190		
Ala	Leu	Asn	Glu	Leu	Leu	Val	Phe	Ile	Phe	Gly	Ser	Leu	Phe	Val	Met
		195					200					205			
Ser	Ser	Ile	Ile	Thr	Ile	Leu	Ile	Ser	Tyr	Val	Phe	Ile	Ile	Leu	Thr
	210					215					220				
Val	Val	Arg	Ile	Arg	Ser	Lys	Glu	Arg	Lys	Tyr	Lys	Ala	Phe	Ser	Thr
225					230					235					240
Cys	Thr	Ser	His	Leu	Met	Ala	Val	Ser	Leu	Phe	His	Gly	Thr	Ile	Val
				245					250					255	
Phe	Met	Tyr	Phe	Gln	Pro	Ala	Asn	Asn	Phe	Ser	Leu	Asp	Lys	Asp	Lys
			260					265					270		
Ile	Met	Ser	Leu	Phe	Tyr	Thr	Val	Val	Ile	Pro	Met	Leu	Asn	Pro	Leu
	275						280					285			
Ile	Tyr	Ser	Trp	Arg	Asn	Lys	Glu	Val	Lys	Asp	Ala	Leu	His	Arg	Ala

290 295 300
 Ile Ala Thr Ala Val Leu Phe His
 305 310

<210> 2728
 <211> 162
 <212> PRT
 <213> Unknown (XLORXR1)

<400>2728
 Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys
 1 5 10 15
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp
 20 25 30
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser
 35 40 45
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu
 50 55 60
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser
 65 70 75 80
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile
 85 90 95
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala
 130 135 140
 Pro Lys Gln Asp Gln Phe Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro
 145 150 155 160
 Leu Leu

<210> 2729
 <211> 161
 <212> PRT
 <213> Unknown (XLORXR2)

<400>2729
 Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys
 1 5 10 15
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala
 20 25 30
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser
 35 40 45
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly
 65 70 75 80
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val
 85 90 95
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys
 100 105 110
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Gly Ser Ile Ile Cys Leu Tyr Met Arg Pro Thr Lys Ser Ile Ser
 130 135 140
 Pro Asn Gln Asp Val Phe Ala Leu Leu Tyr Ala Val Leu Val Pro Met
 145 150 155 160
 Leu

<210> 2730
 <211> 155
 <212> PRT
 <213> Unknown (XLORXR3)

<400>2730
 Val Ala Ile Cys Met Pro Met Leu Tyr Ser Leu Ile Met Lys Lys Ser
 1 5 10 15
 Ile Cys Ala Leu Leu Ala Ser Val Ser Trp Phe Met Gly Ala Met Asp
 20 25 30
 Ser Phe Met Phe Trp Tyr Leu Val Ser Asn Ser Ser Phe Cys Asp His
 35 40 45
 Gln Glu Ile Asn His Phe Phe Cys Asp Leu Lys Thr Leu Met Lys Leu
 50 55 60
 Ser Cys Arg Gly Ala Glu Thr Ile Lys Ile Val Ile Ile Val Ala Ser
 65 70 75 80
 Ala Val Leu Gly Phe Leu Pro Phe Cys Leu Ile Leu Ile Ser Tyr Ala
 85 90 95
 Asn Ile Ile Ser Ser Val Ser Lys Ile Arg Thr Ala Ala Gly Lys Leu
 100 105 110
 Lys Ile Phe Ser Ser Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
 115 120 125
 Cys Gly Thr Cys Leu Ser Leu Tyr Met Lys Pro Asp Ser Gly Asn Ser
 130 135 140
 Gln Glu Asn Glu Glu Leu Leu Ser Leu Leu Tyr
 145 150 155

<210> 2731
 <211> 162
 <212> PRT
 <213> Unknown (XLORXR5)

<400>2731
 Val Ala Ile Cys Gln Pro Leu Leu Tyr Ala Val Ile Met Asn Arg Lys
 1 5 10 15
 Val Val Ile Ile Phe Val Val Gly Val Tyr Leu Ser Gly Ile Phe Thr
 20 25 30
 Ala Ser Ile His Thr Ala Cys Thr Leu Thr Leu Ser Phe Cys Gly Pro
 35 40 45
 Asn Thr Ile Asn His Phe Tyr Cys Asp Ile Pro Pro Leu Met Glu Leu
 50 55 60
 Ser Cys Ser Asp Thr Tyr Ile His Lys Thr Val Ile Phe Val Val Val
 65 70 75 80
 Phe Cys Leu Gly Leu Phe Asn Val Ala Val Ile Leu Ala Ser Tyr Ser
 85 90 95
 Tyr Ile Phe Phe Thr Ile Ile His Ile Gln Ser Ser Cys Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Cys Val Ser Leu Phe
 115 120 125
 Tyr Gly Thr Val Phe Phe Met Tyr Leu Arg Pro Ala Ser Lys Tyr Ser
 130 135 140
 Val Ser Gln Asp Lys Val Val Ser Val Phe Tyr Thr Met Val Ile Pro
 145 150 155 160
 Met Met

<210> 2732
 <211> 163
 <212> PRT
 <213> Unknown (XLORXR9)

<400>2732

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Leu Ala Ile Cys Phe Pro Leu Asn Tyr Cys Leu Ile Met Ser Gln Ser
 1           5           10           15
Leu Arg Cys Arg Leu Val Val Val Cys Trp Ala Cys Gly Leu Val Asn
           20           25           30
Ser Leu Val Gln Ala Phe Ser Ile Ser His Leu Asp Phe Cys Gly Pro
           35           40           45
Asn Val Val Asp His Phe Phe Cys Asp Val Thr Pro Leu Phe Lys Leu
           50           55           60
Ser Cys Ser Asp Thr Arg Val Ser Glu Thr Ile Phe Leu Leu Val Val
65           70           75           80
Ala Val Ala Gly Met Gly Pro Leu Thr Phe Ile Leu Val Thr Tyr Gly
           85           90           95
His Ile Ile Leu Ala Ile Thr Arg Ile Thr Ser Ser His Gly Arg Tyr
           100          105          110
Lys Thr Phe Ser Thr Cys Ala Ser His Phe Thr Val Val Ala Leu Tyr
           115          120          125
Tyr Gly Ser Gly Ile Phe Ser Tyr Ile Trp Pro Thr Ser Thr Tyr Ala
           130          135          140
Met Asn Lys Asp Val Lys Val Val Ala Val Leu Tyr Thr Val Met Thr
145           150           155           160
Pro Met Leu

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<210> 2733

<211> 159

<212> PRT

<213> Unknown (XLORXR13)

<400>2733

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Val Ala Ile Ser Lys Pro Leu Arg Tyr Met Thr Ile Met Asn Trp Lys
 1           5           10           15
Val Cys Ala Val Leu Gly Val Ala Met Trp Thr Ala Gly Thr Val His
           20           25           30
Ser Ile Ser Phe Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro
           35           40           45
Asp Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Glu Leu
           50           55           60
Ala Cys Thr Asp Thr Arg Ile Thr Glu Ile Leu Val Val Ser Asn Ser
65           70           75           80
Gly Met Ile Ser Met Val Cys Phe Val Ile Ile Val Val Ser Tyr Ala
           85           90           95
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Asp Gly Lys Arg Lys
           100          105          110
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu
           115          120          125
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Ile Ser Leu Pro Glu
           130          135          140
Asp Lys Ile Val Ser Ala Phe Phe Thr Ala Val Thr Pro Leu Leu
145           150           155

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<210> 2734

<211> 162

<212> PRT

<213> Unknown (XLORXR17)

<400>2734

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Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn

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	20		25		30										
Ser	Leu	Ile	His	Thr	Ile	Leu	Thr	Phe	Met	Leu	Pro	Phe	Cys	Gly	Ser
	35						40					45			
Asn	Ala	Ile	Asp	Ser	Phe	Phe	Cys	Asp	Met	Pro	Pro	Leu	Leu	Lys	Leu
	50					55					60				
Ala	Cys	Thr	Asp	Thr	Leu	Val	Asn	Gln	Ile	Val	Ile	Phe	Val	Thr	Gly
65					70					75					80
Ser	Cys	Ile	Ile	Ala	Gly	Pro	Phe	Met	Leu	Thr	Val	Phe	Ser	Tyr	Val
				85					90					95	
Gln	Ile	Ile	Ser	Thr	Ile	Val	Ser	Ile	Arg	Ser	Ser	Ser	Arg	Lys	Lys
			100					105					110		
Lys	Ala	Phe	Ser	Thr	Cys	Thr	Ser	His	Ile	Thr	Ala	Val	Val	Ile	Phe
	115						120					125			
Tyr	Val	Pro	Ser	Ile	Cys	Ile	Tyr	Phe	Arg	Pro	Lys	Ser	Asn	Gln	Ala
	130					135					140				
Met	Ile	Gln	Asp	Lys	Met	Ala	Thr	Val	Ile	Cys	Ala	Val	Ile	Thr	Pro
145					150					155					160
Leu	Leu														

<210> 2735

<211> 223

<212> PRT

<213> Unknown (XLORXR42)

<400>2735

Cys	Asn	Leu	Ser	Ser	Leu	Asp	Ile	Ala	Tyr	Thr	Ser	Val	Thr	Ala	Pro
1			5						10					15	
Lys	Leu	Ile	His	Ile	Phe	Ala	Val	Asn	Asn	His	Arg	Ile	Ser	Phe	Trp
			20					25				30			
Gln	Cys	Ile	Ala	Gln	Leu	Tyr	Phe	Phe	Ile	Ala	Phe	Gly	Ser	Thr	Glu
	35					40						45			
Tyr	Leu	Leu	Leu	Thr	Leu	Met	Ser	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys
	50				55						60				
Lys	Pro	Leu	His	Tyr	Arg	Val	Val	Met	Ser	Pro	Met	Leu	Cys	Arg	Ala
65				70					75					80	
Gly	Ala	Ala	Gly	Thr	Trp	Ile	Gly	Gly	Leu	Leu	Ala	Ser	Ile	Pro	Thr
			85					90					95		
Ala	Thr	Ala	Ala	Ala	Asn	Ile	Tyr	Tyr	Cys	Ser	Asn	Asn	Ile	Ile	Ile
			100					105					110		
Asn	His	Phe	Phe	Cys	Asp	Met	Met	Ala	Leu	Val	Lys	Leu	Ala	Cys	Ser
	115					120						125			
Asp	Thr	Thr	Met	Thr	Arg	Ala	Val	Ile	Phe	Val	Glu	Gly	Met	Leu	Ile
	130				135						140				
Leu	Met	Thr	Cys	Phe	Leu	Leu	Thr	Val	Ile	Ser	Tyr	Ile	Cys	Ile	Leu
145					150					155				160	
Ser	Thr	Ile	Val	Arg	Ile	His	Ser	Ser	Gly	Gly	Lys	Phe	Lys	Ala	Phe
			165					170					175		
Ser	Thr	Cys	Ala	Ser	His	Leu	Ser	Val	Val	Ser	Ile	Phe	Tyr	Val	Leu
		180					185						190		
Ile	Phe	Tyr	Leu	Tyr	Leu	Lys	Pro	Lys	Ser	Glu	Ile	Ser	Leu	Ser	Gln
	195					200					205				
Gly	Lys	Leu	Leu	Thr	Val	Leu	Tyr	Val	Tyr	Phe	Ile	Pro	Met	Phe	
	210					215					220				

<210> 2736

<211> 217

<212> PRT

<213> Unknown (XLORXR46)

<400>2736

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Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
          20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
          35           40           45
Ala Ala Asp Arg Tyr Val Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
          50           55           60
Ile Ile Thr Lys Lys Leu Thr Ala Ile Phe Cys Ser Cys Phe Trp Val
65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
          85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
          100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
          115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
          130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
          165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Leu Ala Asn
          180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
          195          200          205
Met Tyr Thr Phe Leu Pro His Leu Ala
          210          215

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<210> 2737

<211> 217

<212> PRT

<213> Unknown (XLORXR106)

<400>2737

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Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
          20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
          35           40           45
Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
          50           55           60
Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val
65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
          85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
          100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
          115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
          130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
          165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn
          180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
          195          200          205

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Met Tyr Thr Phe Leu Pro His Leu Ala
210 215

<210> 2738

<211> 217

<212> PRT

<213> Unknown (XLORXR116)

<400>2738

Leu Leu Phe Asp Thr Ile Thr Leu Pro Lys Ile Ile Ala Lys Tyr Trp
1 5 10 15
Phe Gly Ala Arg Ser Ile Ser Phe Tyr Gly Cys Ile Phe Gln Leu Phe
20 25 30
Cys Val His Ser Leu Gly Ser Leu Asp Ser Phe Ile Ile Met Leu Met
35 40 45
Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Arg Tyr His Ser
50 55 60
Ile Ile Ser Asn Lys Leu Val Thr Leu Leu Cys Tyr Phe Phe Trp Val
65 70 75 80
Leu Ala Ala Leu Ile Gly Ser Ile Val Ala Val Ile Ala Gly Gln Leu
85 90 95
Pro Tyr Cys Gly Pro Asn Arg Val Arg Asn Cys Phe Cys Val Asn Ser
100 105 110
Ala Val Thr Val Leu Ala Cys Val Asp Val Thr Leu Ala Arg Arg Thr
115 120 125
Val Phe Thr Leu Ala Met Cys Val Leu Leu Leu Pro Leu Ala Phe Ile
130 135 140
Ile Leu Ser Tyr Ile Leu Ile Ile Arg Val Ile His Ser Ser Thr Asn
145 150 155 160
Asn Glu Asn Ser Trp Lys Ala Phe Tyr Thr Cys Thr Thr His Leu Met
165 170 175
Val Ile Gly Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Ser Thr Ser
180 185 190
Gln Ile Pro Leu Ile Leu Asp Val Asp Ile Asn Val Leu Leu Leu Cys
195 200 205
Leu Tyr Thr Phe Val Pro His Leu Ala
210 215

<210> 2739

<211> 217

<212> PRT

<213> Unknown (XLORXR117)

<400>2739

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
1 5 10 15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
20 25 30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
35 40 45
Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
50 55 60
Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val
65 70 75 80
Leu Gly Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
85 90 95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
100 105 110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
115 120 125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile

130	135	140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His		
145	150	155
Ser Asp Asn Trp Gln Lys Pro Phe Tyr Thr Cys Thr Thr His Leu Leu		
	165	170
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn		
	180	185
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr		
	195	200
Met Tyr Thr Phe Leu Pro His Leu Ala		205
210	215	

<210> 2740

<211> 222

<212> PRT

<213> Unknown (XLORXR171)

<400>2740

Gln Gln Leu Ser Val Cys Asp Leu Leu Gln Thr Ala Cys Thr Val Pro	
1 5 10 15	
Leu Leu Leu Trp Thr Ile Ile Asn Asp Gly Thr Thr Ile Ser Val Gly	
20 25 30	
Gly Cys Ile Thr Gln Phe Tyr Phe Phe Asn Ala Ser Glu Ser Val Glu	
35 40 45	
Cys Leu Leu Leu Thr Val Met Ser Phe Asp Arg Tyr Leu Ala Ile Cys	
50 55 60	
Asn Pro Leu Arg Tyr Thr Ser Leu Met Asn Pro Lys Leu Cys Val Lys	
65 70 75 80	
Leu Thr Leu Ile Pro Trp Leu Leu Gly Phe Ser Ile Ile Leu Ile Thr	
85 90 95	
Ala Asn Ala Ile Ala Thr Leu Gln Phe Cys Asn Gln Asn Thr Ile Asn	
100 105 110	
His Tyr Phe Cys Asp Tyr Phe Pro Leu Leu Glu Leu Ser Cys Met Asp	
115 120 125	
Thr Phe Phe Val Gln Thr Glu Ala Ile Leu Gln Ala Val Pro Val Val	
130 135 140	
Phe Ile Pro Ile Ile Leu Ile Ile Ile Ser Tyr Val Phe Ile Ile His	
145 150 155 160	
Thr Leu Leu Lys Ile Val Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser	
165 170 175	
Thr Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Ser Leu	
180 185 190	
Ile Gly Ile Tyr Val Val Pro Ser Arg Lys Gln Ser Pro Thr Ile Ser	
195 200 205	
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Leu	
210 215 220	

<210> 2741

<211> 220

<212> PRT

<213> Unknown (XLORXR181)

<400>2741

Gln Gln Leu Ser Leu Ser Asp Leu Leu Gly Ser Thr Asn Ile Val Pro	
1 5 10 15	
Thr Leu Leu Glu Thr Ile Ile Leu Gly Arg Ala Ser Ile Ser Leu Val	
20 25 30	
Asp Cys Ile Thr Gln Phe Asn Val Phe Gly Gly Ser Glu Thr Phe Val	
35 40 45	
Gly Phe Leu Leu Ala Val Met Ser Asn Asp Arg Tyr Val Ala Ile Cys	
50 55 60	

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Ile Pro Leu Arg Tyr Thr Ser Ile Thr Ser Tyr Asn Ile Cys Asn Lys
65          70          75          80
Leu Ile Leu Val Ser Trp Leu Leu Gly Leu Gly Ala Ile Leu Ile Thr
85          90          95
Ala Asn Leu Ile Ala Thr Leu Tyr Phe Cys Asp Gln Asn Ile Ile Asn
100         105         110
His Phe Phe Cys Asp Phe Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp
115         120         125
Thr Phe Ile Val Gln Leu Glu Val Ile Leu Leu Ser Ile Pro Val Ile
130         135         140
Ile Tyr Pro Phe Ile Leu Ile Ile Val Ser Tyr Ile Cys Ile Ala His
145         150         155         160
Ala Ile Leu Lys Ile Val Ser Asn Thr Gly Arg Gln Lys Ala Phe Ser
165         170         175
Thr Cys Ser Ser His Leu Ala Val Val Ser Ile Phe Tyr Gly Ala Leu
180         185         190
Thr Ala Val Tyr Val Ala Pro Pro Arg Lys Glu Ser Gln Thr Leu Ser
195         200         205
Lys Val Phe Ser Leu Leu Tyr Thr Val Met Ile Pro
210         215         220

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<210> 2742

<211> 220

<212> PRT

<213> Unknown (XLOR185)

<400>2742

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Ser Gln Leu Ser Thr Ser Asp Ile Val Ile Ser Thr Thr Val Cys Pro
1          5          10          15
Asn Leu Leu Tyr Ile Thr Trp Asn Glu Gly Ala Tyr Ile Ser Ile Thr
20         25         30
Gly Cys Ile Trp Gln Phe Asn Met Phe Ser Val Ser Ser Val Thr Glu
35         40         45
Cys Phe Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Cys
50         55         60
Lys Pro Leu His Tyr Ala Ser Ile Met Thr Trp Arg Ser Cys Ile Phe
65         70         75         80
Leu Val Met Ser Cys Trp Ser Leu Gly Phe Leu Leu Ser Met Ile Val
85         90         95
Thr Val Met Ile His Tyr Leu His Phe Cys Gly Pro Tyr Thr Ile Asp
100        105        110
His Leu Phe Cys Asp Tyr Thr Pro Leu Met Gln Leu Ser Cys Ser Asp
115        120        125
Thr Thr Ile Leu Lys Met Thr Val Phe Leu Ile Ala Thr Pro Gly Thr
130        135        140
Val Leu Gln Pro Phe Phe Ile Ile Ala Thr Tyr Ile Asn Ile Ile Leu
145        150        155        160
Asn Ile Leu Arg Ile Ser Ser Ser Ser Lys Arg Gln Lys Ala Phe Ser
165        170        175
Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Tyr Tyr Gly Thr Leu
180        185        190
Ile Ala Thr Tyr Ala Thr Pro Thr Asp Gly Arg Leu Ser Thr Arg Asn
195        200        205
Lys Leu Leu Ser Leu Ile Tyr Thr Val Gly Thr Pro
210        215        220

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<210> 2743

<211> 222

<212> PRT

<213> Unknown (XLORXR206)

<400>2743

Gly Asn Leu Ser Phe Val Asp Ile Ser Phe Ile Ser Val Thr Val Pro
 1 5 10 15
 Leu Met Val Ala His Leu Leu Thr Asp Lys Lys Ser Ile Ser Phe Thr
 20 25 30
 Gly Cys Met Thr Gln Leu Phe Phe Phe Ile Trp Ile Ala Val Leu Glu
 35 40 45
 Cys Leu Ile Leu Thr Ile Met Ala Tyr Asp Arg Leu Val Ala Ile Thr
 50 55 60
 Asn Pro Leu Arg Tyr Leu Ser Ile Leu Asp Arg Lys Thr Cys Trp Ser
 65 70 75 80
 Leu Ile Thr Phe Ser Trp Ile Leu Ser Phe Leu His Ser Leu Leu Tyr
 85 90 95
 Ala Ser Thr Ile Ser Ser Leu Asp Tyr Cys Gly Leu Asn Lys Val Asn
 100 105 110
 Glu His Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asn
 115 120 125
 Pro Ala Ser Leu Glu Leu Leu Val Tyr Thr Glu Gly Ser Val Met Ala
 130 135 140
 Met Ser Pro Phe Val Leu Ile Met Val Ser Tyr Leu Arg Ile Ile Lys
 145 150 155 160
 Thr Ile Leu Ser Ile His Ser Ser Ser Gly Arg Tyr Arg Ala Phe Ser
 165 170 175
 Thr Cys Ser Ser His Leu Ile Ser Val Gly Leu Phe Phe Val Thr Ile
 180 185 190
 Phe Val Ser Tyr Leu Gln Pro Ala Ser Ala Gly Ala Val Glu Thr Asn
 195 200 205
 Arg Pro Ile Ala Leu Val Tyr Ser Ile Leu Thr Pro Leu Pro
 210 215 220

<210> 2744

<211> 222

<212> PRT

<213> Unknown (XLORXR214)

<400>2744

Ser Asn Met Ser Phe Leu Glu Ile Arg Tyr Ile Ser Val Thr Leu Pro
 1 5 10 15
 Asn Leu Leu Val Asn Thr Leu Ser Lys Asp Met Ser Ile Ser Leu Ala
 20 25 30
 Gly Cys Met Ala Gln Leu Tyr Phe Phe Ile Ser Leu Met Cys Thr Glu
 35 40 45
 Cys Val Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Ile Ala Val Cys
 50 55 60
 His Pro Leu His Tyr Val Thr Ile Val Ser Asn Lys Leu Cys Ile Gln
 65 70 75 80
 Leu Ala Ala Ala Ser Trp Ile Ala Gly Phe Thr Val Ser Val Ile Lys
 85 90 95
 Val Tyr Phe Ile Ser Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Asn
 100 105 110
 His Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ala Cys Val Asp
 115 120 125
 Met Ser Leu Ala Glu Phe Val Asp Phe Val Leu Ala Leu Val Ile Leu
 130 135 140
 Leu Thr Pro Leu Phe Val Thr Val Ala Ser Tyr Leu Cys Ile Ile Phe
 145 150 155 160
 Thr Ile Leu Lys Ile Pro Thr Asn Thr Gly Arg Gln Lys Ala Phe Ser
 165 170 175
 Thr Cys Ala Ser His Leu Thr Val Val Thr Ile Phe Phe Ser Thr Thr
 180 185 190
 Leu Phe Met Tyr Ala Arg Pro Lys Lys Ala Lys Ser Leu Asp Tyr Phe

195 200 205
 Lys Ile Leu Ser Leu Leu Tyr Ala Val Ph Thr Pro Met Leu
 210 215 220

 <210> 2745
 <211> 312
 <212> PRT
 <213> Unknown (HOR5beta3)

 <400>2745
 Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
 1 5 10 15
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
 20 25 30
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
 35 40 45
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
 85 90 95
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
 100 105 110
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
 115 120 125
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
 130 135 140
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
 145 150 155 160
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
 165 170 175
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp
 195 200 205
 Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
 210 215 220
 Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
 225 230 235 240
 Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
 245 250 255
 Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
 260 265 270
 Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
 275 280 285
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
 290 295 300
 Leu Ser Lys His Arg Phe Ser Arg
 305 310

<210> 2746
 <211> 310
 <212> PRT
 <213> Unknown (HOR5beta2 (translated via ORDEAL))

<220>
 <221> VARIANT
 <222> (1)...(310)
 <223> Xaa = Any Amino Acid

<400>2746

Thr His Asn Ala Ala Pro Phe Leu Leu Pro Gly Phe Ser Val Leu Glu
 1 5 10 15
 Ala Thr Tyr His Ser Ile Ser Ile Pro Phe Phe Ala Val Tyr Val Cys
 20 25 30
 Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr Leu Ile Lys His Asp His
 35 40 45
 Ser Leu His Glu Pro Met Tyr Cys Phe Leu Ala Thr Leu Arg Gln Asp
 50 55 60
 Leu Met Val Lys Leu Thr Met Met Pro Thr Val Met Gly Val Leu Trp
 65 70 75 80
 Met Asn His Lys Glu Val Ile His Gly Ala Cys Phe Leu Gln Val Tyr
 85 90 95
 Ile Ile His Ser His Tyr Pro Leu Ala Glu Ser Gly Ile Leu Leu Ser
 100 105 110
 Met Ala Tyr Asp Arg Phe Ile Ile Ile His Met Leu Leu Arg Tyr Asn
 115 120 125
 Ser Ile Ser Thr Lys Ser Trp Val Lys Ile Glu Leu Trp Leu Phe Met
 130 135 140
 Arg Asp Phe Leu Ser Leu Val Pro Pro Ile Leu Pro Leu His Cys Phe
 145 150 155 160
 Pro Tyr Cys His Ser His Val Leu Phe His Thr Phe Phe Leu His Gln
 165 170 175
 Asp Val Leu Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn His Leu Tyr
 180 185 190
 Pro Ala Ile Leu Val Ala Leu Ile Phe Phe Leu Asp Ala Leu Ile Ile
 195 200 205
 Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Ile Gly Ile Ala Ser
 210 215 220
 Arg Lys Glu Gln Ala Lys Ala Leu Asn Met Cys Val Ser His Ile Ser
 225 230 235 240
 Cys Val Leu Val Phe His Ile Thr Val Ile Ser Glu Thr Phe Ile His
 245 250 255
 Arg Phe Gly Lys His Ala Pro His Val Val His Ile Thr Val Ser Xaa
 260 265 270
 Xaa Leu Ile Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr Ser Ile
 275 280 285
 Lys Pro Ser Arg Ser Lys Glu Ala Leu Xaa Arg Leu Phe Ser Gly His
 290 295 300
 Arg Met Ala Xaa Ala Leu
 305 310

<210> 2747

<211> 310

<212> PRT

<213> Unknown (HOR5beta1)

<400>2747

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
 1 5 10 15
 Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
 20 25 30
 Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
 35 40 45
 Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
 50 55 60
 Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
 65 70 75 80
 Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
 85 90 95
 Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu

	100		105		110
Leu Val	Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg				
	115		120		125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly					
	130		135		140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu					
145			150		155
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys					
	165		170		175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn					
	180		185		190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala					
	195		200		205
Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly					
	210		215		220
Ile Ala Ser Gly Gln Glu Ala Lys Ser Leu Asn Thr Cys Val Ser					
225			230		235
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser					
	245		250		255
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr					
	260		265		270
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile					
	275		280		285
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe					
	290		295		300
Ser Gly Gln Ser Arg Ala					
305					
	310				

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